

**Study Title**

Bioinformatics Evaluation of the Cry1Ac Protein Present in MON 87701 Soybean  
Utilizing the AD8, TOXIN6, and PROTEIN Databases

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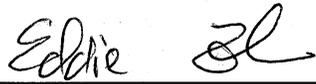
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### Summary of Quality Control Review

This report was checked to ensure that it accurately reflects the raw data. The raw data were audited for compliance with the Monsanto Company Guidelines for Keeping Research Records (GRR Sept. 2008 v. 2), and where applicable, to Monsanto SOPs.

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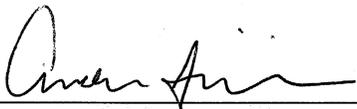
**Study Certification**

This report is an accurate and complete representation of the study/project activities.

**Signatures of Final Report Approval:**

  
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### Study Information

**Study Number:** REG-08-444

**Title:** Bioinformatics Evaluation of the Cry1Ac Protein Present in MON 87701 Soybean Utilizing the AD8, TOXIN6, and PROTEIN Databases

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### **Abbreviations and Definitions**

aa	Amino acid
AD8	Allergen, gliadin, and glutenin protein sequence database
BLOCKS	A database of amino acid motifs found in protein families
BLOSUM	BLOcks SUBstitution Matrix, used to score similarities between pairs of distantly related protein or nucleotide sequences
Cry1Ac	Class I (lepidopteran-specific) crystal protein
FASTA	Algorithm used to find local high scoring alignments between a pair of protein or nucleotide sequences
GenBank	A public genetic database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD
GI	Gene sequence identification number
NCBI	National Center of Biotechnology Information at the National Institutes of Health, Bethesda, MD
PROTEIN	Protein sequence database comprised of GenBank release 163.0
TOXIN6	Toxin protein sequence database

## 1.0 Summary

Monsanto Company has developed insect-protected soybean MON 87701 that produces the Cry1Ac insecticidal crystal (Cry) protein ( $\delta$ -endotoxin) derived from *Bacillus thuringiensis* (*B.t.*) var. *kurstaki*. The Cry1Ac protein provides protection from feeding damage caused by targeted lepidopteran insect pests. The nucleotide sequence of the *cry1Ac* gene in MON 87701 was confirmed by molecular characterization study (Arackal et al., 2008).

The safety assessment of biotechnology-derived crops evaluates potential health effects through a comprehensive approach, which includes bioinformatic analysis of the amino acid sequence of the introduced protein to ensure the protein is not similar to allergenic, toxic, or other proteins that may adversely affect animal or human health. Bioinformatic analyses were performed to assess the potential for allergenicity, toxicity, or biological activity of the Cry1Ac protein sequence.

The FASTA sequence alignment tool was used to assess structural similarity between the Cry1Ac protein sequence and known allergens, toxins, or other biologically active proteins. Although the FASTA program directly compares amino acid sequences (i.e., primary protein structure), the alignment data may be used to infer higher order structural similarities (i.e., secondary and tertiary protein structures). Proteins that share a high degree of similarity throughout their entire lengths are often homologous. Homologous proteins share secondary structure and common three-dimensional folds. Therefore, proteins homologous to allergens are more likely to share linear and/or conformational cross-reactive allergenic epitopes than are unrelated proteins. Potential structural similarities between the Cry1Ac protein sequence and known allergens (AD8 allergen database) were examined. The extent of each similarity was evaluated by visual inspection of the alignment, the calculated percent identity, and the *E*-score value for that alignment. Guidelines were also followed regarding the minimum identity and alignment length for FASTA results from the AD8 search for potential allergenicity of novel proteins in food crops (Codex, 2003). The current allergen, gliadin, and glutenin sequence database (AD8) was assembled from sequences found on the FARRP allergen database dated January 2008 located at <http://www.allergenonline.com> (FARRP, 2008). Potential structural similarities between the Cry1Ac protein sequence and potential toxins were examined using an all-inclusive protein database (PROTEIN database).

The Cry1Ac protein sequence was also screened against the AD8 sequence database using an eight amino acid sliding window search. In these analyses, any sequences of eight or more linearly contiguous amino acids that were found to be identical between the Cry1Ac protein and proteins in the AD8 database were defined as immunologically relevant, in that they may indicate the presence of potentially cross-reactive allergenic epitopes.

These bioinformatic search results indicate that no biologically relevant structural similarities to allergens, human and animal toxins, or other proteins that may adversely affect animal or human health were observed for the Cry1Ac protein sequence. Furthermore, no short (eight amino acid) polypeptide matches were shared between the Cry1Ac protein sequence and proteins in the allergen database.

Taken together, these bioinformatic search data indicate the lack of both structurally and immunologically relevant similarities between the Cry1Ac protein sequence and known allergens, toxins or other biologically active proteins that may have an adverse effect on the health of human or animals.

## 2.0 Introduction

Monsanto Company has developed insect-protected soybean MON 87701 that produces the Cry1Ac insecticidal crystal (Cry) protein ( $\delta$ -endotoxin) derived from *Bacillus thuringiensis* (*B.t.*) var. *kurstaki*. The Cry1Ac protein provides protection from feeding damage caused by targeted lepidopteran insect pests. The nucleotide sequence of the *cry1Ac* gene in MON 87701 was confirmed by molecular characterization study (Arackal et al., 2008). The Cry1Ac protein sequence was used as a query for FASTA and eight amino acid sliding window searches using the Allergen Database (version 8.0, AD8) and for a FASTA search of a public protein sequence database (PROTEIN).

The safety assessment of genetically enhanced crops evaluates potential health effects through a comprehensive approach, which includes bioinformatic analysis of the amino acid sequence of the introduced protein to ensure that the protein does not have homologous similarity to allergenic, toxic, or potentially biologically active proteins that are known to cause adverse health effects. Bioinformatic analyses were performed to assess the potential for allergenicity, toxicity, or biological activity of the Cry1Ac protein sequence.

Exposure to allergens in foods may cause sudden, severe life-threatening reactions in susceptible individuals. Gliadins and glutenins are suspected to cause celiac disease, a non-IgE mediated allergic disorder (gluten-sensitive enteropathy), and are also considered important immunologically active proteins. Screening the amino acid sequences of proteins introduced into plants by modern biotechnology for similarity to sequences of known allergens, gliadins, and glutenins is one of many assessments performed to support product safety. Similarly, the amino acid sequences of introduced proteins are also screened against a toxin-enriched dataset as well as all known proteins in publicly available genetic databases.

The FASTA algorithm can be used to evaluate the extent of sequence similarity between a query protein sequence and several database sequences. In principle, if two proteins share sufficient linear sequence similarity and identity, they will also likely share three-

dimensional structure and, therefore, functional homology. By definition, proteins with enough similarity to be homologous proteins share secondary structure and common three-dimensional folds (Pearson, 2000). Because the degree of similarity between homologs varies widely, the data need to be carefully evaluated in order to maximize their potential predictive value. The allergenicity assessment is used to identify known allergens or potentially cross-reactive proteins. While related (homologous) proteins may share 25% amino acid identity in a 200 amino acid overlap (Pearson, 2000), this is not generally sufficient to indicate IgE mediated cross-reactivity (Aalberse et al., 2001). Indeed, allergenic cross-reactivity caused by proteins is rare at 50% identity and typically requires >70% amino acid identity across the full length of the protein sequences (Aalberse, 2000). A conservative approach is currently applied by which related protein sequences are identified as potentially cross-reactive if linear identity is 35% or greater in an 80 amino acid overlap (Thomas et al., 2005; Codex, 2003). Such high levels of identity are readily detected using FASTA. Additionally, proteins closely related to gliadins or glutenins, the proteins that trigger celiac disease, can be easily identified using FASTA. A second bioinformatics tool was used to specifically identify short linear polypeptide matches to known or suspected allergens. It is possible that proteins structurally unrelated to allergens, gliadins, and glutenins may still contain smaller immunologically significant epitopes. A query sequence may be considered allergenic if it has a sequence identity of at least eight linearly contiguous amino acids with a potential allergen epitope (Metcalf et al., 1996; Hileman et al., 2002; Goodman et al., 2002). However, most allergen epitopes have not been confirmed and the amino acid length for those that have been identified can vary widely, thus the relevance of an exact match of eight amino acids may have limited immunological relevance (Thomas et al., 2005). The eight amino acid bioinformatic strategy is currently an *in silico* search that can produce matches containing significant uncertainty depending on the length of the query sequence (Silvanovich et al., 2006).

This report describes the bioinformatics assessment of the Cry1Ac protein present in MON 87701 soybean. Inspection of the bioinformatic alignment analysis can be used to indicate whether the Cry1Ac protein sequence is structurally congruent and significantly similar to known allergens, toxins, or other biologically active proteins.

### 3.0 Purpose

The purpose of this study was to evaluate, using bioinformatics techniques, the level of similarity of the MON 87701 soybean Cry1Ac protein sequence to known allergens, toxins, or other biologically active proteins. Sequence identity and amino acid similarities to known allergens, toxins, and other proteins were assessed using the FASTA and sliding eight amino acid window searches.

## 4.0 Methods

### 4.1 Sequence Database Preparation.

The allergen, gliadin, and glutenin sequence database (AD8) was assembled from sequences obtained from the FARRP allergen database<sup>1</sup> (FARRP, 2008). The protein sequences in the FARRP allergen database were assembled and evaluated for evidence of allergenicity by an international panel of allergy experts. Gene identification (GI) numbers for each of the 1,311 sequences found in the FARRP database were used to assemble a list, and this list was used to batch query the NCBI protein sequence database<sup>2</sup>. For obsolete GI numbers found using the batch search, the GenPept format flat file associated with each obsolete GI number was examined and an up-to-date GI number was used to replace the obsolete GI number. Due to the removal of obsolete GI numbers, collation of short peptide sequences into larger proteins, and removal of duplicates derived from the same species, a total of 1,250 GI numbers were found to be valid. These 1,250 GI numbers were used to assemble a searchable database AD8 (Appendix 1, release date; January 11, 2008).

The PROTEIN database, consisting of protein and polypeptide sequences from GenBank, release 163.0 (December 15, 2007), was downloaded from NCBI and formatted for use in this bioinformatic analysis. This database is referred to as the PROTEIN database and represents a current compilation of publicly available amino acid sequences. Toxins and other bioactive proteins that may be identified in the bioinformatic alignment search can also be identified using this same PROTEIN database.

### 4.2 Sequence Database Searches

FASTA analyses using the AD8, TOXIN6 and PROTEIN database were performed on a desktop computer loaded with a SUSE LINUX version 10.1 operating system and FASTA version 3.4t26 July 7, 2006. The DNA sequence used for translation to the amino acid sequence was supplied in the molecular characterization report for MON 87701 soybean (Arackal et al., 2008). The translated protein sequence shown in Figure 1 includes four additional amino acids, CMQA, at the N-terminus relative to native Cry1Ac that were identified as part of the characterization of plant-produced Cry1Ac protein (Bell et al., 2008). These additional amino acids are the product resulting from incomplete removal of the chloroplast targeting peptide. The DNA to amino acid sequence translation was performed with the DNASTar SeqEdit program (version 7.0.0). The structural similarity of the translated protein sequences to sequences in AD8 was assessed using the FASTA algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). FASTA comparisons are initiated by aligning the

<sup>1</sup> located at <http://www.allergenonline.com>

<sup>2</sup> located at <http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi>

first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Default FASTA comparison parameters for wordsize (k-tuple) of two, a gap creation penalty and, a gap extension penalty were used. The expectation threshold (*E*-score) limit was set to one. The *E*-score is a statistical measure of the likelihood that the observed similarity score could have occurred by chance in a search. A larger *E*-score indicates a lower degree of similarity between the query sequence and the sequence from the database. Typically, alignments between two sequences will need to have an *E*-score of less than  $1 \times 10^{-5}$  to be considered to have significant homology. FASTA comparisons were performed using the BLOSUM50 scoring matrix (Henikoff and Henikoff, 1992). Multiple alignments are made between the query sequence and each sequence in the database with a score calculated for each alignment. Only the best scoring alignment is extensively analyzed for each database sequence. The BLOSUM matrix series (Henikoff and Henikoff, 1992) was derived from a set of aligned, ungapped regions from protein families, called the BLOCKS database. Sequences from each block were clustered based on the percent of identical residues in the alignments (Henikoff and Henikoff, 1996). The BLOSUM50 matrix will identify blocks of conserved residues that are at least 50% identical. BLOSUM50 works well for identifying sequence similarities that include gaps, and thus recognizes distant evolutionary relationships (Pearson, 2000).

The extent of structural relatedness was evaluated by visual inspection of the aligned sequences, the calculated percent identity, and *E*-score. The *E*-score reflects the degree of amino acid similarity between a pair of sequences and can be used to evaluate the significance of the alignment. Similar amino acids are structurally related and share polar, hydrophobic, or charged states. Such substitutions are referred to as "conservative" since they are unlikely to change the structure of the protein and, by inference, the function of homologous proteins. The calculated *E*-score depends on the overall length of joined (gapped) local sequence alignments, the quality (percent identity, similarity) of the overlap, and the size of the database (Pearson and Lipman, 1988; Baxevanis and Ouellette, 1998). For a pair of sequences, a very small *E*-score may indicate a structurally relevant similarity. Conversely, large *E*-scores are typically associated with alignments that do not represent biologically relevant similarity.

In addition to the FASTA comparisons of the Cry1Ac protein sequence to known allergens (to assess overall structural similarity), an eight amino acid sliding-window search was performed. An algorithm was developed to identify whether or not a linearly contiguous match of eight amino acids existed between the query sequence and sequences within the allergen database (AD8). This program compares the query sequence to each protein sequence in the allergen database using a sliding-window of eight amino acids; that is, with a seven amino acid overlap relative to the preceding window. While there have been recommendations for using a shorter scanning

window (Gendel, 1998; Kleter and Peijnenburg, 2002), only a few studies have actually investigated the ability of six, seven, or eight amino acid search windows to identify allergens (Hileman et al., 2002; Goodman et al., 2002; Stadler and Stadler, 2003). In these studies, randomly or specifically selected protein sequences were used as query sequences in FASTA and six, seven, and eight amino acid window searches against allergen databases. The results demonstrated that searches with six and seven amino acid windows led to high rates of false positive matches between non-allergenic query sequences and allergen database sequences. Additionally, searches with a six or seven amino acid window identified apparently random matches between totally unrelated proteins, such that the matched proteins were not likely to share any structural or sequence similarities that could act as cross-reactive epitopes. These studies concluded that six or seven amino acid sliding-window searches yielded such a high rate of false positive hits that they were of no predictive value. Furthermore, Silvanovich et al. (2006) recently demonstrated the lack of value for six or seven amino acid sliding-window searches in a comprehensive analysis of short peptide match frequencies by analyzing the match frequencies of peptides derived from ~1.95 million published protein sequences. In order to provide the best predictive capability to identify potentially cross-reactive proteins, a window of eight contiguous amino acids was used in the current study to represent the smallest immunologically relevant sequential, or linear IgE binding epitope (Metcalf et al., 1996).

### 4.3 Significance of the Alignment

The FASTA alignments using the AD8 database were judged according to international guidelines for potential allergenicity of proteins transferred to food crops (Codex Alimentarius, 2003). Any alignments with a minimum of 35% shared identity over at least 80 amino acids are indicative of potential allergenicity. Any exact eight amino acid matches are visually inspected for their potential to indicate shared immunologically significant epitopes.

All alignments are judged based on an *E*-score of  $1 \times 10^{-5}$  ( $1 \times 10^{-5}$ ) which was set as an initial cut-off value for alignment significance. Although all alignments were inspected visually, any sequence alignments that yielded an *E*-score less than  $1 \times 10^{-5}$  were analyzed further to determine if such an alignment represented relevant sequence similarity and potential homology.

## 5.0 Results and Discussion

Bioinformatics analysis was performed on the MON 87701 soybean Cry1Ac protein sequence (Figure 1) to assess for potential similarity to allergens, toxins, or other biologically active proteins. Summaries of the best similarities from the analysis are

shown in Tables 1-3. The supporting dataset output files for the analysis are presented in Appendices 2-5.

### **5.1 Assessment of Potential Allergenicity:**

Potential structural identity and similarity shared between the Cry1Ac protein and proteins in the allergen database were evaluated using the FASTA sequence alignment program (Appendix 2). These bioinformatic results show that no significant structural similarities were shared between Cry1Ac and proteins in the allergen database and that specifically, no sequence alignments exceeded the Codex Alimentarius guidelines (2003) for a minimum 35% shared identity over 80 amino acids (Table 1).

No immunologically relevant sequences of eight contiguous amino acid identities were detected when the the Cry1Ac protein sequence (Figure 1) was compared to the AD8 sequence database (Appendix 1) as assessed from the eight amino acid sliding window search data (Appendix 3).

### **5.2 Assessment of Potential Adverse Biological Activity:**

Potential structural similarities shared between the Cry1Ac protein and proteins in the PROTEIN database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 5).

The FASTA program identified and aligned a total of 1728 proteins in the PROTEIN database that yielded an alignment *E*-score of less than 1 and of those, 1583 displayed an *E*-score less  $1 \times 10^{-5}$ . Visual inspection of these 1583 alignments revealed that most alignments were with proteins described as crystal and/or insecticidal proteins from *Bacillus thuringiensis* and the top alignment observed was to a crystal protein homolog (GI-142722) (Table 2). The alignment demonstrated 99.4% identity over 1178 amino acids with an *E*-score of 0. Upon evaluation of the alignments, none of the crystal or insecticidal proteins from *Bacillus thuringiensis* nor any of the other non-crystal proteins indicate any concern for adverse biological activity. Therefore, based on these data, the Cry1Ac protein does not share any structural congruence with any proteins that may have adverse biological activity animals or humans.

### **5.3 Assessment of Potential Toxicity:**

Potential structural similarities shared between the Cry1Ac protein and proteins in the toxin database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 4).

The most significant similarity observed (Table 3) was to a delta-endotoxin (GI-142740), demonstrating 98.98% shared identity over 1178 amino acids with an *E*-score of 0 and this alignment is expected because the Cry1Ac protein present in MON 87701 soybean is a specific insecticidal toxin that shares homology with many other sequences of this family of proteins. There were no alignments to proteins other than insect-specific toxins from the TOXIN6 database. Therefore, the Cry1Ac protein present in MON 87701 soybean does not share any sequence similarity with proteins that may present toxicity to humans or animals.

## 6.0 Conclusions

A bioinformatics analysis of the MON 87701 soybean Cry1Ac protein sequences was conducted to determine if the protein shared significant structural similarities with allergens, bioactive proteins or toxins. The bioinformatics results indicate that no biologically relevant sequence similarities were observed between the full length Cry1Ac protein sequence and any known allergens, biologically active proteins, or human and animal toxins.

Taken together, these bioinformatic analyses support the lack of similarity between the Cry1Ac protein sequences and known allergens and toxins. Therefore, it is unlikely that the Cry1Ac protein present in MON 87701 soybean possess any potential for allergenicity or toxicity and support the conclusion that this protein is not harmful to human or animal health.

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**Table 1.** Top Alignment Observed for the Cry1Ac Pprotein Sequence from a FASTA Search against the AD8 Allergen Database.

<b>Database</b>	<b>GI #</b>	<b>Description</b>	<b>E-score</b>	<b>% Identity</b>	<b>aa Overlap</b>
AD8	-	-	-	-	-

**Table 2.** Top Alignment Observed for the Cry1Ac Protein Sequence from a FASTA Search against the PROTEIN Database.

<b>Database</b>	<b>GI #</b>	<b>Description</b>	<b>E-score</b>	<b>% Identity</b>	<b>aa Overlap</b>
PROTEIN	142722	Crystal protein	0	99.4	1178

**Table 3.** Top Alignment with a Protein Being Described as a Toxin Observed for the Cry1Ac Protein Sequence from a FASTA Search against the TOXIN6 Database.

<b>Database</b>	<b>GI #</b>	<b>Description</b>	<b>E-score</b>	<b>% Identity</b>	<b>aa Overlap</b>
TOXIN6	142740	Delta-endotoxin	0	98.98	1178

**Figure 1. Amino Acid Sequence of Cry1Ac**

CMQAMDNNPN	INECIPYNCL	SNPEVEVLGG	ERIETGYTPI	DISLSLTQFL
LSEFVPGAGF	VLGLVDIIWG	IFGPSQWDAF	LVQIEQLINQ	RIEEFARNQA
ISRLEGLSNL	YQIYAESFRE	WEADPTNPAL	REEMRIQFND	MNSALTTAIP
LFVAVQNYQVP	LLSVYVQAAN	LHLSVLRDVS	VFGQRWGFDA	ATINSRYNDL
TRLIGNYTDH	AVRWYNTGLE	RVWGPDSRDW	IRYNQFRREL	TLTVLDIVSL
FPNYDSRTYP	IRTVSQLTRE	IYTNPVLENF	DGSFRGSAQG	IEGSIRSPHL
MDILNSITIIY	TDHRGEYYW	SGHQIMASPV	GFSGPEFTFP	LYGTMGNAAP
QQRIVAQLGQ	GVYRTLSTL	YRRPFNIGIN	NQQLSVLDGT	EFAYGTSSNL
PSAVYRKSGT	VDSLDEIPPQ	NNNVPPRQGF	SHRLSHVSMF	RSGFSNSSVS
IIRAPMFSWI	HRSAEFNII	ASDSITQIPA	VKGNFLFNGS	VISGPGFTGG
DLVRLNSSGN	NIQNRGYIEV	PIHFPSTSTR	YRVRVRYASV	TPIHLNVNWG
NSSIFSNTVP	ATATSLDNLQ	SSDFGYFESA	NAFTSSLGNI	VGVRNFSGTA
GVIIDRFEFI	PVTATLEAEY	NLERAQKAVN	ALFTSTNQLG	LKTNVTDYHI
DQVSNLVTYL	SDEFCLDEKR	ELSEKVKHAK	RLSDERNLLQ	DSNFKDINRQ
PERGWGGSTG	ITIQGGDDVF	KENYVTLSGT	FDECYPTYLY	QKIDESKLKA
FTRYQLRGI	EDSQDLEIYS	IRYNAKHETV	NVPGTGSLWP	LSAQSPIGKC
GEPNRCAPHL	EWNPDLDLDCSC	RDGEKCAHHS	HHFSLDIDVG	CTDLNEDLGV
WVIFKIKTQD	GHARLGNLEF	LEEKPLVGEA	LARVKRAEKK	WRDKREKLEW
ETNIVYKEAK	ESVDALFVNS	QYDQLQADTN	IAMIHAADKR	VHSIREAYLP
ELSVIPGVNA	AIFEELEGRI	FTAFSLYDAR	NVIKNGDFNN	GLSCWNVKGH
VDVEEQNNQR	SVLVVPEWEA	EVSQEVVCP	GRGYILRVTA	YKEGYGEGCV
TIHEIENNTD	ELKFSNCVEE	EIYPNNTVTC	NDYTVNQEEY	GGAYTSRNRG
YNEAPSVPAD	YASVYEEKSY	TDGRRENPC	FNRGYRDTYP	LPVGYVTKEL
EYFPETDKVW	IEIGETEGTF	IVDSVELLLM	EE	

## Appendix 1 Allergen, gliadin, and glutenin protein sequence database (AD8)

### Aeroallergens Animals

Species	Comments	GI #	AA
Canis lupus familiaris	precursor Can f II [Canis familiaris].	29292272	177
Canis lupus familiaris	precursor Can f II [Canis familiaris].	29292274	179
Canis lupus familiaris	Major allergen Can f 1 precursor (Allergen Dog 1).	3121745	174
Canis lupus familiaris	Minor allergen Can f 2 precursor (Allergen Dog 2).	3121746	180
Canis lupus familiaris	albumin [Canis familiaris].	3319897	585
Canis lupus familiaris	albumin [Canis familiaris].	633938	265
Canis lupus familiaris	albumin [Canis familiaris].	6687188	608
Cavia porcellus	Major allergen Cav p 2.	32363133	15
Cavia porcellus	Major urinary protein (MUP) (Allergen Cav p 1).	32469617	15
Felis catus	Major allergen I polypeptide chain 1 precursor (Allergen Fel d 1-A)	1169665	92
Felis catus	fel d I chain 1 precursor with leader B [Felis catus].	1364212	88
Felis catus	fel d I chain 1 precursor with leader A [Felis catus].	1364213	92
Felis catus	major allergen I.	163825	92
Felis catus	major allergen I.	163827	88
Felis catus	cystatin [Felis catus].	17939981	98
Felis catus	Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B)	232086	109
Felis catus	fel d I chain 2 precursor [Felis catus].	395407	107
Felis catus	Fel d 4 allergen [Felis catus].	45775300	186
Felis catus	albumin precursor [Felis catus].	886485	608
Mus musculus	Major urinary protein 6 precursor (MUP 6) (Alpha-2U-globulin)	20178291	180
Rattus norvegicus	PREDICTED: similar to Major urinary protein precursor (MUP)	109474987	181
Rattus norvegicus	Major urinary protein precursor (MUP) (Alpha-2u-globulin)	127533	181
Rattus norvegicus	Alpha-2u globulin.	81890324	181
Thaumetopoea pityocampa	Tha p 1.	74798355	18

### Aeroallergens Fungi

Species	Comments	GI #	AA
Alternaria alternata	60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).	1350779	110
Alternaria alternata	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	14423684	438
Alternaria alternata	Heat shock 70 kDa protein (Allergen Alt a 3).	14423730	152
Alternaria alternata	major allergen Alt a 1 subunit [Alternaria alternata].	1842045	157
Alternaria alternata	ribosomal P2 phosphoprotein [Alternaria alternata].	1850540	113
Alternaria alternata	putative nuclear transport factor 2 [Alternaria alternata].	21748153	124
Alternaria alternata	major allergen alt a1 [Alternaria alternata].	21913174	115
Alternaria alternata	glutathione-S-transferase [Alternaria alternata].	41057621	231
Alternaria alternata	major allergen Alt a 1 subunit [Alternaria alternata].	45680856	157
Alternaria alternata	minor allergen, ribosomal protein [Alternaria alternata].	467617	113
Alternaria alternata	minor allergen [Alternaria alternata].	467619	204
Alternaria alternata	aldehyde dehydrogenase (NAD+) [Alternaria alternata].	76666767	497
Alternaria alternata	Protein disulfide-isomerase (PDI) (Allergen Alt a 4).	85701160	436
Arthroderma benhamiae	tri m 4 allergen [Arthroderma benhamiae].	23894232	726
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894240	292
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894244	404
Aspergillus oryzae	Oryzin precursor (Alkaline proteinase) (ALP) (Aspergillus	129235	403
Aspergillus fumigatus	enolase [Aspergillus fumigatus].	13925873	438
Aspergillus fumigatus	manganese superoxide dismutase [Aspergillus fumigatus].	1648970	221
Aspergillus fumigatus	large subunit ribosomal protein L3 [Aspergillus fumigatus].	21215170	392
Aspergillus fumigatus	cellular serine proteinase [Aspergillus fumigatus].	2143220	495
Aspergillus niger	xylosidase [Aspergillus niger].	2181180	804
Aspergillus fumigatus	rAsp f 9 [Aspergillus fumigatus].	2879890	302
Aspergillus niger	serine protease.	289172	533
Aspergillus fumigatus	rAsp f 4 [Aspergillus fumigatus].	3005839	286
Aspergillus fumigatus	Aspf1 allergen [Aspergillus fumigatus].	3021324	125
Aspergillus fumigatus	allergen [Aspergillus fumigatus].	3643813	427
Aspergillus niger	beta-xylosidase [Aspergillus niger].	4235093	804
Aspergillus fumigatus	PP1ase [Aspergillus fumigatus].	5019414	178

Aspergillus fumigatus	Ribonuclease mitogillin precursor (Major allergen Asp f 1) (Asp f	54039254	176
Aspergillus fumigatus	Asp FII [Aspergillus fumigatus].	664852	250
Aspergillus fumigatus Af293	allergen Asp F3 [Aspergillus fumigatus Af293].	66845476	168
Aspergillus fumigatus Af293	major allergen Asp F2 [Aspergillus fumigatus Af293].	66849502	304
Aspergillus fumigatus	rAsp f 8 [Aspergillus fumigatus].	6686524	111
Aspergillus flavus	Allergen Asp fl 1.	74665726	403
Aspergillus fumigatus	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	83288046	438
Aspergillus fumigatus	Major allergen Asp f 2 precursor (Asp f II).	83300352	310
Aspergillus fumigatus	Allergen Asp f 4 precursor.	83300369	322
Aspergillus fumigatus	Allergen Asp f 7 precursor.	83300389	270
Aspergillus fumigatus	Heat shock protein 90 (Heat shock protein hsp1) (65 kDa IgE-binding	83303658	706
Aspergillus fumigatus	60S ribosomal protein L3 (Allergen Asp f 23).	83305621	392
Aspergillus fumigatus	60S acidic ribosomal protein P2 (Allergen Asp f 8) (AfP2).	83305635	111
Aspergillus fumigatus	Superoxide dismutase [Mn], mitochondrial precursor (Allergen Asp f	83305645	210
Aspergillus fumigatus	Probable glycosidase crf1 precursor (Crh-like protein 1) (Allergen	85540942	395
Aspergillus fumigatus	major allergen I 18kDa antigen [Aspergillus fumigatus].	9280360	150
Aspergillus oryzae	Alpha-amylase A type-1/2 precursor (Taka-amylase A) (TAA)	94706935	499
Aspergillus fumigatus	aspergillopepsin i [Aspergillus fumigatus].	963013	395
Candida albicans	Enolase 1 (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	232054	440
Candida albicans	29 kDa IgE-binding protein [Candida albicans].	37548637	236
Cochliobolus lunatus	enolase [Curvularia lunata].	14585753	440
Coprinus comatus	Cop c1 allergen [Coprinus comatus].	4538529	81
Davidiella tassiana	Minor allergen Cla h 7 (Cla h 5) (Cla h V).	1168970	204
Davidiella tassiana	60S acidic ribosomal protein P2 (Allergen Cla h 3) (Cla h III).	1173074	111
Davidiella tassiana	60S acidic ribosomal protein P2 (Minor allergen Cla h 4) (Cla h	21542440	111
Davidiella tassiana	putative nuclear transport factor 2 [Davidiella tassiana].	21748151	125
Davidiella tassiana	hydrophobin [Davidiella tassiana].	22796153	105
Davidiella tassiana	enolase; phosphopyruvate hydratase [Davidiella tassiana].	467660	440
Davidiella tassiana	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	6015094	440
Davidiella tassiana	Heat shock 70 kDa protein (Allergen Cla h 4) (Cla h IV).	729764	643
Davidiella tassiana	aldehyde dehydrogenase (NAD+) [Davidiella tassiana].	76666769	496
Davidiella tassiana	Probable NADP-dependent mannitol dehydrogenase (MtDH) (Mannitol	85701146	267
Epicoccum nigrum	Major allergen Epi p 1 (Epi n 14625*).	24636820	18
Fusarium culmorum	thioredoxin-like protein [Fusarium culmorum].	19879659	121
Fusarium culmorum	helix-loop-helix protein [Fusarium culmorum].	25361513	450
Gibberella zeae PH-1	RLA2_ALTAL 60S acidic ribosomal protein P2 (Minor allergen Alt a 6)	46122455	109
Malassezia sympodialis	Chain B, Cross-Reactivity And Crystal Structure Of Malassezia	119390336	121
Malassezia furfur	Major allergen Mal f 1 precursor (Pit o 1).	13959403	350
Malassezia sympodialis	allergen [Malassezia sympodialis].	19069920	342
Malassezia sympodialis	manganese superoxide dismutase [Malassezia sympodialis].	28569698	237
Malassezia furfur	MF1 [Malassezia furfur].	3445490	177
Malassezia furfur	Putative peroxiredoxin (Thioredoxin reductase) (Allergen Mal f 3)	3914387	166
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138171	172
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138173	162
Malassezia sympodialis	allergen [Malassezia sympodialis].	4138175	187
Malassezia furfur	major allergenic protein Mal f4 [Malassezia furfur].	4587985	342
Malassezia sympodialis	allergen [Malassezia sympodialis].	7271239	179
Malassezia sympodialis	mala s 12 allergen precursor [Malassezia sympodialis].	78038796	618
Penicillium oxalicum	vacuolar serine protease [Penicillium oxalicum].	12005497	503
Penicillium citrinum	vacuolar serine protease [Penicillium citrinum].	12005501	358
Penicillium citrinum	enolase [Penicillium citrinum].	13991101	438
Penicillium chrysogenum	vacuolar serine protease [Penicillium chrysogenum].	14215732	494
Penicillium citrinum	Heat shock 70 kDa protein (Allergen Pen c 19).	14423733	503
Penicillium chrysogenum	alkaline serine protease [Penicillium chrysogenum].	21069093	398
Penicillium citrinum	unknown [Penicillium citrinum].	38326693	228
Penicillium citrinum	Pen c 1; alkaline serine protease [Penicillium citrinum].	4587983	397
Penicillium citrinum	alkaline serine protease Pen c2 [Penicillium citrinum].	4588118	457
Penicillium citrinum	peroxisomal membrane protein [Penicillium citrinum].	5326864	167
Penicillium brevicompactum	60S acidic ribosomal P1 phosphoprotein Pen b 26 [Penicillium	59894749	107
Penicillium chrysogenum	allergen Pen n 13 [Penicillium chrysogenum].	6684758	397
Penicillium chrysogenum	allergen Pen n 18 [Penicillium chrysogenum].	7963902	494
Penicillium chrysogenum	68 kDa allergen [Penicillium chrysogenum].	999009	117
Rhodotorula mucilaginosa	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	37078092	439
Rhodotorula mucilaginosa	vacuolar serine protease [Rhodotorula mucilaginosa].	54654335	342

Scomber japonicus	parvalbumin [Scomber japonicus].	29420793	109
Trichophyton schoenleinii	tri s 4 allergen [Trichophyton schoenleinii].	23894227	726
Trichophyton schoenleinii	tri m 2 allergen [Trichophyton schoenleinii].	23894260	405
Trichophyton rubrum	Tri r 4 allergen [Trichophyton rubrum].	5813788	726
Trichophyton rubrum	Tri r 2 allergen [Trichophyton rubrum].	5813790	412

## Aeroallergens Insects

Species	Comments	GI #	AA
Argas reflexus	Arg r 1 precursor [Argas reflexus].	58371884	159
Blattella germanica	allergen Bla g 4.	1166573	182
Blattella germanica	Aspartic protease Bla g 2 precursor (Allergen Bla g II).	1703445	352
Blattella germanica	major allergen Bla g 1.02 [Blattella germanica].	4240395	492
Blattella germanica	major allergen Bla g 1.0101 [Blattella germanica].	4572592	412
Blattella germanica	36 kda allergen {peptide 143-111} [Blattella germanica=German	544618	20
Blattella germanica	36 kda allergen {peptide 143-115} [Blattella germanica=German	544619	25
Blattella germanica	Glutathione S-transferase (GST class-sigma) (Major allergen Bla g	6225491	204
Blattella germanica	Chain A, The Structure Of Mutant (N93q) Of Bla G 2.	62738637	330
Blattella germanica	tropomyosin [Blattella germanica].	8101069	284
Lepisma saccharina	tropomyosin [Lepisma saccharina].	20387027	284
Lepisma saccharina	tropomyosin [Lepisma saccharina].	20387029	243
Periplaneta americana	allergen [Periplaneta americana].	1531589	631
Periplaneta americana	allergen [Periplaneta americana].	1580792	685
Periplaneta americana	allergen [Periplaneta americana].	1580794	470
Periplaneta americana	allergen [Periplaneta americana].	1580797	393
Periplaneta fuliginosa	tropomyosin [Periplaneta fuliginosa].	19310971	284
Periplaneta americana	Cr-P11 allergen [Periplaneta americana].	2231297	446
Periplaneta americana	Cr-P11 allergen [Periplaneta americana].	2253610	274
Periplaneta americana	Cr-P11 [Periplaneta americana].	2580504	395
Periplaneta americana	allergen [Periplaneta americana].	2897849	228
Periplaneta americana	major allergen Per a 1.0105 [Periplaneta americana].	30144660	124
Periplaneta americana	major allergen Per a 1.0101 [Periplaneta americana].	4240399	231
Periplaneta americana	tropomyosin [Periplaneta americana].	4378573	284
Periplaneta americana	tropomyosin [Periplaneta americana].	4468639	284
Plodia interpunctella	arginine kinase [Plodia interpunctella].	15886861	355
Suidasia medanensis	group 2 allergen Sui m 2 [Suidasia medanensis].	45738062	141

## Aeroallergens Mites

Species	Comments	GI #	AA
Acarus siro	lipid binding protein [Acarus siro].	4049356	64
Blomia tropicalis	Blo t 21 allergen [Blomia tropicalis].	111120420	129
Blomia tropicalis	Blo t 21 allergen [Blomia tropicalis].	111120424	129
Blomia tropicalis	Blo t 21 allergen [Blomia tropicalis].	111120428	129
Blomia tropicalis	Blo t 21 allergen [Blomia tropicalis].	111120432	129
Blomia tropicalis	Blo t 21 allergen [Blomia tropicalis].	111494253	129
Blomia tropicalis	allergen [Blomia tropicalis].	1377859	130
Blomia tropicalis	cysteine protease precursor [Blomia tropicalis].	14276828	221
Blomia tropicalis	paramyosin allergen [Blomia tropicalis].	21954740	875
Blomia tropicalis	trypsin [Blomia tropicalis].	25989482	266
Blomia tropicalis	Blo t 1 allergen [Blomia tropicalis].	33667928	333
Blomia tropicalis	Blo t 3 allergen [Blomia tropicalis].	33667930	266
Blomia tropicalis	Blo t 13 allergen [Blomia tropicalis].	37958153	130
Blomia tropicalis	major IgE-binding protein Blo t 5 [Blomia tropicalis].	4204917	134
Chironomus thummi thummi	Globin CTT-III precursor (Erythrocrurin III).	121219	151
Chironomus thummi thummi	Globin CTT-IV precursor.	121227	151
Chironomus thummi thummi	Globin CTT-VIII.	121237	151
Chironomus thummi thummi	Globin CTT-VIIB-3 precursor.	121244	161
Chironomus thummi thummi	Globin CTT-VIIB-6 precursor.	121248	161
Chironomus thummi thummi	Globin CTT-VIIB-7 precursor.	121249	162
Chironomus thummi thummi	Globin CTT-III A.	121256	151
Chironomus thummi thummi	Globin CTT-X.	121259	151
Chironomus thummi thummi	Globin CTT-II beta precursor.	1707908	160
Chironomus thummi thummi	Globin CTT-I/CTT-IA precursor (Erythrocrurin).	2506460	158

Chironomus thummi thummi	Globin CTT-VI precursor.	2506461	162
Chironomus thummi thummi	Globin CTT-VIIB-4 precursor (Erythrocrucorin).	56405052	161
Chironomus thummi thummi	Globin CTT-VIIB-5/CTT-VIIB-9 precursor.	56405054	161
Chironomus kiiensis	tropomyosin [Chironomus kiiensis].	7321108	285
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	10189811	215
Dermatophagoides pteronyssinus	Der p 7 allergen polypeptide.	1045602	215
Dermatophagoides microceras	Peptidase 1 (Major mite fecal allergen Der m 1) (Allrgen Der m I).	127205	30
Dermatophagoides farinae	Der f 3 mite allergen.	1314736	232
Dermatophagoides pteronyssinus	Alpha-amylase (Allergen Der p 4) (Der p IV).	1351935	19
Dermatophagoides pteronyssinus	Mite group 2 allergen Der p 2 precursor (Der p II) (DPX).	1352237	146
Dermatophagoides pteronyssinus	Mite allergen Der p 5 (Der P V) (IgE-binding allergen).	1352238	132
Dermatophagoides pteronyssinus	Mite allergen Der p 6 (Der p VI) (DP5).	1352239	20
Dermatophagoides farinae	Mag44 [Dermatophagoides farinae].	1359436	299
Dermatophagoides farinae	paramyosin-like allergen [Dermatophagoides farinae].	13785807	692
Dermatophagoides farinae	Mite allergen Der f 6 precursor (Der f VI) (DF5).	14424450	279
Dermatophagoides pteronyssinus	cysteine protease [Dermatophagoides pteronyssinus].	1460058	211
Dermatophagoides farinae	Mag3 [Dermatophagoides farinae].	1545803	349
Dermatophagoides farinae	major Der f 2 isoform [Dermatophagoides farinae].	17978844	129
Dermatophagoides pteronyssinus	group 14 allergen protein [Dermatophagoides pteronyssinus].	20385544	1662
Dermatophagoides pteronyssinus	Chain A, X-Ray Structure Of Der P 2, The Major House Dust Mite	21465915	129
Dermatophagoides farinae	gelsolin-like allergen Der f 16 [Dermatophagoides farinae].	21591547	480
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725560	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725562	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725564	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725566	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725568	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725570	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725572	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725574	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725576	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725578	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725580	222
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725582	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725584	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725586	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725588	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725590	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725592	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725594	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725596	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725600	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725602	129
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	21725604	129
Dermatophagoides farinae	mite allergen Der f II precursor [Dermatophagoides farinae].	217306	146
Dermatophagoides farinae	mite allergen Der f II precursor [Dermatophagoides farinae].	217308	138
Dermatophagoides pteronyssinus	serine protease [Dermatophagoides pteronyssinus].	22595342	244
Dermatophagoides pteronyssinus	tropomyosin [Dermatophagoides pteronyssinus].	2353266	284
Dermatophagoides pteronyssinus	tropomyosin [Dermatophagoides pteronyssinus].	2440053	284
Dermatophagoides farinae	Mite allergen Der f 7 precursor (Der f VII).	2498299	213
Dermatophagoides farinae	Mite allergen Der f 3 precursor (Der f III).	2507248	259
Dermatophagoides farinae	Der f 1 allergen preproenzyme [Dermatophagoides farinae].	27530349	321
Dermatophagoides farinae	60 kDa allergen Der f 18p [Dermatophagoides farinae].	27550039	462
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	28798085	132
Dermatophagoides pteronyssinus	HDM allergen [Dermatophagoides pteronyssinus].	37778944	875
Dermatophagoides farinae	Der f 7 allergen [Dermatophagoides farinae].	37958165	213
Dermatophagoides pteronyssinus	Tertiary Structure Of The Major House Dust Mite Allergen Der P 2,	3891991	129
Dermatophagoides farinae	DF5=allergen {N-terminal} [Dermatophagoides farinae=mites, Peptide	404371	20
Dermatophagoides pteronyssinus	alpha-amylase [Dermatophagoides pteronyssinus].	5059162	496
Dermatophagoides pteronyssinus	Der p 3 allergen.	511476	261
Dermatophagoides farinae	Der f II [Dermatophagoides farinae].	546852	142
Dermatophagoides farinae	mite allergen Der f 2 [Dermatophagoides farinae].	55859466	146
Dermatophagoides farinae	Der f 2 [Dermatophagoides farinae].	55859468	146
Dermatophagoides farinae	mite allergen Der f 2 [Dermatophagoides farinae].	55859470	146
Dermatophagoides farinae	group 2 allergen [Dermatophagoides farinae].	56378069	146

Dermatophagoides pteronyssinus	glutathione transferase mu class Dp7019C10 [Dermatophagoides	60920878	219
Dermatophagoides pteronyssinus	Der p 1 allergen [Dermatophagoides pteronyssinus].	61608445	216
Dermatophagoides pteronyssinus	group 18 allergen protein [Dermatophagoides pteronyssinus].	67975085	462
Dermatophagoides farinae	Allergen Mag.	729979	341
Dermatophagoides farinae	Peptidase 1 precursor (Major mite fecal allergen Der f 1) (Allergen	730035	321
Dermatophagoides pteronyssinus	Peptidase 1 precursor (Major mite fecal allergen Der p 1) (Allergen	730036	320
Dermatophagoides farinae	Der f 1 allergen precursor [Dermatophagoides farinae].	76097507	276
Dermatophagoides pteronyssinus	Der p 2 allergen precursor [Dermatophagoides pteronyssinus].	76097509	129
Dermatophagoides farinae	Der f 2 allergen precursor [Dermatophagoides farinae].	76097511	129
Dermatophagoides pteronyssinus	tropomyosin [Dermatophagoides pteronyssinus].	80553470	281
Dermatophagoides pteronyssinus	major allergen p Dp 15 [Dermatophagoides pteronyssinus].	807138	219
Dermatophagoides pteronyssinus	Chain B, Crystal Structure Of Mature And Fully Active Der P 1	83754033	222
Dermatophagoides siboney	Der s 2 a allergen [Dermatophagoides siboney].	86450747	146
Dermatophagoides pteronyssinus	Der p V allergen [Dermatophagoides pteronyssinus].	913285	132
Dermatophagoides farinae	Chain A, Solution Structure Of Der F 13, Group 13 Allergen From	99031759	131
Dermatophagoides pteronyssinus	Der p 2 allergen precursor [Dermatophagoides pteronyssinus].	99644635	146
Euroglyphus maynei	Mite group 2 allergen Eur m 2 precursor.	14423649	145
Euroglyphus maynei	group 2 allergen Eur m 2 0102 [Euroglyphus maynei].	3941386	135
Glycyphagus domesticus	Gly d 2.03 [Glycyphagus domesticus].	33772588	141
Glycyphagus domesticus	Gly d 2 [Glycyphagus domesticus].	6179520	128
Glycyphagus domesticus	gly d 2.02 isoform [Glycyphagus domesticus].	7160811	125
Lepidoglyphus destructor	Mite allergen Lep d 7 precursor.	14423650	216
Lepidoglyphus destructor	Mite allergen Lep d 5.	14423651	110
Lepidoglyphus destructor	Fatty acid-binding protein (Allergen Lep d 13).	14423714	131
Lepidoglyphus destructor	Tropomyosin (Allergen Lep d 10).	14423956	284
Lepidoglyphus destructor	allergen Lep d 1.01.	1582222	141
Lepidoglyphus destructor	allergen Lep d 1.02.	1582223	141
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213898	141
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213900	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.013 [Lepidoglyphus destructor].	34495274	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.023 [Lepidoglyphus destructor].	34495278	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.024 [Lepidoglyphus destructor].	34495280	140
Lepidoglyphus destructor	type 2 allergen Lep d 2.025 [Lepidoglyphus destructor].	34495282	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.031 [Lepidoglyphus destructor].	34495284	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.035 [Lepidoglyphus destructor].	34495286	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.039 [Lepidoglyphus destructor].	34495288	141
Lepidoglyphus destructor	type 2 allergen Lep d 2.042 [Lepidoglyphus destructor].	34495290	141
Lepidoglyphus destructor	type 2 allergen Lep d 5.02 [Lepidoglyphus destructor].	34495292	171
Lepidoglyphus destructor	type 2 allergen Lep d 5.04 [Lepidoglyphus destructor].	34495294	169
Lepidoglyphus destructor	Lep D 2 allergen [Lepidoglyphus destructor].	999462	141
Tyrophagus putrescentiae	group 2 allergen [Tyrophagus putrescentiae].	2182106	141
Tyrophagus putrescentiae	fatty acid-binding protein [Tyrophagus putrescentiae].	51860756	131

**Aeroallergens Pollen**

<b>Species</b>	<b>Comments</b>	<b>GI #</b>	<b>AA</b>
Agrostis alba	pollen allergen Agr a I - bent grass (fragment).	320606	26
Agrostis alba	Group I allergen Agr a I (Form 2), pollen.	75139987	35
Agrostis alba	Group I allergen Agr a I (Form 1), pollen.	75139989	35
Alnus glutinosa	Aln g I [Alnus glutinosa].	261407	160
Alnus glutinosa	pollen allergen Aln g 4 [Alnus glutinosa].	3319651	85
Ambrosia artemisiifolia	Pollen allergen Amb a 1.1 precursor (Antigen E) (AgE) (Antigen Amb	113475	396
Ambrosia artemisiifolia	Pollen allergen Amb a 1.2 precursor (Antigen E) (Antigen Amb a I)	113476	398
Ambrosia artemisiifolia	Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a I).	113477	397
Ambrosia artemisiifolia	Pollen allergen Amb a 1.4 precursor (Antigen E) (Antigen Amb a I).	113478	392
Ambrosia artemisiifolia	Pollen allergen Amb a 2 precursor (Antigen K) (Antigen Amb a II).	113479	397
Ambrosia elatior	Pollen allergen Amb a 5 (Amb a V) (Allergen Ra5).	114090	45
Ambrosia trifida	Pollen allergen Amb t 5 precursor (Amb t V) (Allergen Ra5G).	114091	73
Ambrosia artemisiifolia	Non-specific lipid-transfer protein precursor (LTP) (Pollen	14285595	118
Ambrosia artemisiifolia	antigen E.	166443	397
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851178	131
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851180	131
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851182	133
Ambrosia elatior	Pollen allergen Amb a 3 (Amb a III) (Allergen Ra3).	416636	101
Ambrosia psilostachya	Amb p V allergen.	515953	77

Ambrosia psilostachya	Amb p V allergen.	515954	77
Ambrosia psilostachya	Amb p V allergen.	515955	77
Ambrosia psilostachya	Amb p V allergen.	515956	77
Ambrosia psilostachya	Amb p V allergen.	515957	77
Ambrosia artemisiifolia	profilin isoallergen 1 [Ambrosia artemisiifolia].	62249502	133
Ambrosia artemisiifolia	profilin isoallergen 2 [Ambrosia artemisiifolia].	62249512	133
Anthoxanthum odoratum	pollen allergen Ant o I - sweet vernal grass (fragment).	320607	26
Anthoxanthum odoratum	Group I allergen Ant o I (Form 1), pollen.	75139986	32
Anthoxanthum odoratum	Group I allergen Ant o I (Form 2), pollen.	75139990	32
Artemisia vulgaris	major pollen allergen Art v 1 precursor [Artemisia vulgaris].	27818335	132
Artemisia vulgaris	Amb a 1-like protein [Artemisia vulgaris].	62530263	396
Artemisia vulgaris	Non-specific lipid-transfer protein (LTP) (Pollen allergen Art v	73621307	37
Artemisia vulgaris	Profilin-1 (Pollen allergen Art v 4.01).	73621415	133
Artemisia vulgaris	Profilin-2 (Pollen allergen Art v 4.02).	73621416	133
Artemisia vulgaris	Allergen Art v 2 (Art v II) (Allergen Ag7).	73622184	71
Betula pendula	allergenic isoflavone reductase-like protein Bet v 6.0102 [Betula	10764491	308
Betula pendula	Major pollen allergen Bet v 1-A (Allergen Bet v I-A).	114922	160
Betula pendula	Chain A, Birch Pollen Allergen Bet V 1 Mutant N28t, K32q, E45s,	11514622	159
Betula pendula	Calcium-binding allergen Bet v 3 (Allergen Bet v III).	1168696	205
Betula pendula	Major pollen allergen Bet v 1-B (Allergen Bet v I-B).	1168701	160
Betula pendula	Major pollen allergen Bet v 1-C (Allergen Bet v I-C).	1168702	160
Betula pendula	Major pollen allergen Bet v 1-D/H (Allergen Bet v I-D/H).	1168703	160
Betula pendula	Major pollen allergen Bet v 1-E (Allergen Bet v I-E).	1168704	160
Betula pendula	Major pollen allergen Bet v 1-F/I (Allergen Bet v I-F/I).	1168705	160
Betula pendula	Major pollen allergen Bet v 1-G (Allergen Bet v I-G).	1168706	160
Betula pendula	Major pollen allergen Bet v 1-J (Allergen Bet v I-J).	1168707	160
Betula pendula	Major pollen allergen Bet v 1-K (Allergen Bet v I-K).	1168708	160
Betula pendula	Major pollen allergen Bet v 1-L (Allergen Bet v I-L).	1168709	160
Betula pendula	Major pollen allergen Bet v 1-M/N (Allergen Bet v I-M/N).	1168710	160
Betula platyphylla var. japonica	Bet vI jap1 [Betula platyphylla var. japonica].	12583681	160
Betula platyphylla var. japonica	Bet vI jap2 [Betula platyphylla var. japonica].	12583683	160
Betula platyphylla var. japonica	Bet vI jap3 [Betula platyphylla var. japonica].	12583685	160
Betula pendula	Profilin (Pollen allergen Bet v 2) (Bet v II).	130975	133
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321714	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321716	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321718	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321720	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321722	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321724	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321726	160
Betula pendula	major allergen Bet v 1 [Betula pendula].	1321728	160
Betula pendula	Polcalcin Bet v 4 (Calcium-binding pollen allergen Bet v 4).	14423850	85
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542861	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542863	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542865	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542867	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542869	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542871	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542873	160
Betula pendula	Chain A, Birch Pollen Allergen Bet V 1.	159162097	159
Betula pendula	Birch Pollen Profilin.	1942360	133
Betula pendula	peptidylprolyl isomerase (cyclophilin) [Betula pendula].	21886603	173
Betula pendula	major allergen Bet v 1 [Betula pendula].	2414158	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564220	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564222	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564224	160
Betula pendula	pollen allergen Betv1 [Betula pendula].	2564228	160
Betula	isoallergen {N-terminal} [birch, pollen, Peptide Partial, 51 aa].	298736	51
Betula	isoallergen {N-terminal} [birch, pollen, Peptide Partial, 51 aa].	298737	51
Betula pendula	allergen Bet v 1x [Betula pendula].	30908931	21
Betula pendula	major pollen allergen Bet v I - European white birch (fragment).	320545	51
Betula pendula	major pollen allergen Bet v II - European white birch (fragment).	320546	51
Betula pendula	Chain A, Birch Pollen Allergen Bet V 1 Mutant E45s.	38492423	159
Betula pendula	pollen allergen Betv1, isoform at8 [Betula pendula].	4006928	160

Betula pendula	pollen allergen Betv1, isoform at10 [Betula pendula].	4006945	160
Betula pendula	pollen allergen Betv1, isoform at14 [Betula pendula].	4006947	120
Betula pendula	pollen allergen Betv1, isoform at37 [Betula pendula].	4006953	160
Betula pendula	pollen allergen Betv1, isoform at42 [Betula pendula].	4006955	160
Betula pendula	pollen allergen Betv1, isoform at45 [Betula pendula].	4006957	160
Betula pendula	pollen allergen Betv1, isoform at50 [Betula pendula].	4006959	160
Betula pendula	pollen allergen Betv1, isoform at59 [Betula pendula].	4006961	160
Betula pendula	pollen allergen Betv1, isoform at87 [Betula pendula].	4006963	120
Betula pendula	pollen allergen Betv1, isoform at5 [Betula pendula].	4006965	160
Betula pendula	pollen allergen Betv1, isoform at7 [Betula pendula].	4006967	160
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376216	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376219	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376220	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376221	159
Betula pendula	pollen allergen, Betv1 [Betula pendula].	4376222	159
Betula pendula	isoallergen bet v 1 b1 [Betula pendula].	4590392	160
Betula pendula	isoallergen Bet v 1 b2 [Betula pendula].	4590394	160
Betula pendula	isoallergen bet v 1 b3 [Betula pendula].	4590396	160
Betula pendula	1 Sc-3 [Betula pendula].	534898	160
Betula pendula	1 Sc2 [Betula pendula].	534900	159
Betula pendula	1-Sc1 [Betula pendula].	534910	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545875	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545877	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545879	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545887	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545891	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545893	160
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545895	161
Carpinus betulus	pollen allergen Car b 1 [Carpinus betulus].	1545897	161
Carpinus betulus	Car b I=major allergen [Carpinus betulus=hornbeam trees, pollen,	239735	40
Carpinus betulus	Car b I [Carpinus betulus].	402745	159
Carpinus betulus	Major pollen allergen Car b 1 isoforms 1A and 1B (Allergen Car b	730048	160
Carpinus betulus	Major pollen allergen Car b 1 isoform 2 (Allergen Car b I).	730049	160
Chamaecyparis obtusa	pollen allergen [Chamaecyparis obtusa].	114841683	419
Chamaecyparis obtusa	Chao1 [Chamaecyparis obtusa].	1514943	375
Chamaecyparis obtusa	Polygalacturonase precursor (PG) (Pectinase) (Major pollen allergen	47606004	514
Chenopodium album	Che a 1 allergen precursor [Chenopodium album].	22074346	168
Chenopodium album	pollen allergen Che a 2 [Chenopodium album].	29465666	131
Chenopodium album	pollen allergen Che a 3 [Chenopodium album].	29465668	86
Crocus sativus	profilin [Crocus sativus].	58700651	131
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841607	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841617	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841629	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841635	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841641	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841653	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841657	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841663	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841665	514
Cryptomeria japonica	pollen allergen [Cryptomeria japonica].	114841671	514
Cryptomeria japonica	Polygalacturonase precursor (PG) (Pectinase) (Major pollen allergen	1171004	514
Cryptomeria japonica	Sugi basic protein precursor (SBP) (Major allergen Cry j 1) (Cry j	1173367	374
Cryptomeria japonica	thaumatin-like protein [Cryptomeria japonica].	139002766	225
Cryptomeria japonica	Cry j 1 precursor [Cryptomeria japonica].	19570315	374
Cryptomeria japonica	isoflavone reductase-like protein CJP-6 [Cryptomeria japonica].	19847822	306
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898904	514
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898906	514
Cryptomeria japonica	allergen Cry j 2 [Cryptomeria japonica].	24898908	514
Cryptomeria japonica	Cry j IB precursor [Cryptomeria japonica].	493634	374
Cryptomeria japonica	class IV chitinase [Cryptomeria japonica].	56550550	281
Cupressus arizonica	major allergen Cup a 1 [Cupressus arizonica].	118197955	347
Cupressus arizonica	putative allergen Cup a 1 [Cupressus arizonica].	19069497	367
Cupressus sempervirens	PR5 allergen Cup s 3.2 precursor [Cupressus sempervirens].	38456228	225
Cupressus sempervirens	PR5 allergen Cup s 3.3 precursor [Cupressus sempervirens].	38456230	225

Cupressus arizonica	cup a 1 protein [Cupressus arizonica].	6562326	346
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101711	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101713	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101715	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101717	367
Cupressus sempervirens	Cup s 1 pollen allergen precursor [Cupressus sempervirens].	8101719	367
Cupressus arizonica	Cup a 3 protein [Cupressus arizonica].	9929163	199
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 1 precursor [Cynodon dactylon].	10314021	244
Cynodon dactylon	B1 protein allergen [Cynodon dactylon].	1247373	71
Cynodon dactylon	B4 protein allergen [Cynodon dactylon].	1247375	73
Cynodon dactylon	Major pollen allergen Cyn d 1.	14423757	246
Cynodon dactylon	acidic allergen Cyn d 1 precursor [Cynodon dactylon].	15384338	244
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 2 precursor [Cynodon dactylon].	16076693	262
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 3 precursor [Cynodon dactylon].	16076695	262
Cynodon dactylon	acidic Cyn d 1 isoallergen isoform 4 precursor [Cynodon dactylon].	16076697	262
Cynodon dactylon	calcium-binding pollen allergen [Cynodon dactylon].	1871507	82
Cynodon dactylon	profilin 1 [Cynodon dactylon].	2154730	131
Cynodon dactylon	major allergen Cyn d I=34 kda polypeptide {N-terminal} [Cynodon	451274	25
Cynodon dactylon	major allergen Cyn d I=29 kda polypeptide {N-terminal} [Cynodon	451275	38
Cynodon dactylon	Cyn d Ib isoallergen {N-terminal} [Cynodon dactylon=Bermuda grass,	691726	34
Dactylis glomerata	allergen Dac g II.	1093120	196
Dactylis glomerata	group 5 allergen precursor [Dactylis glomerata].	14423124	290
Dactylis glomerata	unnamed protein product [Dactylis glomerata].	18093971	265
Dactylis glomerata	unnamed protein product [Dactylis glomerata].	18093991	264
Dactylis glomerata	Dac gIII allergen.	1825459	96
Dactylis glomerata	Major pollen allergen Dac g 4.	32363463	55
Dactylis glomerata	group 1 allergen Dac g 1.01 precursor [Dactylis glomerata].	33149333	240
Dactylis glomerata	pollen allergen (group II) [Dactylis glomerata].	4007040	122
Festuca arundinacea	pollen allergen Fes e I type A - reed fescue (fragment).	320610	17
Festuca arundinacea	pollen allergen Fes e I type B - reed fescue (fragment).	320611	20
Festuca arundinacea	Group I allergen FeS e I, pollen.	75139991	35
Fraxinus excelsior	allergen Fra e 1.0101 [Fraxinus excelsior].	33327133	145
Fraxinus excelsior	allergen Fra e 1 [Fraxinus excelsior].	34978692	146
Fraxinus excelsior	Fra e 1.0102 major allergen [Fraxinus excelsior].	56122438	145
Holcus lanatus	protein with incomplete signal sequence [Holcus lanatus].	1167836	248
Holcus lanatus	pollen allergen Hol 1 5b [Holcus lanatus].	11991229	296
Holcus lanatus	group V grass pollen allergen [Holcus lanatus].	2266623	240
Holcus lanatus	group V allergen [Holcus lanatus].	2266625	264
Holcus lanatus	major group I allergen Hol 1 I [Holcus lanatus].	3860384	263
Holcus lanatus	allergen Hol-II [Holcus lanatus].	414703	265
Humulus japonicus	Humj1 [Humulus japonicus].	33113263	155
Humulus scandens	profilin-like protein [Humulus scandens].	34851174	131
Humulus scandens	profilin-like protein [Humulus scandens].	34851176	131
Juniperus oxycedrus	putative allergen jun o 1 [Juniperus oxycedrus].	15139849	367
Juniperus rigida	PR5 allergen Jun r 3.1 precursor [Juniperus rigida].	38456222	225
Juniperus rigida	PR5 allergen Jun r 3.2 precursor [Juniperus rigida].	38456224	225
Juniperus ashei	pollen major allergen 1-1 [Juniperus ashei].	4138877	367
Juniperus virginiana	Pathogenesis-related protein precursor (Putative major pollen	51316532	110
Juniperus oxycedrus	pollen allergen Jun o 4 [Juniperus oxycedrus].	5391446	165
Juniperus ashei	allergen Jun a 3 [Juniperus ashei].	6940772	225
Juniperus virginiana	pollen major allergen 1-2 [Juniperus virginiana].	8843917	367
Juniperus virginiana	pollen major allergen 1-1 [Juniperus virginiana].	8843921	367
Juniperus ashei	pollen major allergen 2 protein [Juniperus ashei].	9955725	507
Ligustrum vulgare	major allergen [Ligustrum vulgare].	3256210	145
Ligustrum vulgare	major allergen [Ligustrum vulgare].	3256212	145
Lilium longiflorum	polygalacturonase [Lilium longiflorum].	73913442	413
Lolium perenne	Pollen allergen Lol p 1 precursor (Lol p I) (Allergen R7).	126385	263
Lolium perenne	Pollen allergen Lol p 2-A (Lol p II-A).	126386	97
Lolium perenne	Pollen allergen Lol p 3 (Lol p III).	126387	97
Lolium perenne	pollen allergen.	168314	252
Lolium perenne	Major pollen allergen Lol p 5a precursor (Lol p Va) (Lol p Ib).	2498581	308
Lolium perenne	Major pollen allergen Lol p 5b precursor (Lol p Vb).	2498582	339
Lolium italicum	pollen allergen (group II) [Lolium italicum].	4007636	122
Lolium perenne	pollen allergen Lol p VA precursor; major allergen [Lolium	4416516	301

Lolium perenne	Major pollen allergen Lol p 11 (Lol p XI).	47605808	134
Lolium perenne	pollen allergen Lol p 4 [Lolium perenne].	55859464	423
Lolium perenne	pollen allergen [Lolium perenne].	6634467	301
Lolium perenne	Pollen allergen.	75274600	263
Lolium perenne	allergen Lol p II [Lolium perenne].	939932	88
Mercurialis annua	Profilin [Mercurialis annua].	2959898	133
Olea europaea	Superoxide dismutase [Cu-Zn] (Allergen Ole e 5) (Ole e V).	122064581	30
Olea europaea	main olive allergen [Olea europaea].	13195753	130
Olea europaea	major allergen OLE16 - common olive (fragment).	1362128	137
Olea europaea	major allergen OLE17 - common olive (fragment).	1362129	136
Olea europaea	major allergen OLE19 - common olive (fragment).	1362130	136
Olea europaea	major allergen OLE1c - common olive (fragment).	1362131	145
Olea europaea	major allergen OLE20 - common olive (fragment).	1362132	137
Olea europaea	major allergen OLE26 - common olive (fragment).	1362133	136
Olea europaea	major allergen OLE5c - common olive.	1362136	145
Olea europaea	major allergen OLE6 - common olive (fragment).	1362137	136
Olea europaea	beta-1,3-glucanase-like protein [Olea europaea].	14279169	460
Olea europaea	Pollen allergen Ole e 6.	14423643	50
Olea europaea	Calcium-binding allergen Ole e 8 (PCA18/PCA23).	14423648	171
Olea europaea	Major pollen allergen (Allergen Ole e 1) (Ole e I).	14424429	145
Olea europaea	Pollen allergen Ole e 7 (Ole e VII).	22002032	21
Olea europaea	Ole e 1.0102 protein [Olea europaea].	2465127	146
Olea europaea	Ole e 1.0103 protein [Olea europaea].	2465129	146
Olea europaea	Ole e 1 protein [Olea europaea].	2465131	146
Olea europaea	allergen Ole e 10 [Olea europaea].	29465664	123
Olea europaea	Major pollen allergen Ole e 4 (Ole e IV).	32363447	24
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33325111	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33325115	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329732	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329738	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329744	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329748	129
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329750	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329752	131
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329754	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329756	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	33329758	131
Olea europaea	calcium-binding pollen allergen [Olea europaea].	3337403	84
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37548753	132
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37724593	135
Olea europaea	major pollen allergen Ole e 1 [Olea europaea].	37724597	134
Olea europaea	Ole e 3 allergen [Olea europaea].	37725377	52
Olea europaea	Profilin-1 (Pollen allergen Ole e 2).	3914426	134
Olea europaea	Profilin-2 (Pollen allergen Ole e 2).	3914427	134
Olea europaea	Profilin-3 (Pollen allergen Ole e 2).	3914428	134
Olea europaea	Cu /Zn super-oxide dismutase [Olea europaea].	39840779	152
Olea europaea	calcium-binding protein [Olea europaea].	6901654	171
Parietaria officinalis	mAb 2F9-reactive major allergen {N-terminal} [Parietaria	1311509	17
Parietaria officinalis	mAb 8C7-reactive major allergen {N-terminal, band 1} [Parietaria	1311510	15
Parietaria officinalis	mAb 8C7-reactive major allergen {N-terminal, band 2} [Parietaria	1311511	15
Parietaria officinalis	mAb 3F8-reactive major allergen {N-terminal} [Parietaria	1311512	15
Parietaria officinalis	mAb 8B6-reactive major allergen {N-terminal} [Parietaria	1311513	30
Parietaria judaica	Profilin-2 (Pollen allergen Par j 3.0102).	14423869	131
Parietaria judaica	Profilin-1 (Pollen allergen Par j 3.0101).	14423876	132
Parietaria judaica	P8 protein [Parietaria judaica].	1532056	133
Parietaria judaica	P9 protein [Parietaria judaica].	1532058	176
Parietaria officinalis	Par o 1a=acidic allergen isoform {N-terminal} [Parietaria	1836010	25
Parietaria officinalis	Par o 1b=basic allergen isoform {N-terminal} [Parietaria	1836011	24
Parietaria judaica	Probable non-specific lipid-transfer protein 1 precursor (LTP)	2497749	138
Parietaria judaica	Probable non-specific lipid-transfer protein 2 precursor (LTP 2)	2497750	133
Parietaria judaica	Probable non-specific lipid-transfer protein (LTP) (Major pollen	3915783	139
Parietaria judaica	major allergen Par j I.	741844	143
Parietaria officinalis	Pollen major allergen Par o I.	75139847	12
Phalaris aquatica	Major pollen allergen Pha a 1 precursor (Pha a I).	2498576	269

Phalaris aquatica	Major pollen allergen Pha a 5.1 precursor (Pha A 5) (Clone 28).	2498577	320
Phalaris aquatica	Major pollen allergen Pha a 5.2 precursor (Pha a 5) (Clone 14).	2498578	305
Phalaris aquatica	Major pollen allergen Pha a 5.3 precursor (Pha a 5) (Clone 29).	2498579	294
Phalaris aquatica	Major pollen allergen Pha a 5.4 (Pha a 5) (Clone 5).	2498580	175
Phalaris aquatica	Pha a I=34 kda pollen allergen {N-terminal} [Phalaris	409328	20
Phleum pratense	major allergen Phl p Va.	1092249	285
Phleum pratense	group V allergen Phl p 5 precursor [Phleum pratense].	13430402	275
Phleum pratense	Polcalcin Phl p 7 (Calcium-binding pollen allergen Phl p 7) (P7).	14423846	78
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	1684718	281
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	1684720	276
Phleum pratense	unnamed protein product [Phleum pratense].	21725606	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725608	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725610	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725612	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725614	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725616	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725618	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725620	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725622	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725624	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725626	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725628	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725630	287
Phleum pratense	unnamed protein product [Phleum pratense].	21725632	287
Phleum pratense	pollen allergen Phl p 11 [Phleum pratense].	23452313	143
Phleum pratense	Major Pollen Allergen Phl p Va [Phleum pratense].	2398757	286
Phleum pratense	profilin 3 [Phleum pratense].	2415700	131
Phleum pratense	profilin 4 [Phleum pratense].	2415702	131
Phleum pratense	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen	28373838	241
Phleum pratense	Chain N, Crystal Structure Of Phl P 6, A Major Timothy Grass Pollen	28374072	111
Phleum pratense	Pollen allergen Phl p 5b precursor (Phl p Vb).	2851457	284
Phleum pratense	Chain A, Crystal Structure Of The Functional Domain Of The Major	28948464	102
Phleum pratense	phl p5a allergen precursor [Phleum pratense].	29500897	284
Phleum pratense	Phl p6 allergen [Phleum pratense].	3004465	138
Phleum pratense	Phl p6 allergen [Phleum pratense].	3004467	138
Phleum pratense	Phl p6 IgE binding fragment [Phleum pratense].	3004469	106
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135497	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135499	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135501	276
Phleum pratense	major allergen Phl p 5 [Phleum pratense].	3135503	276
Phleum pratense	group V allergen Phl p 5.0103 precursor [Phleum pratense].	3309039	312
Phleum pratense	group V allergen Phl p 5.0203 precursor [Phleum pratense].	3309041	295
Phleum pratense	group V allergen Phl p 5.0206 precursor [Phleum pratense].	3309045	290
Phleum pratense	group V allergen Phl p 5.0207 precursor [Phleum pratense].	3309047	287
Phleum pratense	pollen allergen Phl pI [Phleum pratense].	3901094	263
Phleum pratense	Phlp5 [Phleum pratense].	398830	312
Phleum pratense	PHL PII, pollen allergen [Phleum pratense].	415896	122
Phleum pratense	PHLP5A protein - common timothy (fragment).	422005	257
Phleum pratense	unnamed protein product [Phleum pratense].	45108967	500
Phleum pratense	unnamed protein product [Phleum pratense].	45108973	500
Phleum pratense	unnamed protein product [Phleum pratense].	45823012	240
Phleum pratense	Profilin-1 (Pollen allergen Phl p 12) (Phl p 11).	464471	131
Phleum pratense	Phl p I allergen [Phleum pratense].	473360	263
Phleum pratense	allergen Phl p Vb - common timothy.	481397	280
Phleum pratense	polygalacturonase [Phleum pratense].	4826572	394
Phleum pratense	pollen allergen Phl p 4 [Phleum pratense].	54144332	508
Phleum pratense	Pollen allergen Phl p V.	75139900	24
Phleum pratense	major pollen allergen Phl p 4 precursor [Phleum pratense].	82492267	525
Phoenix dactylifera	profilin [Phoenix dactylifera].	21322677	131
Platanus x acerifolia	putative invertase inhibitor precursor [Platanus x acerifolia].	26190140	179
Platanus x acerifolia	polygalacturonase [Platanus x acerifolia].	49523394	377
Poa pratensis	Pollen allergen KBG 31 precursor (Pollen allergen Poa p 9) (Poa p	113560	373
Poa pratensis	Pollen allergen KBG 41 precursor (Pollen allergen Poa p 9) (Poa p	113561	333
Poa pratensis	Pollen allergen KBG 60 precursor (Pollen allergen Poa p 9) (Poa p	113562	307

Poa pratensis	pollen allergen Poa p 5 [Poa pratensis].	11991227	303
Poa pratensis	pollen allergen Poa-pI - Kentucky bluegrass (fragment).	280414	20
Poa pratensis	pollen allergen Poa p I - Kentucky bluegrass (fragment).	320620	26
Poa pratensis	pollen allergen (group II) [Poa pratensis].	4007655	122
Poa pratensis	group I pollen allergen [Poa pratensis].	4090265	263
Poa pratensis	pollen allergen (clone 7.2) - Kentucky bluegrass (fragment).	539056	131
Quercus alba	major pollen allergen Que a I - white oak (fragment).	543675	24
Salsola kali	Pollen allergen Sal k 1.	25090947	42
Salsola kali	pectin-methyltransferase precursor [Salsola kali].	51242679	362
Salsola kali	pectin methylesterase allergenic protein [Salsola kali].	59895728	339
Salsola kali	pectin methylesterase allergenic protein [Salsola kali].	59895730	339
Syringa vulgaris	allergen-like protein Syr v I isoform 1 - Syringa vulgaris.	631911	145
Syringa vulgaris	allergen-like protein Syr v I isoform 2 - Syringa vulgaris.	631912	145
Syringa vulgaris	allergen-like protein Syr v I isoform 3 - Syringa vulgaris.	631913	145

### Food Allergens Animals

Species	Comments	GI #	AA
Batillus cornutus	Tropomyosin (Major allergen Tur c 1).	47117349	146
Bos taurus	kappa-casein [Bos taurus].	1228078	190
Bos taurus	alpha-lactalbumin precursor (EC 2.4.1.22).	162644	142
Bos taurus	albumin [Bos taurus].	162648	607
Bos taurus	alpha-s1-casein.	162650	93
Bos taurus	beta-lactoglobulin.	162748	151
Bos taurus	beta-lactoglobulin.	162750	14
Bos taurus	alpha-s1-casein precursor.	162792	214
Bos taurus	alpha-S1-casein.	162794	214
Bos taurus	beta-casein precursor.	162797	224
Bos taurus	beta-casein.	162805	224
Bos taurus	kappa-casein precursor.	162811	190
Bos taurus	alpha-s1-casein.	162927	76
Bos taurus	alpha-s2-like casein precursor.	162929	222
Bos taurus	beta-casein precursor.	162931	224
Bos taurus	Protein S100-A7 (S100 calcium-binding protein A7) (Allergen Bos d	2493414	101
Bos taurus	alpha-lactalbumin [Bos taurus].	295774	142
Bos taurus	lactotransferrin [Bos taurus].	30794292	708
Bos taurus	bovine serum albumin [Bos taurus].	3336842	607
Bos taurus	beta-casein A3 [Bos taurus].	459292	224
Bos taurus	beta-lactoglobulin [Bos taurus].	520	178
Bos taurus	beta-lactoglobulin variant B precursor [Bos taurus].	669061	178
Bos taurus	major allergen BDA20 [Bos taurus].	886215	172
Charybdis feriatius	heat stable allergen tropomyosin [Charybdis feriatius].	7024506	264
Chionoecetes opilio	tropomyosin slow-tonic isoform [Chionoecetes opilio].	125995167	284
Crassostrea gigas	tropomyosin [Crassostrea gigas].	15419048	233
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977825	109
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977827	109
Erimacrus isenbeckii	tropomyosin slow-twitch isoform [Erimacrus isenbeckii].	125995169	284
Erimacrus isenbeckii	tropomyosin slow-tonic isoform [Erimacrus isenbeckii].	125995171	284
Farfantepenaeus aztecus	Pen a 1 allergen [Farfantepenaeus aztecus].	73532979	284
Gadus callarias	Parvalbumin beta (Allergen Gad c 1) (Gad c I) (Allergen M).	131112	113
Gadus morhua	parvalbumin beta [Gadus morhua].	14531014	109
Gadus morhua	parvalbumin beta [Gadus morhua].	14531016	109
Gallus gallus	PREDICTED: similar to Ovomuroid precursor (Allergen Gal d 1) (Gal d	118097409	208
Gallus gallus	Ovomucoid precursor (Allergen Gal d 1) (Allergen Gal d I).	124757	210
Gallus gallus	Lysozyme C precursor (1,4-beta-N-acetylmuramidase C) (Allergen Gal	126608	147
Gallus gallus	Ovalbumin (Egg albumin) (Plakalbumin) (Allergen Gal d 2) (Allergen	129293	386
Gallus gallus	Ovotransferrin precursor (Conalbumin) (Serum transferrin) (Allergen	1351295	705
Gallus gallus	Chain A, Loop-Inserted Structure Of P1-P1' Cleaved Ovalbumin Mutant	15826578	385
Gallus gallus	lysozyme protein.	212279	24
Gallus gallus	Chain D, Crystal Structure Of S-Ovalbumin At 1.9 Angstrom	34811333	385
Gallus gallus	unnamed protein product [Gallus gallus].	63052	155
Gallus gallus	preproalbumin (serum albumin) [Gallus gallus].	63748	615
Gallus gallus	ovotransferrin [Gallus gallus].	757851	705
Gallus gallus	unnamed protein product [Gallus gallus].	808969	386
Helix aspersa	tropomyosin [Helix aspersa].	4468224	284

Homarus americanus	Tropomyosin (Allergen Hom a 1).	14285796	284
Homarus americanus	fast tropomyosin isoform [Homarus americanus].	2660868	284
Litopenaeus vannamei	arginine kinase [Litopenaeus vannamei].	115492980	356
Marsupenaeus japonicus	tropomyosin fast isoform [Marsupenaeus japonicus].	125995159	284
Metapenaeus ensis	tropomyosin.	607633	274
Mimachlamys nobilis	tropomyosin [Mimachlamys nobilis].	9954253	284
Octopus vulgaris	tropomyosin [Octopus vulgaris].	83715936	284
Ommastrephes bartramii	tropomyosin [Ommastrephes bartramii].	83715934	284
Pandalus eous	tropomyosin fast isoform [Pandalus eous].	125995161	284
Panulirus stimpsoni	Tropomyosin (Allergen Pan s 1) (Pan s I).	14285797	274
Paralithodes camtschaticus	tropomyosin fast isoform [Paralithodes camtschaticus].	125995163	284
Paralithodes camtschaticus	tropomyosin slow-tonic isoform [Paralithodes camtschaticus].	125995165	284
Penaeus monodon	tropomyosin fast isoform [Penaeus monodon].	125995157	284
Penaeus monodon	allergen Pen m 2 [Penaeus monodon].	27463265	356
Perna viridis	tropomyosin [Perna viridis].	9954251	284
Rana esculenta	parvalbumin alpha [Rana esculenta].	20796729	110
Rana sp. CH-2001	parvalbumin alpha [Rana sp. CH-2001].	20796733	110
Rana esculenta	parvalbumin beta protein [Rana esculenta].	20797081	109
Rana sp. CH-2001	parvalbumin beta protein [Rana sp. CH-2001].	20797085	109
Salmo salar	Parvalbumin beta 2 (Major allergen Sal s 1).	18281421	108
Salmo salar	Parvalbumin beta 1 (Major allergen Sal s 1).	2493445	109
Sepia esculenta	tropomyosin [Sepia esculenta].	83715928	284
Sepioteuthis lessoniana	tropomyosin [Sepioteuthis lessoniana].	83715930	284
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531018	109
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531020	109
Todarodes pacificus	tropomyosin [Todarodes pacificus].	83715932	284
Trachurus japonicus	dark muscle parvalbumin [Trachurus japonicus].	77799800	107

## Food Allergens Plants

Species	Comments	GI #	AA
Actinidia deliciosa	unnamed protein product [Actinidia deliciosa].	15984	380
Actinidia deliciosa	actinidin.	166317	380
Actinidia deliciosa	phytolectin [Actinidia deliciosa].	40807635	116
Actinidia chinensis	Thaumatococin-like protein (Allergen Act c 2).	68064399	20
Actinidia deliciosa	thaumatococin-like protein [Actinidia deliciosa].	71057064	225
Actinidia deliciosa	Kiwellin (Allergen Act d 5).	85701136	189
Anacardium occidentale	vicilin-like protein [Anacardium occidentale].	21666498	536
Anacardium occidentale	vicilin-like protein [Anacardium occidentale].	21914823	538
Anacardium occidentale	2s albumin [Anacardium occidentale].	24473800	138
Anacardium occidentale	allergen Ana o 2 [Anacardium occidentale].	25991543	457
Ananas comosus	profilin [Ananas comosus].	14161637	131
Ananas comosus	Fruit bromelain precursor (Allergen Ana c 2).	75277440	351
Apium graveolens	Major allergen Api g 1 (Api g 1.0101) (Allergen Api g I).	1346568	154
Apium graveolens	Api g 1.0201 allergen [Apium graveolens].	1769847	159
Apium graveolens	Allergen Api g 5.	33300920	86
Apium graveolens	profilin [Apium graveolens].	4761578	134
Arachis hypogaea	iso-Ara h3 [Arachis hypogaea].	112380623	512
Arachis hypogaea	Allergen Ara h 1, clone P17 precursor (Ara h I).	1168390	614
Arachis hypogaea	Allergen Ara h 1, clone P41B precursor (Ara h I).	1168391	626
Arachis hypogaea	unnamed protein product [Arachis hypogaea].	14347293	207
Arachis hypogaea	Chain A, Allergen Ara h 6 From Peanut (Arachis Hypogaea).	159163254	127
Arachis hypogaea	conglutin [Arachis hypogaea].	17225991	144
Arachis hypogaea	allergen Ara h 3/Ara h 4 [Arachis hypogaea].	21314465	538
Arachis hypogaea	trypsin inhibitor [Arachis hypogaea].	22135348	219
Arachis hypogaea	peanut agglutinin precursor; prePNA [Arachis hypogaea].	253289	273
Arachis hypogaea	allergen Ara h 2.02 [Arachis hypogaea].	26245447	172
Arachis hypogaea	allergen Ara h 2 isoform [Arachis hypogaea].	31322017	169
Arachis hypogaea	glycinin [Arachis hypogaea].	3703107	507
Arachis hypogaea	Ara h 8 allergen [Arachis hypogaea].	37499626	157
Arachis hypogaea	conarachin [Arachis hypogaea].	46560472	303
Arachis hypogaea	conarachin [Arachis hypogaea].	46560474	299
Arachis hypogaea	conarachin [Arachis hypogaea].	46560476	428
Arachis hypogaea	glycinin [Arachis hypogaea].	5712199	530
Arachis hypogaea	profilin [Arachis hypogaea].	5902968	131

Arachis hypogaea	allergen Ara h 6 [Arachis hypogaea].	5923742	129
Arachis hypogaea	allergen [Arachis hypogaea].	5931948	160
Bertholletia excelsa	2S sulfur-rich seed storage protein precursor (Allergen Ber e 1)	112754	146
Bertholletia excelsa	2S albumin [Bertholletia excelsa].	17713	154
Bertholletia excelsa	11S globulin [Bertholletia excelsa].	30313867	465
Brassica napus	pollen allergen group II (clone 42) - rape.	2129801	83
Brassica napus	pollen allergen group II (clone 44) - rape.	2129802	83
Brassica rapa	pollen allergen group II (clone 4) - turnip (fragment).	2129805	80
Brassica napus	recombinant 1b pronapin precursor [Brassica napus].	26985163	109
Brassica rapa subsp. rapa	Chitin-binding allergen Bra r 2.	32363456	91
Brassica juncea	Bra j IE small chain=allergen [Brassica juncea=oriental-mustard,	407609	37
Brassica juncea	Bra j IE large chain=allergen [Brassica juncea=oriental-mustard,	407610	92
Brassica rapa subsp. rapa	Polcalcin Bra r 1 (Calcium-binding pollen allergen Bra r 1).	59800144	79
Brassica rapa subsp. rapa	Polcalcin Bra r 2 (Calcium-binding pollen allergen Bra r 2).	59800146	83
Capsicum annuum	profilin [Capsicum annuum].	16555785	131
Carica papaya	papain precursor.	167391	345
Castanea sativa	chitinase 1b [Castanea sativa].	1359600	316
Castanea sativa	ypr10 [Castanea sativa].	16555781	160
Castanea sativa	CAS S 1 major allergen.	75199059	24
Citrus sinensis	lipid transfer protein [Citrus sinensis].	50199132	91
Citrus sinensis	Germin-like protein (Allergen Cit s 1).	52782810	25
Citrus limon	Non-specific lipid-transfer protein (LTP) (Allergen Cit 13).	52783176	20
Citrus sinensis	Non-specific lipid-transfer protein (LTP) (Allergen Cit s 3.0101).	52783177	20
Citrus sinensis	Profilin (Allergen Cit s 2).	54036219	10
Citrus sinensis	profilin [Citrus sinensis].	56000996	131
Corylus avellana	putative luminal binding protein [Corylus avellana].	10944737	668
Corylus avellana	major allergen variant Cor a 1.0402 [Corylus avellana].	11762102	161
Corylus avellana	major allergen variant Cor a 1.0403 [Corylus avellana].	11762104	161
Corylus avellana	major allergen variant Cor a 1.0404 [Corylus avellana].	11762106	161
Corylus avellana	minor allergen hazelnut profilin [Corylus avellana].	12659206	131
Corylus avellana	minor allergen hazelnut profilin [Corylus avellana].	12659208	131
Corylus avellana	major allergen Cor a 1 [Corylus avellana].	1321731	160
Corylus avellana	major allergen Cor a 1 [Corylus avellana].	1321733	160
Corylus avellana	lipid transfer protein precursor [Corylus avellana].	13507262	115
Corylus avellana	11S globulin-like protein [Corylus avellana].	18479082	515
Corylus avellana	48-kDa glycoprotein precursor [Corylus avellana].	19338630	448
Corylus avellana	major allergen [Corylus avellana].	22684	160
Corylus avellana	major allergen [Corylus avellana].	22686	160
Corylus avellana	major allergen [Corylus avellana].	22690	160
Corylus avellana	oleosin [Corylus avellana].	29170509	140
Corylus avellana	major allergen Cor a 1.0401 [Corylus avellana].	5726304	161
Corylus avellana	Major pollen allergen Cor a 1 isoforms 5, 6, 11 and 16 (Allergen	584968	160
Cucumis melo	profilin [Cucumis melo].	31559374	131
Cucumis melo	Pathogenesis-related protein (PR-1) (Allergen Cuc m 3).	46396595	41
Cucumis melo var. cantalupensis	profilin [Cucumis melo var. reticulatus].	57021110	131
Cucumis melo	profilin [Cucumis melo].	58263793	131
Cucumis melo	pre-pro-cucumis [Cucumis melo].	807698	731
Daucus carota	pathogenesis-related protein.	1335877	168
Daucus carota	cr16 [Daucus carota].	1663522	154
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Fagopyrum esculentum	legumin-like protein [Fagopyrum esculentum].	2317674	504
Fagopyrum esculentum	major allergenic storage protein [Fagopyrum esculentum].	4895075	538
Fagopyrum esculentum	BW 16kDa allergen [Fagopyrum esculentum].	61970231	127
Fagopyrum gracilipes	22kDa storage protein [Fagopyrum gracilipes].	6979766	191
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Glycine max	hull allergen Gly m 2 - soybean (fragment).	1362049	20
Glycine max	beta-conglycinin-alpha subunit.	169927	218
Glycine max	beta-conglycinin storage protein [Glycine max].	169929	639
Glycine max	glycinin.	169969	516
Glycine max	glycinin precursor.	169971	240
Glycine max	unnamed protein product [Glycine max].	18536	605
Glycine max	unnamed protein product [Glycine max].	18609	485
Glycine max	unnamed protein product [Glycine max].	18615	495
Glycine max	glycinin subunit G1 [Glycine max].	18635	495
Glycine max	glycinin subunit G2 [Glycine max].	18637	485
Glycine max	glycinin subunit G3 [Glycine max].	18639	481
Glycine max	glycinin [Glycine max].	18641	562
Glycine max	unnamed protein product [Glycine max].	18744	158
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Glycine max	CG4 beta-conglycinin [Glycine max].	256427	439
Glycine max	Kunitz trypsin inhibitor; KTi [Glycine max].	256429	216
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Glycine max	hydrophobic seed protein precursor-like [Glycine max].	76782247	134
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Hordeum vulgare	amylase/protease inhibitor.	167077	117
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Malus x domestica	major allergen Mal d1 [Malus x domestica].	1313972	160

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Vigna radiata	pathogenesis-related protein 10 [Vigna radiata].	60418924	155
Vitis sp.	Non-specific lipid-transfer protein P3 (LTP P3).	145559502	91
Vitis sp.	Non-specific lipid-transfer protein P2 (LTP P2).	462717	38
Vitis sp.	Non-specific lipid-transfer protein P4 (LTP P4).	462719	37
Zea mays	EXPB10 [Zea mays].	105969543	99
Zea mays	EXPB10 [Zea mays].	105969545	269
Zea mays	pollen profilin variant 1 [Zea mays].	110644952	131
Zea mays	pollen profilin variant 2 [Zea mays].	110644954	131
Zea mays	pollen profilin variant 3 [Zea mays].	110644956	131
Zea mays	pollen profilin variant 4 [Zea mays].	110644958	131
Zea mays	pollen profilin variant 5 [Zea mays].	110644960	131
Zea mays	pollen profilin variant 6 [Zea mays].	110644962	131
Zea mays	pollen profilin variant 7 [Zea mays].	110644964	130
Zea mays	Chain X, Crystal Structure Of Expb1 (Zea M 1), A Beta-Expansin And	114794319	245
Zea mays	Non-specific lipid-transfer protein precursor (LTP) (Phospholipid	128388	120
Zea mays	beta-expansin 1 [Zea mays].	14193761	269
Zea mays	Zm13.	1588669	170
Zea mays	profilin [Zea mays].	2642324	131
Zea mays	beta-expansin 9 protein [Zea mays].	28630919	269
Zea mays	beta-expansin 1 protein [Zea mays].	28630923	269
Zea mays	thioredoxin h1 protein [Zea mays].	66841002	128
Zea mays	Zea m 1 allergen [Zea mays].	89892721	263
Zea mays	Zea m 1 allergen [Zea mays].	89892723	252
Zea mays	Zea m 13 allergen [Zea mays].	89892725	410
Zea mays	Zea m 13 allergen [Zea mays].	89892727	404
Zea mays	Zea m 13 allergen [Zea mays].	89892729	411
Ziziphus mauritiana	allergen Ziz m 1 [Ziziphus mauritiana].	61225281	330

**Nematodes and Worms**

<b>Species</b>	<b>Comments</b>	<b>GI #</b>	<b>AA</b>
Ancylostoma caninum	secreted protein ASP-2 precursor [Ancylostoma caninum].	3608493	218
Ancylostoma duodenale	ancylostoma-secreted protein 1 precursor [Ancylostoma duodenale].	3719257	425
Ancylostoma caninum	ancylostoma-secreted protein 1 precursor; ASP-1 [Ancylostoma	4884851	424
Ancylostoma caninum	Aspartic protease.	74936004	442
Anisakis simplex	ani s 4 allergen [Anisakis simplex].	110346534	115
Anisakis simplex	SXP/RAL-2 family protein [Anisakis simplex].	121308878	152
Anisakis simplex	protease inhibitor [Anisakis simplex].	121308880	84
Anisakis simplex	Allergen Ani s 4.	47605398	14
Anisakis simplex	Major allergen Ani s 1 precursor (Excretory gland allergen Ans1)	47605452	194
Anisakis simplex	troponin-like protein [Anisakis simplex].	6065738	161
Anisakis simplex	paramyosin [Anisakis simplex].	8117843	869
Anisakis simplex	paramyosin isoform [Anisakis simplex].	8453086	473
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735096	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735098	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735102	133
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735106	133
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735108	267
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735110	267
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735112	267

Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735114	134
Ascaris lumbricoides	ABA-1 allergen [Ascaris lumbricoides].	2735118	134
Ascaris suum	major allergen ABA-1=TBA-1 allergen homolog {N-terminal} [Ascaris	299550	68
Ascaris suum	Polyprotein ABA-1 precursor (Body fluid allergen 1) (Allergen Asc s	77416849	1365
Schistosoma japonicum	22.6 kDa tegumental antigen [Schistosoma japonicum].	2739154	191
Schistosoma japonicum	hypothetical protein, putative Profilin/allergen [Schistosoma	29841461	129

**Other Contact Allergens**

Species	Comments	GI #	AA
Equus caballus	Latherin precursor (Dander allergen Equ c 4/Equ c 5).	152031631	228
Equus caballus	Dander allergen Equ c 2.0101.	3121755	29
Equus caballus	Dander allergen Equ c 2.0102.	3121756	19
Equus caballus	Major allergen Equ c 1 precursor.	3121758	187
Equus caballus	preproalbumin [Equus caballus].	399672	607
Hevea brasiliensis	IgE-binding protein MnSOD [Hevea brasiliensis].	10862818	205
Hevea brasiliensis	Chain A, Latex Profilin Hevb8.	11513601	131
Hevea brasiliensis	beta-1,3-glucanase.	1184668	374
Hevea brasiliensis	Pro-hevein precursor (Major hevein) [Contains: Hevein (Allergen Hev	123062	204
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	124294783	374
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	124294785	374
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	124365249	374
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	124365251	374
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	124365253	374
Hevea brasiliensis	Rubber elongation factor protein (REF) (Allergen Hev b 1).	132270	138
Hevea brasiliensis	Profilin-6 (Pollen allergen Hev b 8.0204).	14423856	131
Hevea brasiliensis	Profilin-5 (Pollen allergen Hev b 8.0203).	14423858	131
Hevea brasiliensis	Profilin-4 (Pollen allergen Hev b 8.0202).	14423859	131
Hevea brasiliensis	Profilin-3 (Pollen allergen Hev b 8.0201).	14423860	131
Hevea brasiliensis	Profilin-2 (Pollen allergen Hev b 8.0102).	14423868	131
Hevea brasiliensis	Small rubber particle protein (SRPP) (22 kDa rubber particle	14423933	204
Hevea brasiliensis	putative class I chitinase [Hevea brasiliensis].	14575525	295
Hevea brasiliensis	latex allergen.	1480457	151
Hevea brasiliensis	latex patatin homolog [Hevea brasiliensis].	1916805	388
Hevea brasiliensis	lipid transfer precursor protein [Hevea brasiliensis].	20135538	116
Hevea brasiliensis subsp. brasiliensis	class I chitinase [Hevea brasiliensis subsp. brasiliensis].	27526732	295
Hevea brasiliensis	prohevein [Hevea brasiliensis].	2832430	187
Hevea brasiliensis	latex allergen [Hevea brasiliensis].	3087805	388
Hevea brasiliensis	ENSP-like protein [Hevea brasiliensis].	30909057	391
Hevea brasiliensis	profilin [Hevea brasiliensis].	3183706	131
Hevea brasiliensis	beta-1,3-glucanase [Hevea brasiliensis].	32765543	374
Hevea brasiliensis	latex allergen [Hevea brasiliensis].	3288200	388
Hevea brasiliensis	superoxide dismutase (manganese).	348137	233
Hevea brasiliensis	putative latex allergen hev b 7.02 [Hevea brasiliensis].	41581137	387
Hevea brasiliensis	major latex allergen Hev b 4 [Hevea brasiliensis].	46410859	366
Hevea brasiliensis	MnSOD [Hevea brasiliensis].	5777414	205
Hevea brasiliensis	latex protein allergen Hev b 7 [Hevea brasiliensis].	6707018	388
Hevea brasiliensis	Chain A, Crystal Structure Of A Hev B 6.02 Isoallergen.	73535415	43
Hevea brasiliensis	enolase, isoform 1 [Hevea brasiliensis].	9581744	445
Hevea brasiliensis	enolase, isoform 2 [Hevea brasiliensis].	9581746	445
Nicotiana tabacum	villin 1 [Nicotiana tabacum].	57283137	559
Nicotiana tabacum	villin 2 [Nicotiana tabacum].	57283139	520

**Venoms**

Species	Comments	GI #	AA
Aedes aegypti	D7 protein precursor (Allergen Aed a 2).	118216	321
Aedes aegypti	30 kDa salivary gland allergen Aed a 3 [Aedes aegypti].	2114497	253
Aedes aegypti	apyrase.	556272	562
Aedes albopictus	30 kDa salivary gland allergen 30k-3 [Aedes albopictus].	56417504	271
Aedes albopictus	GE-rich salivary protein 30k-4 [Aedes albopictus].	56417506	266
Aedes aegypti	30 kDa salivary gland allergen variant 2 [Aedes aegypti].	94468546	273
Aedes aegypti	30 kDa salivary gland allergen variant 3 [Aedes aegypti].	94468552	258
Apis mellifera	Melittin precursor (Allergen Api m 3) (Api m III).	126949	70
Apis dorsata	Melittin.	126955	26
Apis mellifera	Phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase)	24418862	167

Apis cerana cerana	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	24638082	134
Apis dorsata	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	47117012	134
Apis mellifera	Hyaluronoglucosaminidase precursor (Hyaluronidase) (Hya) (Allergen)	585279	382
Apis mellifera	melittin, minor - honeybee.	69552	27
Apis cerana	phospholipase A2 (EC 3.1.1.4), venom - Indian honeybee.	7435005	134
Apis mellifera	allergen Api m 6 precursor [Apis mellifera].	94400875	94
Apis mellifera	allergen Api m 6 variant 1 [Apis mellifera].	94400907	92
Apis mellifera	icarapin variant 1 precursor [Apis mellifera].	94471622	223
Apis mellifera	icarapin variant 2 precursor [Apis mellifera].	94471624	175
Bombus terrestris	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase) (Allergen)	14423832	136
Dolichovespula maculata	Hyaluronoglucosaminidase (Hyaluronidase) (Allergen Dol m 2) (Dol m	1346322	331
Dolichovespula maculata	Venom allergen 5.01 precursor (Antigen 5 form 2) (Ag5-2) (Allergen	137395	227
Dolichovespula maculata	Phospholipase A1 2 (Allergen Dol m 1.02) (Dol m I).	1709542	303
Dolichovespula arenaria	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Dol a 5) (Dol a V).	465052	203
Dolichovespula maculata	Phospholipase A1 1 precursor (Allergen Dol m 1.01) (Dol m I).	548449	317
Dolichovespula maculata	Venom allergen 5.02 precursor (Antigen 5 form 3) (Ag5-3) (Allergen	549186	215
Myrmecia pilosula	major allergen Myr p II.	1587177	75
Myrmecia pilosula	Myr p I=allergenic polypeptide {N-terminal} [Myrmecia	1911819	112
Myrmecia pilosula	Pilosulin-2 precursor (Allergen Myr p 2) (Myr p II).	2498604	75
Myrmecia pilosula	Pilosulin-1 precursor (Major allergen Myr p 1) (Myr p I) [Contains:	730091	112
Polistes annularis	Hyaluronoglucosaminidase precursor (Hyaluronidase) (Allergen Pol a	14423735	367
Polistes annularis	Phospholipase A1 (Allergen Pol a 1).	14423833	301
Polistes annularis	allergen 5.	160780	209
Polistes gallicus	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol g 5).	25091511	206
Polistes dominulus	venom serine protease precursor [Polistes dominulus].	30909091	277
Polistes gallicus	Phospholipase A1 (Allergen Pol g 1).	41017429	42
Polistes dominulus	venom phospholipase A1 1 precursor [Polistes dominulus].	45510887	337
Polistes dominulus	venom phospholipase A1 2 precursor [Polistes dominulus].	45510889	316
Polistes dominulus	venom phospholipase A1 3 precursor [Polistes dominulus].	45510891	316
Polistes dominulus	venom phospholipase A1 4 precursor [Polistes dominulus].	45510893	316
Polistes exclamans	allergen Pol e 5 precursor [Polistes exclamans].	51093375	226
Polistes dominulus	allergen Pol d 5 precursor [Polistes dominulus].	51093377	227
Polistes exclamans	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol e 5) (Pol e V).	549187	205
Polistes fuscatus	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol f 5) (Pol f V).	549188	205
Sarcoptes scabiei type hominis	glutathione S-transferase [Sarcoptes scabiei type hominis].	27462836	219
Sarcoptes scabiei type hominis	glutathione transferase mu class Yv5004H11 [Sarcoptes scabiei type	60920770	219
Solenopsis invicta	Sol i 1=antigen {N-terminal} [Solenopsis invicta=imported fire	1336809	58
Solenopsis invicta	Sol i 1=antigen {N-terminal} [Solenopsis invicta=imported fire	1336811	25
Solenopsis invicta	Sol i 1=antigen {N-terminal} [Solenopsis invicta=imported fire	1336812	26
Solenopsis invicta	Sol i 1=antigen {N-terminal} [Solenopsis invicta=imported fire	1336813	26
Solenopsis invicta	Venom allergen 4 precursor (Venom allergen IV) (Allergen Sol i 4)	14424465	137
Solenopsis invicta	Venom allergen 3 precursor (Venom allergen III) (Allergen Sol i 3)	14424466	234
Solenopsis invicta	venom allergen Sol i 4.02 precursor [Solenopsis invicta].	4038411	137
Solenopsis invicta	allergen Sol i 1 precursor [Solenopsis invicta].	51093373	346
Solenopsis invicta	Venom allergen 2 precursor (Venom allergen II) (Allergen Sol i 2)	549179	138
Solenopsis richteri	Venom allergen 2 (Venom allergen II) (Allergen Sol r 2) (Sol r II).	6136162	119
Solenopsis richteri	Venom allergen 3 (Venom allergen III) (Allergen Sol r 3) (Sol r	6136163	211
Solenopsis geminata	venom allergen Sol g 4.01 precursor [Solenopsis geminata].	7638028	137
Solenopsis geminata	venom allergen Sol g 4.02 precursor [Solenopsis geminata].	7638030	137
Triatoma protracta	procalin [Triatoma protracta].	15426413	169
Vespa crabro	Venom allergen 5.01 (Antigen 5-1) (Ag5-1) (Allergen Vesp c 5.01)	549184	202
Vespa crabro	Venom allergen 5.02 (Antigen 5-2) (Ag5-2) (Allergen Vesp c 5.02)	549185	202
Vespa mandarinia	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Vesp m 5).	6136165	202
Vespula vulgaris	Chain A, Ves V 5, An Allergen From Vespula Vulgaris Venom.	11514279	209
Vespula germanica	hyaluronidase [Vespula germanica].	116174180	331
Vespula germanica	hyaluronidase homologue [Vespula germanica].	116174182	323
Vespula vulgaris	Hyaluronoglucosaminidase A (Hyaluronidase A) (Allergen Ves v 2a)	1346323	331
Vespula vulgaris	allergen 5.	162551	227
Vespula maculifrons	Phospholipase A1 (Allergen Ves m 1) (Ves m I).	1709545	300
Vespula vulgaris	allergen 5; antigen 5 [Vespula vulgaris].	4826574	204
Vespula flavopilosa	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).	549189	204
Vespula germanica	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves g 5) (Ves g V).	549190	204
Vespula maculifrons	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves m 5) (Ves m V).	549191	204
Vespula pensylvanica	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).	549192	204

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Vespula squamosa	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves s 5) (Ves s V).	549193	205
Vespula vidua	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves vi 5) (Ves vi V).	549194	206
Vespula vulgaris	hyaluronidase b [Vespula vulgaris].	62147665	340
Vespula germanica	Ves g 5 allergen precursor [Vespula germanica].	74035841	204
Vespula germanica	Ves g 1 allergen precursor [Vespula germanica].	74035843	300
Vespula maculifrons	venom allergen 5 [Vespula maculifrons].	85681830	227
Vespula vulgaris	allergen and phospholipase A1.	897647	336

## Regulatory Product Characterization Team

## Appendix 2 FASTA Alignments with AD8

```
# fasta34 -Q -E 1.0 Cry1Ac_long.fas /home/andre/db/AD8.fasta -O Cry1Ac_long_AD8
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
Please cite:
```

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
Cry1Ac_CMQA, 1182 aa
vs /home/andre/db/AD8.fasta library
```

```

      opt      E()
< 20      0      0:
 22      0      0:          one = represents 3 library sequences
 24      0      0:
 26      0      0:
 28      0      0:
 30      8      2:*==
 32     13      7:===*==
 34     25     18:====*====
 36     50     37:====*====
 38     91     61:====*====
 40    100     85:====*====
 42    103    105:====*====
 44    108    115:====*====
 46    126    117:====*====
 48     98    112:====*====
 50     91    103:====*====
 52     72     90:====*====
 54     79     77:====*====
 56     57     64:====*====
 58     45     53:====*====
 60     54     43:====*====
 62     27     34:====*====
 64     12     27:====*====
 66     11     22:====*====
 68     13     17:====*====
 70     10     13:====*====
 72      3     10:==*====
 74      8      8:==*====
 76      6      6:==*====
 78      9      5:==*====
 80     15      4:==*====
 82      3      3:*====
 84      3      2:*====
 86      4      2:*====
 88      2      1:*          inset = represents 1 library sequences
 90      2      1:*
 92      1      1:*          :*
 94      0      1:*          :*
 96      0      0:          *
 98      1      0:=-       *=-
100      0      0:          *
102      0      0:          *
104      0      0:          *
106      0      0:          *
108      0      0:          *
110      0      0:          *
```

```

112      0      0:          *
114      0      0:          *
116      0      0:          *
118      0      0:          *
>120     0      0:          *
284546 residues in 1250 sequences
Expectation_n fit: rho(ln(x))= 4.50280.00543; mu= 20.9177 0.281
mean_var=84.301725.079, 0's: 0 Z-trim: 0 B-trim: 69 in 1/40
Lambda= 0.139687
Kolmogorov-Smirnov statistic: 0.0611 (N=29) at 40
```

```
FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, open/ext: -10/-2, width: 16
!! No sequences with E() < 1.000000
```

```

1182 residues in 1 query sequences
284546 residues in 1250 library sequences
Scmplib [34t26]
start: Mon Oct 6 17:28:16 2008 done: Mon Oct 6 17:28:16 2008
Total Scan time: 0.170 Total Display time: 0.000
```

Function used was FASTA [version 3.4t26 July 7, 2006]

## Appendix 3 Eight amino acid sliding window search with AD8

```
Sliding 8 amino acid window search
Database searched = AD8
Query = Cry1Ac_CMQA
```

Start time: Mon Oct 6 17:27:34 CDT 2008 Finish time: Mon Oct 6 17:27:34 CDT 2008

No matches exist with the AD8 database

## Appendix 4 FASTA Alignments with TOXIN6

```
# fasta34 -Q -E 1.0 Cry1Ac_long.fas /home/andre/db/TOXIN6.fasta -O
Cry1Ac_long_TOXIN6
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
Please cite:
```

W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```
Cry1Ac_CMQA, 1182 aa
vs /home/andre/db/TOXIN6.fasta library
```

```

      opt      E()
< 20     16      0:==
 22      0      0:          one = represents 14 library sequences
 24      1      0:=-
 26      2      0:=-
```

```

28 4 2:*
30 18 10:*
32 44 38:==*
34 100 103:====*
36 153 212:====*
38 494 351:====*
40 449 490:====*
42 560 598:====*
44 759 660:====*
46 795 672:====*
48 562 644:====*
50 448 587:====*
52 577 516:====*
54 355 441:====*
56 293 368:====*
58 347 302:====*
60 299 245:====*
62 170 196:====*
64 107 156:====*
66 155 123:====*
68 75 97:====*
70 84 76:====*
72 54 59:====*
74 43 46:====*
76 46 36:==*
78 60 28:==*
80 20 22:=*
82 23 17:=*
84 10 13:*
86 11 10:*
88 8 8:* inset = represents 1 library sequences
90 4 6:*
92 4 5:* :====*
94 3 4:* :==*
96 0 3:* : *
98 0 2:* : *
100 0 2:* : *
102 3 1:* :*==
104 0 1:* :*
106 1 1:* :*
108 0 1:* :*
110 0 0:*
112 0 0:*
114 0 0:*
116 0 0:*
118 0 0:*
>120 14 0:== *=====
1830188 residues in 7176 sequences
Expectation_n fit: rho(ln(x))= 5.73950.000845; mu= 11.7494 0.042
mean_var=68.172814.116, 0's: 16 Z-trim: 30 B-trim: 17 in 2/59
Lambda= 0.155335
Kolmogorov-Smirnov statistic: 0.0339 (N=29) at 46

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, open/ext: -10/-2, width: 16
The best scores are:
gi|142740|gb|AAA22338.1| delta-endotoxin (1177) 7794 1756.2 0
gi|142875|gb|AAA22410.1| delta-endotoxin (1181) 6788 1530.7 0
gi|142720|gb|AAA22330.1| entomocidal protoxin (1155) 4503 1018.6 0

```

```

gi|142886|gb|AAA22420.1| 5.3 class delta endotoxin (1155) 4483 1014.2 0
gi|1022728|gb|AAA79694.1| crystal toxin (1155) 3918 887.5 0
gi|208153|gb|AAA73184.1| crystal toxin (597) 1084 252.3 5.6e-67
gi|142734|gb|AAA22336.1| delta-endotoxin (652) 1084 252.3 6e-67
gi|1246432|emb|CAA63860.1| cbm71 mosquitocidal tox (613) 580 139.4 5.7e-33
gi|1922253|emb|CAA67841.1| cbm72 mosquitocidal tox (618) 403 99.7 5e-21
gi|538378|gb|AAA21516.1| delta endotoxin (1186) 308 78.5 2.3e-14
gi|142772|gb|AAA22355.1| delta-endotoxin (1257) 266 69.1 1.6e-11
gi|142763|gb|AAA22352.1| mosquito-toxic crystal pr (643) 175 48.6 1.2e-05
gi|220928|dbj|BAA00854.1| protoxin [Cloning vector (12) 92 29.4 0.14
gi|220926|dbj|BAA00848.1| protoxin [Cloning vector (12) 92 29.4 0.14

>>gi|142740|gb|AAA22338.1| delta-endotoxin (1177 aa)
initn: 4900 initl: 4900 opt: 7794 Z-score: 9426.2 bits: 1756.2 E(): 0
Smith-Waterman score: 7794; 98.981% identity (99.406% similar) in 1178 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|142 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60
10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLYQIYAESFRE
gi|142 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
gi|142 TLTVLDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|142 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPO
gi|142 GYVRTLSSTFYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPO
360 370 380 390 400 410

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300      310      320      330      340      350
Cry1Ac  GVYRLLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
gi|142  GVYRLLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
360      370      380      390      400      410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|142  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
420      430      440      450      460      470
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|142  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
480      490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS
gi|142  TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
480      490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS
gi|142  TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
540      550      560      570      580      590
Cry1Ac  VPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|142  TTNLQFHTSIDGRPLNQGNFSATMSSGNNLQSGSFRVTGFTTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590
Cry1Ac  VPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|142  TTNLQFHTSIDGRPLNQGNFSATMSSGNNLQSGSFRVTGFTTTPFNFSNGSSVFTLSAHVF
600      610      620      630      640      650
Cry1Ac  SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|142  NSGNEVYIDRIEFVPAEVTFAEYDLERAQEAVALFTSPNQIGLKTVDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac  SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|142  NSGNEVYIDRIEFVPAEVTFAEYDLERAQEAVALFTSPNQIGLKTVDYHIDQVSNL
660      670      680      690      700      710
Cry1Ac  VTLYLDFECLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|142  VECLDFECLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPERGWGGSTGITIQGG
660      670      680      690      700      710
Cry1Ac  VTLYLDFECLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|142  VECLDFECLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPERGWGGSTGITIQGG
720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLPGTDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIRYNAK
gi|142  DDVFKENYVTLPGTDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLPGTDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIRYNAK
gi|142  DDVFKENYVTLPGTDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIRYNAK
780      790      800      810      820      830
Cry1Ac  HETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|142  HETVNPVGTGSLWPLSFESSIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
780      790      800      810      820      830
Cry1Ac  HETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|142  HETVNPVGTGSLWPLSFESSIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|142  IDVGCIDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|142  IDVGCIDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIREAYLPELSVIP
gi|142  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIREAYLPELSVIP

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gi|142  KLQLETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac  GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|142  GVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNHRSVLVVP
960      970      980      990      1000      1010
Cry1Ac  EWEAEVQEVVRCVCPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFSNCVVEEYIPNN
gi|142  EWEAEVQEVVRCVCPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFSNCVVEEYVPPNN
1020      1030      1040      1050      1060      1070
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAP----SVPADYASVYEEKSYTDGRRNPCEFN
gi|142  TVTCNEYTANQEEYGGAYTSCNRGYDETYGSNYSVPADYASVYEEKAYTDGRRNPCESN
1080      1090      1100      1110      1120      1130
Cry1Ac  RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|142  RGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELFLMEE
1140      1150      1160      1170      1180
>>gi|142720|gb|AAA22330.1| entomocidal protoxin (1155 aa)
initn: 6347 initl: 3174 opt: 4503 Z-score: 5440.5 bits: 1018.6 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|142  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
70      80      90      100      110      120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|142  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
gi|142  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
gi|142  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL

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gi|142 TLTVLDIVSLFPNYSRTYPIRTVSQTLTREIYTNPVLENFDGFSFRGSAQGIIEGSIKSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVaQLGQ
      .....
gi|142 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVaQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
      .....
gi|142 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNI IASDSITQIPa
      .....
gi|142 NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNI IPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|142 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVRNF
      .....
gi|142 TTNLQFHTSIDGRPINQGNFSATMSSGNSNLQSGSFRTVGFTTFFNFNSGGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFIPVTATLEAEYnLERAQKAVNALFTSTnQLGLKTNVTDYHIDQVSNL
      .....
gi|142 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      .....
gi|142 VECLSDEFCLDEKRElSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENyVTLTSGTFDECyPTyLYQKIDESKlKAFTRyQLRgyIEDSODLEIYSIRYNAK
      .....
gi|142 DDVFKENyVTLTSGTFDECyPTyLYQKIDESKlKAYTRyQLRgyIEDSODLEIYLIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVnVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGECaHSHHfSLD
      .....
gi|142 HETVnVPGTGSWPLSAPSPiGK-----AHHSHHfSLD
      780      790      800

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGvVwVfIKIKTQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE

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      .....
gi|142 IDVGCTDLNEDLGvVwVfIKIKTQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
      810      820      830      840      850      860

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRvHSIREAYLPELSVIP
      .....
gi|142 KLEWETNIVYKEAKESVDALFVNSQYDRlQADTNIAMIHAADKRvHSIREAYLPELSVIP
      870      880      890      900      910      920

      960      970      980      990      1000      1010
Cry1Ac GVNAAlFEELegRIFtAFSLYDARNVIKNGDFNngLSCWNVKghVDVEEQNNQRsvLVVP
      .....
gi|142 GVNAAlFEELegRIFtAFSLYDARNVIKNGDFNngLSCWNVKghVDVEEQNNHRSvLVVP
      930      940      950      960      970      980

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVrVCPGRgyILRvTAYKEgyGEGCVTIHEIENNTDELKfSNCVVEEIPPN
      .....
gi|142 EWEAEVSQEVrVCPGRgyILRvTAYKEgyGEGCVTIHEIENNTDELKfSNCVVEEIPPN
      990      1000      1010      1020      1030      1040

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYtVnQEEYGGAYTSRNRgyNEA----PSVPADYASVYEEKSYTDGRRENpCEFN
      .....
gi|142 TVTCNDYtATQEEYEGTYTSRNRgyDGAYESNssVPADYASAYEEKAYTDGRRDNPcESN
      1050      1060      1070      1080      1090      1100

      1140      1150      1160      1170      1180
Cry1Ac RgyRDYtPLPVgyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
      .....
gi|142 RgyGDYtPLPAGyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
      1110      1120      1130      1140      1150

>>gi|142886|gb|AAA22420.1| 5.3 class delta endotoxin (1155 aa)
initn: 6321 init1: 3168 opt: 4483 Z-score: 5416.3 bits: 1014.2 E(): 0
Smith-Waterman score: 6671; 86.425% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINeCIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGF
      .....
gi|142 MDNPNINeCIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGfGpSQWDAFLVQIEQLINQRIEEFARNQAIrSREGLSNLYQIYAESfRE
      .....
gi|142 VLGLVDIIWIGfGpSQWDAFLVQIEQLINQRIEEFARNQAIrSREGLSNLYQIYAESfRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNdMNSALtTAIPLFAVQNYQVPLlSVVYQAANLHLSVLRdVS
      .....
gi|142 WEADPTNPALREEMRIQFNdMNSALtTAIPLFAVQNYQVPLlSVVYQAANLHLSVLRdVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNyTDHAvRWYNTGLERVWGPDSRDWIRYnQfREL

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gi|142 VFGQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGDSRDWRIRYQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQIEGSIKRSRPHL
.....
gi|142 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQIEGSIKRSRPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITIIYTDHRGEYYSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
.....
gi|142 MDILNSITIIYTDHRGEYYSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

370 380 390 400 410 420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIIPPQ
.....
gi|142 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIIPPQ
360 370 380 390 400 410

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
.....
gi|142 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSANFNIIIPSSQITQIPL
420 430 440 450 460 470

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
.....
gi|142 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
.....
gi|142 TTNLQFHSTIHGRPINQGNFSATMSSGNSLQSGSFRHLGFTTTPFNFSNGSSVFTLSAHVF
540 550 560 570 580 590

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGKLTNTVDYHIDQVSNL
.....
gi|142 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600 610 620 630 640 650

660 670 680 690 700 710
Cry1Ac VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
.....
gi|142 VECLSDDEFCLDEKRELSEKVKHANGLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660 670 680 690 700 710

720 730 740 750 760 770
Cry1Ac DDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
.....
gi|142 DDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770

780 790 800 810 820 830

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Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLD
.....
gi|142 HETVNVPGTGSWLPLSAPSPIGK-----AHSHHFLSLD
780 790 800

840 850 860 870 880 890
Cry1Ac IDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
.....
gi|142 IDVGCTDLNEDLGVVWIFKIKTQDGHARLGILEFLEEKPLVGEALARVKRAEKKWRDKRE
810 820 830 840 850 860

900 910 920 930 940 950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
.....
gi|142 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
870 880 890 900 910 920

960 970 980 990 1000 1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNNQRSVLVVP
.....
gi|142 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNNHRSVLVVP
930 940 950 960 970 980

1020 1030 1040 1050 1060 1070
Cry1Ac EWEAEVSQEVVPCPRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYIPNN
.....
gi|142 EWEAEVSQEVVPCPRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYIPNN
990 1000 1010 1020 1030 1040

1080 1090 1100 1110 1120 1130
Cry1Ac TVTCNDYTYNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPECFN
.....
gi|142 TVTCNDYTYNQEEYGGTYTSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPESN
1050 1060 1070 1080 1090 1100

1140 1150 1160 1170 1180
Cry1Ac RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
.....
gi|142 RGYRDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110 1120 1130 1140 1150

>>gi|1022728|gb|AAA79694.1| crystal toxin (1155 aa)
initn: 4600 init1: 3044 opt: 3918 Z-score: 4732.0 bits: 887.5 E(): 0
Smith-Waterman score: 4945; 65.240% identity (83.048% similar) in 1168 aa overlap
(12-1160:7-1147)

10 20 30 40 50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTP--IDISLSLTQFLLSEFVPGA
.....
gi|102 MEVNHQNECVPNCLKNPKIEMLDIEGISSRSREQVABISLGLTRFLLESLLPGA
10 20 30 40 50

60 70 80 90 100 110
Cry1Ac GFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESF
.....
gi|102 SFGGLFDIIWGVIGPDQWLSFLTQIEQLIDQRIEAEHVRNQAISRLLEGLSDSYEVVIESL
60 70 80 90 100 110

120 130 140 150 160 170

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Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|102 REWEASPNNESLQDVRNRFSNTDNALITAIPILREQGFEIPLLVYVQAANLHLSLRD
120 130 140 150 160 170

180 190 200 210 220 230
Cry1Ac VSVFGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRR
gi|102 AVYFGRWGLDTATVMNHYNRLINLINTYSDHCAQWFNRLDNLN---ARYLDFQR
180 190 200 210 220 230

240 250 260 270 280 290
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSP
gi|102 EVTISVLDIVALFPNYDIRTYPIQTLSQLTREIYTSVAEP---GASLNVDLRNI---LREP
240 250 260 270 280

300 310 320 330 340 350
Cry1Ac HLMIDLNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|102 HLMDFLTRLVIYTGQGGIYHWAGHEISSRTTGNLSSNIQPLYGTSANADRPFNLAHY
290 300 310 320 330 340

360 370 380 390 400 410
Cry1Ac GQGVYRTLSSTLYRRFPNIGINNQLSVDLGTGFAYGTSNLSA--VYRSGTVDSLDE
gi|102 SETIYRTLSAPI--SVSGGISPNRTRAVEGVRFLTARDNNLNSLPFLYRKEGSLDSFTE
350 360 370 380 390 400

420 430 440 450 460 470
Cry1Ac IPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSIT
gi|102 LPPEDENEPPIYGYSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSIT
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac QIPAVKGNFLFNGS--VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYRV
gi|102 QIPWVKAHTLDSGAFVIKPGFTGGDIL---TRPNLGLTALRVTLTGQLPQT---YNI
470 480 490 500 510

540 550 560 570 580
Cry1Ac RVRYASVTPIHNLNVNNGNSSIFSN-----TVPATATSLDNLQSSDFGY--FESANAFTS
gi|102 RIRYASIA-----NRGGTLIFSQPPSYGLTFPKTMDIDEPLTSRFSARTTLFTPIFTQ
520 530 540 550 560 570

590 600 610 620 630 640
Cry1Ac SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNV
gi|102 AQAEEL---NLTIQQGVYIDRIEIPVNATFEAEYDLERAQEAVALFTSSNQLGLKTDL
580 590 600 610 620

650 660 670 680 690 700
Cry1Ac TDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGW
gi|102 TDYHIDQVSNLVDCLSEDFCIDEKRELSKVKHAKRLSDERNLLQDSNFRGINRQPRGW
630 640 650 660 670 680

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710 720 730 740 750 760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQD
gi|102 RGSTDTITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQD
690 700 710 720 730 740

770 780 790 800 810 820
Cry1Ac LEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK
gi|102 LEIYLIRYNAKHETVNVPGTGSWPLSVESPIGKCGEPNRCVPQLEWNSNLDSCRDGEK
750 760 770 780 790 800

830 840 850 860 870 880
Cry1Ac CAHSHHFFSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARKV
gi|102 CAHSHHFFSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARKV
810 820 830 840 850 860

890 900 910 920 930 940
Cry1Ac RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIR
gi|102 RAEKKWRDKRETQLLETNIVYKEAKESVDALFANSQYNRLQADTNIAMIIHAADKRVHRIR
870 880 890 900 910 920

950 960 970 980 990 1000
Cry1Ac EAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEE
gi|102 EAYLPELSVIPGVNAGIFEELEGRIFTAFSLYDARNVIKNSDFNGLSCWNVKGVHDVIEE
930 940 950 960 970 980

1010 1020 1030 1040 1050 1060
Cry1Ac QNNQSVLVVPEWEAEVSVQEVRCVGRGYILRVYAYKEGEGCVTIHEIENNTDELKFS
gi|102 QNNHRSVLVPEWEAEVSKVHVCPGRGYILRVYAYKEGEGCVTIHEIEDHTDELKFR
990 1000 1010 1020 1030 1040

1070 1080 1090 1100 1110 1120
Cry1Ac NCVEEIIYPNNTVTCDYTVNQEYGGAYTSRNRGYNEA---PSPVADYASVYEEKSYT
gi|102 NCEEDEVYPNNTRTCNAYPADQEGYEGACTSRNRGYDEVYGNTPSLPADYAPIYEENAYT
1050 1060 1070 1080 1090 1100

1130 1140 1150 1160 1170 1180
Cry1Ac DGRRENPCFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLME
gi|102 DGRRGNPCSSRGYDTPPLPAGYETKLEYFPETDTVWPRNRYSD
1110 1120 1130 1140 1150

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Cry1Ac E
>>gi|208153|gb|AAA73184.1| crystal toxin (597 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1304.2 bits: 252.3 E(): 5.6e-67
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:44-596)

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30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
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gi|142 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
      540      550      560      570      580
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
      560      570      580      590      600      610
gi|142 APFNQYYFDKTIKGDITLTYNSFNLASFPSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
      590      600      610      620      630      640
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKR
      620      630      640      650      660      670
gi|142 PVN
      650

>>gi|1246432|emb|CAA63860.1| cbm71 mosquitocidal toxin [ (613 aa)
      initn: 477 init1: 149 opt: 580 Z-score: 693.6 bits: 139.4 E(): 5.7e-33
      Smith-Waterman score: 590; 27.797% identity (57.119% similar) in 590 aa overlap
      (60-613:43-608)

      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLV-DIIWGFGPSQWDAFLVQIEQ--
      30      40      50      60      70      80
gi|124 SKGVASVFKVIDTIHNIKNNFNILTQDFIIDTILSILW--EDPNEIEFSSMIEDGE
      20      30      40      50      60      70
Cry1Ac -LINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSAL
      90      100     110     120     130     140
gi|124 TITNKNLSAQTKEGLLNSNSFGLKFKYNNAFRSW-IDNYNPTSIDDVVYRFKDVNSIC
      80      90      100     110     120
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRW-----GFDAATINSRYND
      150     160     170     180     190
gi|124 ENNINEFKVKNYEVTVLPPIYMQIANLHLLLRDGMIDAWNLYRELGF--SDQDSFYNH
      130     140     150     160     170     180
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTY
      200     210     220     230     240     250
gi|124 VLDKTKFYINDCLNYNTGLSNLKLDPNNSWIDITRYCRFMTFYILDMISICPIYDTKVY
      190     200     210     220     230     240
Cry1Ac --PIRTVSQTLTREIYTNPVLENF-DGSFRGSAQGIEGSIRSPHLMIDILNSITITYTDAHRG
      260     270     280     290     300     310
gi|124 DKPI-NMQTLTRKVVSDPV--NFIDENIPISEYEKMYNI-SPELFTSLFISFYTN-KSG
      250     260     270     280     290     300
Cry1Ac EYYWSGH--QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSSTLYRRP
      320     330     340     350     360     370
gi|124 NKFLNGHVRNRHVGTDLNYNGLRETH--YGNYSNYE---VESMAFDDIKAYSNNY----
      310     320     330     340     350
Cry1Ac FNIGINNQQLSVLDGTEFAYGTSSNLPASVYRK--SGTVDSLDEIPPQNNVPPRQGFSGH
      380     390     400     410     420     430

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gi|124 FNNTQNNNPTSV---KSIKFLITKNNDWEIYGEPPDSSNIDFTRNIQGYLSNLN-NESYTH
      360      370      380      390      400
Cry1Ac RLSHVMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK----GNFLF
      440      450      460      470      480
gi|124 SLSDMILANNDKIQINIDTPHSYSYSWIYKGIEDTNYISDKLINQIPLVKEVKLSRHYS
      410      420      430      440      450      460
Cry1Ac NGSVISGPGFTGGDLV--RLNSSGNNIQN---RGYLEVPIH--FPSTSTRYRVRVRYASV
      490      500      510      520      530      540
gi|124 EISVIKGPFTGGDLILSKVHKPANQIPAQYMKNKITIPKTKFPAGSQDFKVRCLYASN
      470      480      490      500      510      520
Cry1Ac TPIHL-NVNWGNSSIFSNTVPATATSLDN--LQSSDFGYF---ESANAFTSSLGNIVGVR
      550      560      570      580      590
gi|124 HDIGLIRLIAGSKYITTTNIQQTFNNTENNPSLIYDDFKYFNFNETLSITSSGIDELYLEF
      530      540      550      560      570      580
Cry1Ac NFSGTAGVIIDRFEF-IPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      600      610      620      630      640      650
gi|124 YYSYTDGNFDFPKLSIPYTRNYS
      590      600      610

>>gi|1922253|emb|CAA67841.1| cbm72 mosquitocidal toxin [ (618 aa)
      initn: 464 init1: 217 opt: 403 Z-score: 479.2 bits: 99.7 E(): 5e-21
      Smith-Waterman score: 519; 25.535% identity (54.434% similar) in 654 aa overlap
      (7-611:2-616)

      10      20      30      40      50
Cry1Ac CMQAMDNNPNI--NECIPYNC---LSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFV
      10      20      30      40      50
gi|192 MNNKKIEQNKIIVEYNSNLDIQPRELNTLNLGL-VFTGAT---VSIILPLIGTTAVV
      10      20      30      40      50
Cry1Ac PGAGFVLGLV---DIIWGFGPSQ---WDAFLVQIEQLINQRIEEFARNQAISRLEGL
      60      70      80      90      100
gi|192 PVVGGVIGIIAALLPVIWPA-GTSSNDNLFDVAMKDEMEMIMDEKISEYVNDAMTRLES
      60      70      80      90      100     110
Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      110     120     130     140     150     160
gi|192 YNLLDYRLSKDFWEKNKDDPLAIAELKERFSLKHSQFIESMAYFKRANYEVLLPAYAN
      120     130     140     150     160     170
Cry1Ac AANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      170     180     190     200     210     220
gi|192 AANLHLLLRGLLNLKVID-NFITEGLHYEEFKTKRSTYIAHCSTWYKGLLENKKNK-T
      180     190     200     210     220
Cry1Ac RDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQ-LTREIYTNPVLENDFDGSFRG
      230     240     250     260     270     280

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gi|192 RDNFNKINKYDAYMNLVSLDIISLFLSYDPYQYDKATKLTTRTTFVSDPLQR-----
230 240 250 260 270 280

Cry1Ac SAQGIIEGSIIRSPHLMILNSITIIYDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMG
290 300 310 320 330 340

gi|192 APRDLIYISPKETLFLKNLGLRAFFA--EGDLVLTGFRNYFRNTYINDQIIIEGDLFGYTT
290 300 310 320 330

Cry1Ac NAAPQORIVAQLGQGVYRTLSSTLYRRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYR
350 360 370 380 390 400

gi|192 N---NERYKLFDTDSKIYKV--TVFIDNVALAIVKLFPHDTDNKEWDFSKTDTITDINKYR
340 350 360 370 380 390

Cry1Ac KSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEF
410 420 430 440 450 460

gi|192 KEEVYLNLL---SNNEIQKEP--SHYLYKMHHYGDNYDSY-----LFQWIHQSSISP
400 410 420 430

Cry1Ac NNII----ASDS--ITQIPAVKGNFLFN-GSV---ISGPGFTGGDLVRLNSSGNNIQNR
470 480 490 500 510

gi|192 ENYLFDKDKDDNYIITQIPAIKASELSNLGELSLQAIKGRPTGGNVIL---SSVSKIDNN
440 450 460 470 480 490

Cry1Ac -----GYIEVPI--HFPSTSTRYRVRVRYASVTPIH-----LNVNWGNSISFNTVPA
520 530 540 550 560

gi|192 DPLYGGTIKIPLLTAFNNTS-KFKIRIYYAANHNYNDYIGALLTINSQHVANFKFKQTF
500 510 520 530 540 550

Cry1Ac TATSLDNLQSSD--FGYFESANAFTSSSLGNIVGVRNF-----SGTAGVIIDRFEPFIP
570 580 590 600 610

gi|192 SGEDYSNLSYNNYQFDYLVQTVAFQNTSDVTLNLQFFYDPKFLNDYKQIVIIDKIEFIP
560 570 580 590 600 610

Cry1Ac VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
620 630 640 650 660 670

gi|192 EN

>>gi|538378|gb|AAA21516.1| delta endotoxin (1186 aa)
initn: 507 initl: 155 opt: 308 Z-score: 359.6 bits: 78.5 E(): 2.3e-14
Smith-Waterman score: 779; 25.196% identity (53.269% similar) in 1147 aa overlap
(50-1075:75-1143)

Cry1Ac LSNPEVEVLGGERIEYTPIDISLSLTQFLLESEFVPGAGVGLVDIIWGFPGSQWDA
20 30 40 50 60 70

gi|538 SFSLTALQGGFSASQGGAFNYLTLLQSGISLAGSFVPGGTVPVAPVNNMVGWLWPHKNT
50 60 70 80 90 100

Cry1Ac F----LVQ----IEQLINQRIEEFARNQAISRLBGLSNLYQIYAESF--REWEA--DPT
80 90 100 110 120

gi|538 ADTENLIKLIIDEIIOQLNKLALDQDRNNWTSFLESIFDTSATVSNAIIDAQWSGTVDDT
110 120 130 140 150 160

Cry1Ac N----PALREEMRI--QFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
130 140 150 160 170

gi|538 NRQOKTPTTSDVLNVVGVKFDSDSSIIITNENQIMNGNFDVAAAPYFVIGATLRLSLYQSY
170 180 190 200 210 220

Cry1Ac SVFGQRW---GFDAATINSRYNDLTRL-----IGNYTDHAVRWYNTGLER-VWGPDS
180 190 200 210 220

gi|538 IKFCNSWIDAVGFS'TNDANTQKANLARTKLTMR'TTINEYTRQVMKVFKDKSKMPTIGTNK
230 240 250 260 270 280

Cry1Ac RDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV--LENFDGFSR
230 240 250 260 270 280

gi|538 FSVDAYNVYKGM'TLNVLDVMAIWSL'YPNDYTSQTAIEQTRVTF'SNMVQEGE'GTDGTLK
290 300 310 320 330 340

Cry1Ac GSAQGIIEGSIIRSPHLM---DILNSITIIYDHRGEYYWSGHQIMASPVGFSGPEFTFPLY
290 300 310 320 330 340

gi|538 --IYNTFDSLSYQHS'LIPN'NNVNLISYYTDELQ----NLELAVYTPKGGSG--YAYP-Y
350 360 370 380 390

Cry1Ac GTMGNAAPQORIVAQLGQGVYRTLSSTLYRR--PFN-IGINNQLSVLDGTEFAYGTSSN
350 360 370 380 390

gi|538 GFILNYAN----SNVYGDNDPTGKPLNKQDGP'IQINAATQNSKYLDG-ETINGIGAS
400 410 420 430 440

Cry1Ac LP-----SAV---YRKSGTVDSLDE-IPPQNNN--VPPRQGFSHRLSHVSMFRSGFSN
400 410 420 430 440

gi|538 LPGYCTTGCSATEQPF'SCTSTANSYKASCNP'SD'TNQKINALYAFTQ'TNVKGSTGKLGVL
450 460 470 480 490 500

Cry1Ac SSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRL
450 460 470 480 490 500

gi|538 SLVPPYDLNPKNVF'GELSD'TNNVI----LKGIPAEKGYFPN'NARPTVVKEWINGASAVPF
510 520 530 540 550 560

Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA---SVTPIHLLNVNWGNSISFNTVPAT
510 520 530 540 550 560

gi|538 YS-GNTL---FMTAT---NLTATQYKIRIRYANPNSDTQIGVLITQNGSQI-SNSNLTIL
570 580 590 600 610

Cry1Ac ATSLDNLQSSDF-----GYFESANAFTS---SLGNIVGVRNFSGTAGVIIDRFE
570 580 590 600

gi|538 YSTTDSMSSNLPQNVVYV'TGENGYTLLDLYSTTNVLS'TGDIT-LKLTGGNQKIFIDRIE
620 630 640 650 660 670

610 620 630

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Cry1Ac FIP-----VTAT-----LEAEYNLERAKAVN
      :::::      :::::      :::::
gi|538 FIPTMPVPAPTNTNTNNGDNGNPPHGGCAIAGTQQLCSGPPKFEQVSDLEKITTQVY
      680      690      700      710      720      730

      640      650      660      670      680
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE-FCLDEKRELSKVKHAKRLSDERNLL
      :::::      :::::      :::::      :::::      :::::
gi|538 MLFKSSSYEELALKVSSYQINQVALKVMALSDEKFC-EKRLRLRKLNVKANQLLEARNLL
      740      750      760      770      780      790

      690      700      710      720      730      740
Cry1Ac QDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLK
      :::::      :::::      :::::      :::::      :::::
gi|538 VGGNF----ETQNWVLTGNAYINYDSFLFNGNYLSLQPA-SGFFTSYAYQKIDESTLK
      800      810      820      830      840

      750      760      770      780      790      800
Cry1Ac AFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGTGLWPLSAQSPIGKCGEPNRCAP
      :::::      :::::      :::::      :::::      :::::
gi|538 PYTRYKVSFIGQSNQVELIISRYGKEIDKILNVYAGPL-PITADASI-TC----CAP
      850      860      870      880      890      900

      810      820      830      840      850      860
Cry1Ac HLEWNPDLDCSCRDEKCAHSHHSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNL
      :::::      :::::      :::::      :::::      :::::
gi|538 EID-----QCDGQS---DSHFFNYSIDVGALHPELNPGLIEIGLKIVQSNGYITISNL
      910      920      930      940      950

      870      880      890      900      910      920
Cry1Ac EFLEEKPLVGEALARVKRAEKWRDKREKLEWETNI--VYKEAKESVDALFVNSQYDQLQ
      :::::      :::::      :::::      :::::      :::::
gi|538 EIIERPLTEMEIQAVNRKDKW--KREKLLCASVSELLQPIINQIDSLFKDANW----
      960      970      980      990      1000

      930      940      950      960      970      980
Cry1Ac ADTNIAMIHAADKRVHSIREAYLPELSV-----IPGVNAAI FEELEGRIFTAFSLYDARN
      :::::      :::::      :::::      :::::      :::::
gi|538 --YNDILPHVTYQTLKNIIVPDLPKLKHWFIDHLPGEYHEIEQKMEALKHAFTQLDEKN
      1010      1020      1030      1040      1050      1060

      990      1000      1010      1020      1030
Cry1Ac VIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVPEWEAEVSVQEVVCP---GRGYILRV
      :::::      :::::      :::::      :::::      :::::
gi|538 LIHNGHFATNLIDWQVGDARMKVLLENALALQLSNWSSVSQSIDILEFDEDEKAYKLRV
      1070      1080      1090      1100      1110      1120

      1040      1050      1060      1070      1080      1090
Cry1Ac TAYKEGYGEGCVTIIEIENNTDELKFSNCVEEIIYPNNTVTCDNYTVNQEEYGGAYTSRN
      :::::      :::::      :::::      :::::      :::::
gi|538 --YAQSGT-----IQFGNCEDEAIQFNTNSFVYKEKIIYFDTPSINLHIQ
      1130      1140      1150      1160

      1100      1110      1120      1130      1140      1150
Cry1Ac RGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDYTPLVGYVTKLEYFPETDK
      :::::      :::::      :::::      :::::      :::::
gi|538 SEGSEFVSSIDLVELSDDE
      1170      1180

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>>gi|142772|gb|AAA22355.1| delta-endotoxin (1257 aa)
      initn: 744 initl: 222 opt: 266 Z-score: 308.3 bits: 69.1 E(): 1.6e-11
      Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
      (33-1058:60-1177)

      10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLSEFVPGAGFV
      :::::      :::::      :::::      :::::      :::::
gi|142 SKYDEMIKAFKWKWKGAQKDLLDVAWYIITGGEIDPLNVKGVLSVL--TLIPEVGTIV
      30      40      50      60      70      80

      70      80      90      100      110
Cry1Ac LG---LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNQAI SRLEGLSNLY
      :::::      :::::      :::::      :::::      :::::
gi|142 ASAASTIVSFIWPKIFGDKPNAKNIFEELKPKQIEALIQQDITNYQDAINQKFKDSLQKTI
      90      100      110      120      130      140

      120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
      :::::      :::::      :::::      :::::      :::::
gi|142 NLYTVAI----DNNDYV---TAKTQLENLNSILTSDISIFIEPEGYETGGLPYYAMVANA
      150      160      170      180      190

      180      190      200      210      220      230
Cry1Ac HLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
      :::::      :::::      :::::      :::::      :::::
gi|142 HILLLRDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTEAVIKAFNLGLDKFKSLDVNSYN
      200      210      220      230      240      250

      240      250      260      270      280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRSTYPIRTVSQLTREIYT---NPVLENFDGS-----
      :::::      :::::      :::::      :::::      :::::
gi|142 KKANYIKGTEMVLDLVALWPTFDPPHYQKEVEIEFTRTISSEPIYQPVKPNMQNTSSSIV
      260      270      280      290      300      310

      290      300      310      320
Cry1Ac -----FRGSAQIEGSIRSPH--LMDILNSI--TIYTDahrGEYyW-----SGHQ
      :::::      :::::      :::::      :::::
gi|142 PSDLPHYQGDLVKLEFSTRTDNDGLAKIFTGIRNTFFYKSPNTHETVHVDFSYNTQSSGNI
      320      330      340      350      360      370

      330      340      350      360      370      380
Cry1Ac IMAS---PVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQGVYRVLSSSTLYRRPFNIGIN
      :::::      :::::      :::::      :::::      :::::
gi|142 SRGSSNPIDLNPIISTCIRNSFYKAIAGSSVLVNFKDG---TQGYAFAQAAPTG-GAW
      380      390      400      410      420      430

      390      400      410      420
Cry1Ac NQQLSVLDGT---EFAYGTSSNLPsAVYRKSgTVDsLDEIppQNN-----NVPPRQg
      :::::      :::::      :::::      :::::
gi|142 DHSFIESDGAPEGHKLNLYITS--PGDTLRDFINVTLISTPTINELSTEKIKGFPKAEKG
      440      450      460      470      480      490

      430      440      450      460      470      480
Cry1Ac FSHRLSHVSMF-RSGFSNSsVSI---RAPMFSWIH--RsaEFNniIASDSITQIPAVKg
      :::::      :::::      :::::      :::::      :::::
gi|142 YKKNQGIKYYGKPEYINGAQPVNLENQQTlifEPHASKTAQYtirIRYAS-TQ--GtKG
      500      510      520      530      540      550

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          490          500          510          520
Cry1Ac  NFLFNGSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|142  YFRLDNQELQTLNIPSTSHNGYVTVGNIGENYDLYTIGSYTITEGNHTLQIHNDKNGMVL
          560          570          580          590          600          610
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
Cry1Ac  PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWGNS-----
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|142  RIEFVPKDSLQSDPQSDPPEVHESTIIIFDKSSPTIWSNKHYSYSHIHLEGSYTSQGSYPH
          620          630          640          650          660          670
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
Cry1Ac  ----SIFSNTPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRFNSGTAGVI
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  NLLINLFHPTDPNRRNHTIHVNNGDMNVVDYKDSVADGLNFNKITATIPSDAWYSGTITSM
          680          690          700          710          720          730
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  --IDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  HLFNDNNFKTITPKFELSNELENIITQVNALFASSAQDTLASNVSDYWIIEQVVMKVDALS
          740          750          760          770          780          790
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  DEVFGKEKKALRKLNVQAKRLSKIRNLLIGGNFDNLV-----AWYMGKDVKKESHELK
          800          810          820          830          840
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  ENYVTLTG--TFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK--HET
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  SDHVLPPPTF---HPSYIFQKVEESKLPNTRYTISGFIAHGEDVELVVSRYGQEIQKV
          850          860          870          880          890          900
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  VNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSDIDV
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  MQVPYEEAL-PLTSESN-SSC-----CVPNLNINETLA-----DPHFYSYIDV
          910          920          930          940
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  GCTDLNEDLGVVIFKIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
          950          960          970          980          990          1000
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIAHADKRVHSIREAYL
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  TEITAIQPVLNQINALYENEDWNGSIRSNSVSYHDLEQIMLPTLLKTEEINCNDYDHPAFL
          1010          1020          1030          1040          1050          1060
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  PE-----LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDVE
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  LKVYHWFMTDRIGEHTILARFQEAALDRAYTQLESRNLLHNGHFTTDTANWTIEGDAHHT
          1070          1080          1090          1100          1110          1120

```

```

          1010          1020          1030          1040          1050          1060
Cry1Ac  EQNNQRSVLVVPWEAEVQSEVVRVCP---GRGYILRVYTAYKEGYGEGCVTIHEIENNTDE
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  ILEDGRRVLRPLPDWSSNATQTIEIEDFDLDDQYQLLIHAK---GKGSITLQHGEEYEV
          1130          1140          1150          1160          1170          1180
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  LKFSNCVEEIEYPNNTVTNCDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYT
          1070          1080          1090          1100          1110          1120
gi|142  ETHTHHTNDFITSQNIPTFKGNQIEVHITSEDEGFLIDHITVIEVSKTDTNTNIENS
          1190          1200          1210          1220          1230          1240
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
>>gi|142763|gb|AAA22352.1| mosquito-toxic crystal protei (643 aa)
      initn: 105 initl: 105 opt: 175 Z-score: 202.8 bits: 48.6 E(): 1.2e-05
      Smith-Waterman score: 203; 19.516% identity (51.452% similar) in 620 aa overlap
      (34-601:25-618)
          10          20          30          40          50
Cry1Ac  AMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVPGAG
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  MEDSSLDLTVSNVNETDFPLYNNYTEPTIAPALIAVAPIAQYLATAIGKWAAKAA
          10          20          30          40          50
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFR
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  FS-KVLSLIFPGSQPATMEKVRTEVETLINQKLSQDRVNLNAEYRGIIEVSDVDFDAYIK
          60          70          80          90          100          110
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  EWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  QPGFTPATA-----KGYFLNLSGAI IQRLPQFEVQTYEGVSIALFTQMCTLHLTLKDG
          120          130          140          150          160
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD-----
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  ILAGSAWGFTQADVDVDFIKLQKLVLDYRTRLMRMYTEFGRLCKVSLKDGLTFRNMCNL
          170          180          190          200          210          220
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  -----W--IRYNQFRRELTTLVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLEN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  YVFPFAEAWSLMRYEGLKQSSLSLWDYVGVSI PVNYNEWGGLVYKLLMGEVNRQLTTVK
          230          240          250          260          270          280
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  FDGSRFGSAQGIIEG--SIRSPH-LMDILNSITIIYTDHRGEYYW---SGHQIMA--SPV
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  FNYSFTEPADIPARENIRGVHPIYDPSSGLTGWIGNGRNTNFFADNNGNEIMEVTRTQT
          290          300          310          320          330          340
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
Cry1Ac  GFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRSLSSLYRPFNIGINNQL--SVLD
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142  FYQNPN-NEPI-----APRD-IINQI---LTAPAPADLFPKNADINVKFTQWFQSTLY
          350          360          370          380          390

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```

      390      400      410      420      430      440
Cry1Ac  GTEFAYGTSSNLPASVYRKSGTVD----SLDEIPPQNNVPPRQ--GFSHRLSHVSMFR
      :  .  .  :  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|142  GWNIKLGTQTVLSS----RTGTIPPNYLAYDGYIRAIACPRGVSALYNDHDLTTLTYNR
      400      410      420      430      440      450

```

```

      450      460      470      480      490
Cry1Ac  SGF-SNSSVSIIR--APMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PGF
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|142  IEYDSPTTENIIVGFAPDNTKDFYSKKSHYLSETNDSYVIPALQFAEVSDRSFLEDTPDQ
      460      470      480      490      500      510

```

```

      500      510      520      530      540      550
Cry1Ac  TGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYR--VVRVYASVTPIHNLV--NWGNS
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|142  ATDGSIKFARTFISNEAKYSIRLNTGF-NTATRYKLIIRVVRYPYRLPAGIRVQSQNSGNN
      520      530      540      550      560      570

```

```

      560      570      580      590      600      610
Cry1Ac  SIFSN-TVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGRNFSGTAGVIIDRFEPFIP
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|142  RMLGSFTANANPEWVDFV--TDAFTFNDLGITTSSTNALFSISSDSLNSGEEWYLSQLFL
      580      590      600      610      620

```

```

      620      630      640      650      660      670
Cry1Ac  VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHLDQVSNLVTYLSDEFCLDEKRE
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|142  VKESAFTTQINPLLK
      630      640

```

```

>>gi|220928|dbj|BAA00854.1| protoxin [Cloning vector pAc (12 aa)
  initn: 92 init1: 92 opt: 92 Z-score: 129.9 bits: 29.4 E(): 0.14
Smith-Waterman score: 92; 100.000% identity (100.000% similar) in 12 aa overlap
(5-16:1-12)

```

```

      10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|220  MDNNPNINECIP
      10

```

```

>>gi|220926|dbj|BAA00848.1| protoxin [Cloning vector pAc (12 aa)
  initn: 92 init1: 92 opt: 92 Z-score: 129.9 bits: 29.4 E(): 0.14
Smith-Waterman score: 92; 100.000% identity (100.000% similar) in 12 aa overlap
(5-16:1-12)

```

```

      10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :  .  .  .  .  :
gi|220  MDNNPNINECIP
      10

```

```

1182 residues in 1 query sequences
1830188 residues in 7176 library sequences
Scomplib [34t26]

```

```

start: Mon Oct 6 17:28:23 2008 done: Mon Oct 6 17:28:24 2008
Total Scan time: 0.990 Total Display time: 0.820

```

Function used was FASTA [version 3.4t26 July 7, 2006]

### Appendix 5 FASTA Alignments with PROTEIN

```

# fasta34 -Q -E 1.0 Cry1Ac_long.fas /home/andre/db/163.fasta -O Cry1Ac_long_163
FASTA searches a protein or DNA sequence data bank version 3.4t26 July 7, 2006
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

```

```

Cry1Ac_CMQA, 1182 aa
vs /home/andre/db/163.fasta library

```

```

      opt      E()
< 20 184854    0:=====
  22  141      0:=
  24  353     12:*
  26 1123     272:*
  28 4879    2939:*
  30 22103   17852:*=
  32 73347   69029:===*
  34 196374  187197:=====*
  36 395055  384459:=====*
  38 643018  635367:=====*
  40 900965  886281:=====*=
  42 1108228 1083371:=====*=
  44 1205052 1195059:=====*=
  46 1210072 1217197:=====*=
  48 1151088 1165326:=====*=
  50 1028097 1063365:=====*=
  52 906488  934875:===== *
  54 771372  798547:=====*
  56 629314  667032:===== *
  58 516341  547620:===== *
  60 420676  443605:=====*
  62 333176  355639:=====*
  64 268927  282838:=====*
  66 214947  223546:=====*
  68 169193  175837:=====*
  70 132633  137796:=====*
  72 106599  107675:=====*
  74 81077   83950:=====*
  76 64690  65340:=====*
  78 48316  50788:=====*
  80 39501  39436:=====*
  82 30087  30168:=====*
  84 23737  23897:=====*
  86 17226  18490:=====*
  88 13925  14307:=====*
  90 10429  11070:=====*
  92 8010   8565:=====*
  94 6310   6627:=====*
  96 5098   5128:=====*

inset = represents 161 library sequences

```

## Regulatory Product Characterization Team

```

98 3918 3968:* :=====
100 2728 3070:* :===== *
102 2038 2375:* :===== *
104 1766 1838:* :=====
106 1299 1422:* :=====
108 1053 1100:* :=====
110 754 851:* :=====
112 574 659:* :=====
114 401 510:* :=====
116 342 394:* :=====
118 231 305:* :=====
>120 2651 236:* :=====
3227582627 residues in 12963194 library sequences
statistics sampled from 60000 to 12958037 sequences
Expectation_n fit: rho(ln(x))= 5.48360.000197; mu= 13.1587 0.011
mean_var=71.868414.662, 0's: 818 Z-trim: 827 B-trim: 7 in 1/63
Lambda= 0.151288
Kolmogorov-Smirnov statistic: 0.0142 (N=29) at 88

FASTA (3.5 Sept 2006) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 39, opt: 27, open/ext: -10/-2, width: 16
The best scores are:
opt bits E(12963194)
gi|142722|gb|AAA22331.1| crystal protein (1178) 7849 1723.1 0
gi|1839246|gb|AAB46989.1| insecticidal delta-endot (1178) 7849 1723.1 0
gi|2584729|emb|CAA05505.1| insecticidal crystal pr (1178) 7849 1723.1 0
gi|1888559|gb|AAB49768.1| CrylAc delta-endotoxin [ (1178) 7849 1723.1 0
gi|1842095|gb|AAC44841.1| crystal protein [Bacillu (1178) 7849 1723.1 0
gi|29293657|gb|AA072077.1| CrylAc [Bacillus thurin (1178) 7849 1723.1 0
gi|1612050|gb|AAB15030.1| Sequence 5 from patent U (1178) 7849 1723.1 0
gi|52783575|gb|AAU87037.1| CrylAc [Bacillus thurin (1178) 7844 1722.0 0
gi|143126|gb|AAA73077.1| [Bacillus thuringiensis g (1178) 7842 1721.5 0
gi|87298907|gb|ABD37053.1| insecticidal crystal pr (1178) 7830 1718.9 0
gi|3979717|emb|CAA10270.1| crystal toxin protein [ (1178) 7827 1718.2 0
gi|23344760|gb|AAN07788.1| insecticidal crystal pr (1177) 7819 1716.5 0
gi|593570|gb|AAA55177.1| Sequence 1 from Patent EP (1177) 7812 1715.0 0
gi|142742|gb|AAA22339.1| cryIA(c)3 (1177) 7812 1715.0 0
gi|157394690|gb|AAX18704.2| CrylAc [Bacillus thuri (1177) 7812 1715.0 0
gi|82698017|gb|ABB89046.1| delta-endocytotoxin [Baci (1177) 7806 1713.7 0
gi|142740|gb|AAA22338.1| delta-endotoxin (1177) 7794 1711.0 0
gi|118566334|gb|ABL01535.1| crystal protein [Bacil (1177) 7788 1709.7 0
gi|34422369|gb|AAQ68348.1| Sequence 2 from patent (1177) 7782 1708.4 0
gi|68236022|gb|AAY88347.1| Cry [Bacillus thuringie (1177) 7777 1707.3 0
gi|33321716|gb|AAQ06607.1| CrylAc [Bacillus thurin (1177) 7775 1706.9 0
gi|1610958|gb|AAB13937.1| Sequence 34 from patent (1188) 7743 1699.9 0
gi|5987870|gb|AAE17035.1| Sequence 34 from patent (1188) 7743 1699.9 0
gi|5973547|gb|AAE12827.1| Sequence 34 from patent (1182) 7732 1697.5 0
gi|1608064|gb|AAB11019.1| Sequence 34 from patent (1182) 7732 1697.5 0
gi|90568470|gb|ABD94160.1| insecticidal crystal pr (1164) 7727 1696.4 0
gi|67089175|gb|AAY66992.1| CrylAc [Bacillus thurin (1164) 7727 1696.4 0
gi|594153|gb|AAA55760.1| Sequence 1 from Patent EP (1182) 7716 1694.0 0
gi|34426442|gb|AAQ070695.1| Sequence 5 from patent (1178) 7687 1687.7 0
gi|594598|gb|AAA56205.1| Sequence 8 from Patent EP (1178) 7401 1625.3 0
gi|112061966|gb|ABH98784.1| Sequence 34 from paten (1177) 7222 1586.2 0
gi|77376722|gb|ABA70269.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|29718515|gb|AAP01239.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|47257347|gb|AAT23510.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|31688820|gb|AAP60985.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|16242914|gb|AAE80144.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|15126309|gb|AAE73545.1| Sequence 34 from patent (1177) 7222 1586.2 0

```

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gi|162500744|gb|ABY14168.1| Sequence 34 from paten (1177) 7222 1586.2 0
gi|12824343|gb|AAE49249.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|53937594|gb|AAV01845.1| Sequence 34 from patent (1177) 7222 1586.2 0
gi|37728786|gb|AAO39719.1| insecticidal crystal pr (1181) 7186 1578.3 0
gi|15126304|gb|AAE73540.1| Sequence 12 from patent (1177) 7159 1572.4 0
gi|19577427|emb|CAD28601.1| unnamed protein produc (1177) 7159 1572.4 0
gi|16242909|gb|AAE80139.1| Sequence 12 from patent (1177) 7159 1572.4 0
gi|12824338|gb|AAE49244.1| Sequence 12 from patent (1177) 7159 1572.4 0
gi|20221572|gb|AAE87145.1| Sequence 12 from patent (1177) 7159 1572.4 0
gi|15126307|gb|AAE73543.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|29718513|gb|AAP01237.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|20221575|gb|AAE87148.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|12824341|gb|AAE49247.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|162500742|gb|ABY14166.1| Sequence 28 from paten (1177) 7109 1561.5 0
gi|40189706|gb|AAR76446.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|83329855|gb|ABC06984.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|19577443|emb|CAD28604.1| unnamed protein produc (1177) 7109 1561.5 0
gi|31688818|gb|AAP60983.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|112061963|gb|ABH98782.1| Sequence 28 from paten (1177) 7109 1561.5 0
gi|16242912|gb|AAE80142.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|53937592|gb|AAV01843.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|77376720|gb|ABA70267.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|47257345|gb|AAT23508.1| Sequence 28 from patent (1177) 7109 1561.5 0
gi|20221573|gb|AAE87146.1| Sequence 14 from patent (1177) 7084 1556.1 0
gi|15126305|gb|AAE73541.1| Sequence 14 from patent (1177) 7084 1556.1 0
gi|19577429|emb|CAD28602.1| unnamed protein produc (1177) 7084 1556.1 0
gi|16242910|gb|AAE80140.1| Sequence 14 from patent (1177) 7084 1556.1 0
gi|12824339|gb|AAE49245.1| Sequence 14 from patent (1177) 7084 1556.1 0
gi|112061962|gb|ABH98781.1| Sequence 26 from paten (1177) 7065 1551.9 0
gi|29718512|gb|AAP01236.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|162500741|gb|ABY14165.1| Sequence 26 from paten (1177) 7065 1551.9 0
gi|20221574|gb|AAE87147.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|40189705|gb|AAR76445.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|19577441|emb|CAD28603.1| unnamed protein produc (1177) 7065 1551.9 0
gi|83329854|gb|ABC06983.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|15126306|gb|AAE73542.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|31688817|gb|AAP60982.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|53937591|gb|AAV01842.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|16242911|gb|AAE80141.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|47257344|gb|AAT23507.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|77376719|gb|ABA70266.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|12824340|gb|AAE49246.1| Sequence 26 from patent (1177) 7065 1551.9 0
gi|37048803|gb|AAQ88259.1| crylA toxin [Bacillus t (1177) 7049 1548.4 0
gi|68236024|gb|AAY88348.1| Cry [Bacillus thuringie (1177) 7049 1548.4 0
gi|31688814|gb|AAP60979.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|12824337|gb|AAE49243.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|47257343|gb|AAT23506.1| Sequence 14 from patent (1177) 7046 1547.8 0
gi|83329851|gb|ABC06980.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|53937588|gb|AAV01839.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|47257342|gb|AAT23505.1| Sequence 12 from patent (1177) 7046 1547.8 0
gi|112061957|gb|ABH98778.1| Sequence 10 from paten (1177) 7046 1547.8 0
gi|77376716|gb|ABA70263.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|47257341|gb|AAT23504.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|19577425|emb|CAD28600.1| unnamed protein produc (1177) 7046 1547.8 0
gi|15126303|gb|AAE73539.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|40189703|gb|AAR76443.1| Sequence 12 from patent (1177) 7046 1547.8 0
gi|53937590|gb|AAV01841.1| Sequence 14 from patent (1177) 7046 1547.8 0
gi|20221571|gb|AAE87144.1| Sequence 10 from patent (1177) 7046 1547.8 0
gi|162500740|gb|ABY14164.1| Sequence 14 from paten (1177) 7046 1547.8 0

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gi	112061960	gb ABH98780.1	Sequence 14 from paten	(1177)	7046	1547.8	0	gi	21239436	gb AAM44305.1	AF510713_1 crystal prote	(1180)	6523	1433.6	0
gi	40189702	gb AAR76442.1	Sequence 10 from patent	(1177)	7046	1547.8	0	gi	4666284	dbj BAA77213.1	BtT84A1 crystal protein	(1180)	6523	1433.6	0
gi	29718510	gb AAP01234.1	Sequence 12 from patent	(1177)	7046	1547.8	0	gi	37781497	gb AAP40639.1	CryIAa [Bacillus thurin	(1183)	6493	1427.1	0
gi	83329853	gb ABC06982.1	Sequence 14 from patent	(1177)	7046	1547.8	0	gi	34426443	gb AAQ70696.1	Sequence 6 from patent	(1184)	6471	1422.3	0
gi	31688816	gb AAP60981.1	Sequence 14 from patent	(1177)	7046	1547.8	0	gi	5669035	gb AAD46139.1	AF081790_1 insecticidal c	(1176)	6463	1420.5	0
gi	40189704	gb AAR76444.1	Sequence 14 from patent	(1177)	7046	1547.8	0	gi	5669019	gb AAD46137.1	AF081248_1 lepidoteran-sp	(1176)	6388	1404.2	0
gi	77376717	gb ABA70264.1	Sequence 12 from patent	(1177)	7046	1547.8	0	gi	34423556	gb AAQ68985.1	Sequence 2 from patent	(1179)	6321	1389.5	0
gi	162500738	gb ABY14162.1	Sequence 10 from paten	(1177)	7046	1547.8	0	gi	1247711	emb CAA01880.1	PS81RR1 endotoxin [Baci	(1179)	6309	1386.9	0
gi	53937589	gb AAV01840.1	Sequence 12 from patent	(1177)	7046	1547.8	0	gi	142744	gb AAA22340.1	cryIA(d)	(1179)	6299	1384.7	0
gi	112061959	gb ABH98779.1	Sequence 12 from paten	(1177)	7046	1547.8	0	gi	911029	gb AAA70483.1	Sequence 1 from Patent US	(1179)	6299	1384.7	0
gi	16242908	gb AAE80138.1	Sequence 10 from patent	(1177)	7046	1547.8	0	gi	53932143	gb AAV00425.1	Sequence 2 from patent	(1176)	6295	1383.9	0
gi	77376718	gb ABA70265.1	Sequence 14 from patent	(1177)	7046	1547.8	0	gi	118907896	gb ABL55894.1	Sequence 2 from patent	(1176)	6295	1383.9	0
gi	31688815	gb AAP60980.1	Sequence 12 from patent	(1177)	7046	1547.8	0	gi	12819673	gb AAE47787.1	Sequence 2 from patent	(1176)	6295	1383.9	0
gi	29718509	gb AAP01233.1	Sequence 10 from patent	(1177)	7046	1547.8	0	gi	33734262	gb AAQ38643.1	Sequence 2 from patent	(1176)	6295	1383.9	0
gi	162500739	gb ABY14163.1	Sequence 12 from paten	(1177)	7046	1547.8	0	gi	3012929	gb AAC11772.1	I76775 Sequence 2 from pa	(1176)	6295	1383.9	0
gi	29718511	gb AAP01235.1	Sequence 14 from patent	(1177)	7046	1547.8	0	gi	911500	gb AAA70954.1	Sequence 4 from patent US	(969)	6224	1368.3	0
gi	83329852	gb ABC06981.1	Sequence 12 from patent	(1177)	7046	1547.8	0	gi	34426444	gb AAQ70697.1	Sequence 7 from patent	(1188)	5911	1300.1	0
gi	594597	gb AAA56204.1	Sequence 4 from Patent EP	(1177)	7007	1539.3	0	gi	911502	gb AAA70956.1	Sequence 6 from patent US	(969)	5519	1214.5	0
gi	2095433	gb AAB57615.1	I42028 Sequence 17 from p	(1181)	6978	1532.9	0	gi	5973542	gb AAE12822.1	Sequence 29 from patent	(1174)	5443	1197.9	0
gi	47270466	gb AAT27228.1	Sequence 13 from patent	(1181)	6978	1532.9	0	gi	1610953	gb AAB13932.1	Sequence 29 from patent	(1174)	5443	1197.9	0
gi	21690367	emb CAD37456.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	5987865	gb AAE17030.1	Sequence 29 from patent	(1174)	5443	1197.9	0
gi	47270464	gb AAT27227.1	Sequence 11 from patent	(1181)	6978	1532.9	0	gi	1608059	gb AAB11014.1	Sequence 29 from patent	(1174)	5443	1197.9	0
gi	21694629	emb CAD37807.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	412688	emb CAA00485.1	bt18 [synthetic construc	(1171)	5381	1184.4	0
gi	47270470	gb AAT27230.1	Sequence 17 from patent	(1181)	6978	1532.9	0	gi	142752	gb AAA22345.1	cryIE(a)	(1171)	5375	1183.1	0
gi	5942795	gb AAE02327.1	Sequence 11 from patent	(1181)	6978	1532.9	0	gi	58397442	gb AAW72936.1	insecticidal delta endo	(1171)	5375	1183.1	0
gi	21713551	emb CAD38228.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	1610413	gb AAB13385.1	Sequence 2 from patent U	(1171)	5375	1183.1	0
gi	12808293	gb AAE43513.1	Sequence 28 from patent	(1181)	6978	1532.9	0	gi	1610414	gb AAB13386.1	Sequence 4 from patent U	(1171)	5375	1183.1	0
gi	21713538	emb CAD38222.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	17979619	gb AAL50330.1	AF202531_1 Cry032 [Bacil	(1171)	5375	1183.1	0
gi	21713540	emb CAD38223.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	1253214	gb AAA94473.1	Sequence 2 from patent U	(1171)	5375	1183.1	0
gi	5942805	gb AAE02337.1	Sequence 28 from patent	(1181)	6978	1532.9	0	gi	593575	gb AAA55182.1	Sequence 1 from Patent EP	(1171)	5375	1183.1	0
gi	12808286	gb AAE43506.1	Sequence 17 from patent	(1181)	6978	1532.9	0	gi	1946622	gb AAD04732.1	CryIEa [Bacillus thurin	(1171)	5373	1182.6	0
gi	2095430	gb AAB57612.1	I42025 Sequence 11 from p	(1181)	6978	1532.9	0	gi	3990784	gb AAC84211.1	AR000634 Sequence 4 from	(1171)	5369	1181.8	0
gi	21690373	emb CAD37459.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	53984833	gb AAV26509.1	Sequence 4 from patent	(1171)	5369	1181.8	0
gi	12808284	gb AAE43504.1	Sequence 13 from patent	(1181)	6978	1532.9	0	gi	15105603	gb AAE66197.1	Sequence 4 from patent	(1171)	5369	1181.8	0
gi	21713544	emb CAD38225.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	2298886	emb CAA02750.1	unnamed protein product	(1171)	5369	1181.8	0
gi	2095431	gb AAB57613.1	I42026 Sequence 13 from p	(1181)	6978	1532.9	0	gi	40257	emb CAA37933.1	crystal protein [Bacillus	(1171)	5369	1181.8	0
gi	21690369	emb CAD37457.1	unnamed protein produc	(1181)	6978	1532.9	0	gi	40282	emb CAA39609.1	crystal protein [Bacillus	(1171)	5369	1181.8	0
gi	47270484	gb AAT27237.1	Sequence 28 from patent	(1181)	6978	1532.9	0	gi	160221245	gb ABX11258.1	CryIEa [Bacillus thuri	(1171)	5353	1178.3	0
gi	12808283	gb AAE43503.1	Sequence 11 from patent	(1181)	6978	1532.9	0	gi	1610956	gb AAB13935.1	Sequence 32 from patent	(1184)	5302	1167.1	0
gi	5942796	gb AAE02328.1	Sequence 13 from patent	(1181)	6978	1532.9	0	gi	5987868	gb AAE17033.1	Sequence 32 from patent	(1184)	5302	1167.1	0
gi	2095440	gb AAB57622.1	I42035 Sequence 28 from p	(1181)	6978	1532.9	0	gi	5987863	gb AAE17028.1	Sequence 25 from patent	(1174)	5301	1166.9	0
gi	5942798	gb AAE02330.1	Sequence 17 from patent	(1181)	6978	1532.9	0	gi	53932146	gb AAV00428.1	Sequence 8 from patent	(1174)	5301	1166.9	0
gi	21690371	emb CAD37458.1	unnamed protein produc	(1181)	6974	1532.1	0	gi	1608062	gb AAB11017.1	Sequence 32 from patent	(1174)	5301	1166.9	0
gi	47270468	gb AAT27229.1	Sequence 15 from patent	(1181)	6974	1532.1	0	gi	3012932	gb AAC11775.1	I76778 Sequence 8 from pa	(1174)	5301	1166.9	0
gi	2095432	gb AAB57614.1	I42027 Sequence 15 from p	(1181)	6974	1532.1	0	gi	1610951	gb AAB13930.1	Sequence 25 from patent	(1174)	5301	1166.9	0
gi	21713542	emb CAD38224.1	unnamed protein produc	(1181)	6974	1532.1	0	gi	118907899	gb ABL55897.1	Sequence 8 from patent	(1174)	5301	1166.9	0
gi	5942797	gb AAE02329.1	Sequence 15 from patent	(1181)	6974	1532.1	0	gi	142758	gb AAA22348.1	insecticidal crystal prot	(1174)	5301	1166.9	0
gi	12808285	gb AAE43505.1	Sequence 15 from patent	(1181)	6974	1532.1	0	gi	34423559	gb AAQ68988.1	Sequence 8 from patent	(1174)	5301	1166.9	0
gi	142875	gb AAA22410.1	delta-endotoxin	(1181)	6788	1491.5	0	gi	12819676	gb AAE47790.1	Sequence 8 from patent	(1174)	5301	1166.9	0
gi	216284	dbj BAA00257.1	unnamed protein product	(1176)	6652	1461.8	0	gi	1608057	gb AAB11012.1	Sequence 25 from patent	(1174)	5301	1166.9	0
gi	32344731	gb AAP80146.1	AF384211_1 delta-endotox	(1176)	6652	1461.8	0	gi	33734265	gb AAQ38646.1	Sequence 8 from patent	(1174)	5301	1166.9	0
gi	1613206	gb AAB16186.1	Sequence 10 from patent	(1176)	6645	1460.3	0	gi	15110438	gb AAE68102.1	Sequence 6 from patent	(1174)	5301	1166.9	0
gi	6687073	emb CAA70856.1	delta-endotoxin [Bacill	(1176)	6645	1460.3	0	gi	5973540	gb AAE12820.1	Sequence 25 from patent	(1174)	5301	1166.9	0
gi	40267	emb CAA31886.1	unnamed protein product	(1176)	6636	1458.3	0	gi	5973545	gb AAE12825.1	Sequence 32 from patent	(1174)	5301	1166.9	0
gi	535781	dbj BAA04468.1	insecticidal crystal pro	(1176)	6634	1457.9	0	gi	42682716	gb AAS28779.1	Sequence 6 from patent	(1174)	5301	1166.9	0
gi	142765	gb AAA22353.1	crystal protein	(1176)	6632	1457.4	0	gi	142756	gb AAA22347.1	cryIF	(1174)	5301	1166.9	0
gi	1612051	gb AAB15031.1	Sequence 6 from patent U	(1176)	6623	1455.5	0	gi	5973549	gb AAE12829.1	Sequence 36 from patent	(1175)	5205	1146.0	0
gi	5901703	gb AAD55382.1	AF154676_1 135 kDa insect	(1176)	6604	1451.3	0	gi	5987872	gb AAE17037.1	Sequence 36 from patent	(1175)	5205	1146.0	0
gi	67089177	gb AAY66993.1	CryIAa [Bacillus thurin	(1163)	6551	1439.7	0	gi	15105604	gb AAE66198.1	Sequence 6 from patent	(1186)	5176	1139.6	0

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gi	2298888 emb CAA02751.1	unnamed protein product	(1186)	5176	1139.6	0	gi	14103737 gb AAE55171.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	53984834 gb AAV26510.1	Sequence 6 from patent	(1186)	5176	1139.6	0	gi	17920873 gb AAE86493.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	3990785 gb AAC84212.1	AR000635 Sequence 6 from	(1186)	5176	1139.6	0	gi	56664637 gb AAW18062.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	15110440 gb AAE68104.1	Sequence 15 from patent	(1156)	5122	1127.8	0	gi	56642270 gb AAW11988.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	42682718 gb AAS28781.1	Sequence 15 from patent	(1156)	5122	1127.8	0	gi	158456669 gb ABW41342.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	3211608 gb AAC21368.1	I83311 Sequence 2 from pa	(1176)	5029	1107.5	0	gi	14112742 gb AAE58157.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	37540106 gb AAG35409.1	insecticidal crystal pr	(1176)	5029	1107.5	0	gi	23325082 gb AAN23782.1	Sequence 8 from patent	(1189)	4994	1099.9	0
gi	3939847 gb AAC81580.1	I95377 Sequence 2 from pa	(1176)	5029	1107.5	0	gi	56664636 gb AAW18061.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	56642302 gb AAW12020.1	Sequence 59 from patent	(1189)	5011	1103.6	0	gi	56642269 gb AAW11987.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	23325114 gb AAN23814.1	Sequence 59 from patent	(1189)	5011	1103.6	0	gi	158456668 gb ABW41341.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	56664669 gb AAW18094.1	Sequence 59 from patent	(1189)	5011	1103.6	0	gi	23325081 gb AAN23781.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	158456701 gb ABW41374.1	Sequence 59 from paten	(1189)	5011	1103.6	0	gi	17920872 gb AAE86492.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	17920905 gb AAE86525.1	Sequence 59 from patent	(1189)	5011	1103.6	0	gi	14112741 gb AAE58156.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	56642267 gb AAW11985.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	14103736 gb AAE55170.1	Sequence 6 from patent	(1189)	4993	1099.7	0
gi	17920870 gb AAE86490.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	14111212 gb AAE57661.1	Sequence 8 from patent	(1189)	4988	1098.6	0
gi	23325079 gb AAN23779.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	62771822 gb AAY01599.1	Sequence 8 from patent	(1189)	4988	1098.6	0
gi	56664634 gb AAW18059.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	27436034 gb AAO13295.1	AF336114_1 crystal delta	(1174)	4979	1096.6	0
gi	158456666 gb ABW41339.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	2958666 emb CAA80235.1	crystal protein [Bacilla	(1174)	4979	1096.6	0
gi	14103734 gb AAE55168.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	53932145 gb AAV00427.1	Sequence 6 from patent	(1189)	4978	1096.4	0
gi	14112739 gb AAE58154.1	Sequence 2 from patent	(1189)	5009	1103.2	0	gi	142750 gb AAA22343.1	cryIC(b)	(1189)	4978	1096.4	0
gi	1612052 gb AAB15032.1	Sequence 7 from patent U	( 934)	5007	1102.7	0	gi	118907898 gb AB55896.1	Sequence 6 from patent	(1189)	4978	1096.4	0
gi	551713 gb AAA22552.1	insecticidal crystal prot	( 934)	5007	1102.7	0	gi	12819675 gb AAE47789.1	Sequence 6 from patent	(1189)	4978	1096.4	0
gi	23325115 gb AAN23815.1	Sequence 61 from patent	(1189)	5004	1102.1	0	gi	3012931 gb AAC11774.1	I76777 Sequence 6 from pa	(1189)	4978	1096.4	0
gi	56664670 gb AAW18095.1	Sequence 61 from patent	(1189)	5004	1102.1	0	gi	33734264 gb AAQ38645.1	Sequence 6 from patent	(1189)	4978	1096.4	0
gi	17920906 gb AAE86526.1	Sequence 61 from patent	(1189)	5004	1102.1	0	gi	3010036 gb AAC10641.1	I73895 Sequence 4 from pa	(1168)	4970	1094.7	0
gi	158456702 gb ABW41375.1	Sequence 61 from paten	(1189)	5004	1102.1	0	gi	10059079 gb AAE35985.1	Sequence 4 from patent	(1168)	4970	1094.7	0
gi	56642303 gb AAW12021.1	Sequence 61 from patent	(1189)	5004	1102.1	0	gi	2982744 dbj BAA25298.1	CryINA67-1 [Bacillus th	(1168)	4966	1093.8	0
gi	158456667 gb ABW41340.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	6650206 gb AAF21767.1	AF062350_1 crystal protei	(1169)	4949	1090.1	0
gi	56664635 gb AAW18060.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	1247709 emb CAA01879.1	PS81A2 endotoxin [Bacil	(1174)	4870	1072.8	0
gi	14103735 gb AAE55169.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	911030 gb AAA70484.1	Sequence 3 from Patent US	(1174)	4868	1072.4	0
gi	18913153 gb AAL79362.1	delta-endotoxin [Bacill	(1189)	5002	1101.7	0	gi	3010035 gb AAC10640.1	I73894 Sequence 2 from pa	(1174)	4868	1072.4	0
gi	23325080 gb AAN23780.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	142754 gb AAA22346.1	cryIE(b)	(1174)	4868	1072.4	0
gi	19880135 gb AAW00264.1	AF362020_1 insecticidal	(1189)	5002	1101.7	0	gi	10059078 gb AAE35984.1	Sequence 2 from patent	(1174)	4868	1072.4	0
gi	14112740 gb AAE58155.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	34422133 gb AAQ68244.1	Sequence 4 from patent	(1174)	4868	1072.4	0
gi	37540181 gb AAG50438.1	Cry1Ca [Bacillus thurin	(1189)	5002	1101.7	0	gi	82468528 gb ABB76664.1	Cry1A-type pesticidal c	( 850)	4786	1054.4	0
gi	34423558 gb AAQ68987.1	Sequence 6 from patent	(1189)	5002	1101.7	0	gi	46409857 gb AAE93796.1	cry1A type crystal prot	( 793)	4762	1049.2	0
gi	56642268 gb AAW11986.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	5052774 gb AAD38701.1	AF148644_1 insecticidal p	( 723)	4715	1038.9	0
gi	17920871 gb AAE86491.1	Sequence 4 from patent	(1189)	5002	1101.7	0	gi	546641 gb AAB30710.1	insecticidal protein Cry	( 723)	4677	1030.6	0
gi	56642272 gb AAW11990.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	112088055 gb ABI06962.1	Sequence 40 from paten	(1167)	4592	1012.2	0
gi	14103739 gb AAE55173.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	13537915 emb CAC35767.1	unnamed protein produc	(1167)	4592	1012.2	0
gi	56664639 gb AAW18064.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	33765730 gb AAQ52381.1	Sequence 40 from patent	(1167)	4592	1012.2	0
gi	158456671 gb ABW41344.1	Sequence 12 from paten	(1189)	5000	1101.2	0	gi	3010046 gb AAC10651.1	I73905 Sequence 27 from p	(1174)	4562	1005.6	0
gi	17920875 gb AAE86495.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	10059089 gb AAE35995.1	Sequence 27 from patent	(1174)	4562	1005.6	0
gi	14112744 gb AAE58159.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	37524001 gb AAQ92302.1	truncated CRYIA(b) [syn	( 818)	4503	992.7	0
gi	23325084 gb AAN23784.1	Sequence 12 from patent	(1189)	5000	1101.2	0	gi	1610957 gb AAB13936.1	Sequence 33 from patent	(1165)	4504	993.0	0
gi	14103738 gb AAE55172.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	5987869 gb AAE17034.1	Sequence 33 from patent	(1165)	4504	993.0	0
gi	17920874 gb AAE86494.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	594314 gb AAA55921.1	Sequence 3 from Patent EP	(1154)	4503	992.7	0
gi	56664638 gb AAW18063.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	21713536 emb CAD38221.1	unnamed protein produc	(1155)	4503	992.7	0
gi	56642271 gb AAW11989.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	2095429 gb AAB57611.1	I42024 Sequence 9 from pa	(1155)	4503	992.7	0
gi	7141141 gb AAF37224.1	AF215647_1 toxin Cry1Ca6	(1189)	4998	1100.8	0	gi	117553202 gb ABK35130.1	Cry1Ab [Bacillus thuri	(1155)	4503	992.7	0
gi	14112743 gb AAE58158.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	47270462 gb AAT27226.1	Sequence 9 from patent	(1155)	4503	992.7	0
gi	23325083 gb AAN23783.1	Sequence 10 from patent	(1189)	4998	1100.8	0	gi	5973546 gb AAE12826.1	Sequence 33 from patent	(1155)	4503	992.7	0
gi	158456670 gb ABW41343.1	Sequence 10 from paten	(1189)	4998	1100.8	0	gi	3746545 gb AAC64003.1	crystal protein [Bacillu	(1155)	4503	992.7	0
gi	40294 emb CAA30396.1	unnamed protein product [	(1189)	4997	1100.6	0	gi	142720 gb AAA22330.1	entomocidal protoxin	(1155)	4503	992.7	0
gi	15105602 gb AAE66196.1	Sequence 2 from patent	(1189)	4996	1100.3	0	gi	216280 dbj BAA00071.1	delta-endotoxin [Bacillu	(1155)	4503	992.7	0
gi	3990783 gb AAC84210.1	AR000633 Sequence 2 from	(1189)	4996	1100.3	0	gi	143124 gb AAA22561.1	crystal protein precursor	(1155)	4503	992.7	0
gi	2298884 emb CAA02749.1	unnamed protein product	(1189)	4996	1100.3	0	gi	21690365 emb CAD37455.1	unnamed protein produc	(1155)	4503	992.7	0
gi	53984832 gb AAV26508.1	Sequence 2 from patent	(1189)	4996	1100.3	0	gi	490188 emb CAA00840.1	delta-endotoxin [Bacillu	(1155)	4503	992.7	0
gi	1247717 emb CAA01886.1	bt15 [Bacillus thuringi	(1189)	4996	1100.3	0	gi	58759040 gb AAW81956.1	Cry1Ab [Chloroplast tra	(1155)	4503	992.7	0

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gi 5942794 gb AAE02326.1	Sequence 9 from patent U (1155)	4503	992.7	0	gi 34423557 gb AAQ68986.1	Sequence 4 from patent (1165)	3774	833.6	0
gi 40273 emb CAA38701.1	unnamed protein product [ (1155)	4503	992.7	0	gi 12819674 gb AAE47788.1	Sequence 4 from patent (1165)	3774	833.6	0
gi 27436100 gb AAO13302.1	AF358861_2 crystal endot (1155)	4503	992.7	0	gi 118907897 gb ABU55895.1	Sequence 4 from patent (1165)	3774	833.6	0
gi 412204 emb CAA00303.1	MGE1 protein [Bacillus t (1155)	4503	992.7	0	gi 33734263 gb AAQ38644.1	Sequence 4 from patent (1165)	3774	833.6	0
gi 12808282 gb AAE43502.1	Sequence 9 from patent (1155)	4503	992.7	0	gi 62771821 gb AA01598.1	Sequence 6 from patent (1165)	3774	833.6	0
gi 594204 gb AAA55811.1	Sequence 4 from Patent EP (1155)	4503	992.7	0	gi 412690 emb CAA00486.1	bt4 [synthetic construct (1165)	3774	833.6	0
gi 1608063 gb AAB11018.1	Sequence 33 from patent (1155)	4503	992.7	0	gi 490266 emb CAA01235.1	bt4 [Bacillus thuringien (1165)	3774	833.6	0
gi 25990352 gb AAN76494.1	AF254640_1 insecticidal (1155)	4503	992.7	0	gi 40280 emb CAA38099.1	unnamed protein product [ (1165)	3774	833.6	0
gi 594472 gb AAA56079.1	Sequence 6 from Patent EP (1156)	4503	992.7	0	gi 53932144 gb CAA00426.1	Sequence 4 from patent (1165)	3774	833.6	0
gi 594020 gb AAA55627.1	Sequence 6 from Patent EP (1156)	4503	992.7	0	gi 3012930 gb AAC11773.1	I76776 Sequence 4 from pa (1165)	3774	833.6	0
gi 10440886 gb AAG16877.1	delta endotoxin [Bacill (1155)	4496	991.2	0	gi 14111120 gb AAE57660.1	Sequence 6 from patent (1165)	3774	833.6	0
gi 151655610 gb ABS18384.1	delta-endotoxin CryIAb (1155)	4495	991.0	0	gi 1247715 emb CAA01885.1	bt4 [Bacillus thuringie (1165)	3774	833.6	0
gi 48734426 gb AAT46415.1	parasporal crystal prot (1156)	4495	991.0	0	gi 911501 gb AAA70955.1	Sequence 5 from patent US ( 695)	3753	828.9	0
gi 159024156 gb ABW87320.1	endotoxin [Bacillus th (1155)	4489	989.7	0	gi 33765721 gb AAQ52372.1	Sequence 22 from patent (1168)	3755	829.5	0
gi 56900936 gb AAW31761.1	CryIAb [Bacillus thurin (1155)	4488	989.5	0	gi 13537904 emb CAC35765.1	unnamed protein produc (1168)	3755	829.5	0
gi 143099 gb AAA22551.1	insecticidal protein (1155)	4487	989.2	0	gi 112088040 gb ABI06953.1	Sequence 22 from paten (1168)	3755	829.5	0
gi 14190061 gb AAK55546.1	AF375608_1 CryIAb16 [Bac (1155)	4484	988.6	0	gi 3410670 gb AAC31092.1	I90730 Sequence 6 from pa (1168)	3713	820.3	0
gi 142886 gb AAA22420.1	5.3 class delta endotoxin (1155)	4483	988.4	0	gi 2958624 emb CAA82024.1	crystal protein [Bacillu (1160)	3702	817.9	0
gi 40255 emb CAA28405.1	unnamed protein product [ (1155)	4476	986.8	0	gi 13899010 gb AAK48937.1	AF358862_2 insecticidal (1160)	3688	814.9	0
gi 1612047 gb AAB15027.1	Sequence 2 from patent U (1155)	4476	986.8	0	gi 53984837 gb AAV26513.1	Sequence 12 from patent (1242)	3604	796.5	0
gi 40278 emb CAA31620.1	unnamed protein product [ (1155)	4473	986.2	0	gi 15105607 gb AAE66201.1	Sequence 12 from patent (1242)	3604	796.5	0
gi 34426441 gb AAQ70694.1	Sequence 4 from patent (1155)	4467	984.9	0	gi 3006691 gb AAC09533.1	I70556 Sequence 2 from pa (1167)	3566	788.2	0
gi 593702 gb AAA55309.1	Sequence 1 from Patent EP (1155)	4465	984.4	0	gi 2096162 gb AAB54994.1	Sequence 2 from patent U (1167)	3566	788.2	0
gi 1608054 gb AAB11009.1	Sequence 19 from patent (1155)	4459	983.1	0	gi 6001559 gb AAE22521.1	Sequence 2 from patent U (1167)	3566	788.2	0
gi 5973537 gb AAE12817.1	Sequence 19 from patent (1155)	4459	983.1	0	gi 474892 gb AAA22341.1	crystal protein (1167)	3566	788.2	0
gi 1610948 gb AAB13927.1	Sequence 19 from patent (1155)	4459	983.1	0	gi 125172655 gb ABN37587.1	Sequence 4 from patent (1168)	3534	781.2	0
gi 5987860 gb AAE17025.1	Sequence 19 from patent (1155)	4459	983.1	0	gi 15143041 emb CAC50779.1	unnamed protein produc (1168)	3534	781.2	0
gi 13173238 gb AAK14336.1	insecticidal crystal pr (1118)	4417	974.0	0	gi 21517410 gb AAM60740.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 46409861 gb AAS93798.1	cryIA type crystal prot ( 793)	4399	969.9	0	gi 208155 gb AAA72985.1	cryIA(a) ( 615)	3423	756.9	1.4e-215
gi 42717976 gb AAS38435.1	cryIACAT modified toxin ( 675)	4379	965.5	0	gi 33736852 gb AAQ40697.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 27447986 gb AAO13756.1	AF288683_1 delta-endotox (1169)	4365	962.6	0	gi 15119962 gb AAE72056.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 4097876 gb AAD10291.1	insecticidal crystal pro (1169)	4351	959.6	0	gi 20230203 gb AAE91346.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 296087 emb CAA80236.1	crystal protein [Bacillu (1172)	4295	947.3	0	gi 12827415 gb AAE50565.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 45387401 gb AAS60191.1	crystal protein [Bacill (1170)	4209	928.6	0	gi 15119964 gb AAE72058.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 295862 emb CAA80233.1	crystal protein [Bacillu (1166)	4205	927.7	0	gi 15117049 gb AAE70575.1	Sequence 10 from patent ( 615)	3423	756.9	1.4e-215
gi 143227 gb AAA22613.1	insecticidal endotoxin (1156)	4163	918.5	0	gi 36244769 gb AAE85125.1	CryIAb1 [synthetic cons ( 617)	3420	756.2	2.2e-215
gi 61696667 gb AAAX53094.1	insecticidal crystal pr (1044)	4142	913.9	0	gi 111983520 gb ABH85230.1	Sequence 1 from patent ( 617)	3418	755.8	2.9e-215
gi 2414156 emb CAA70925.1	delta-endotoxin [Bacill ( 618)	4102	905.1	0	gi 809635 emb CAA01733.1	bt2 (cryIAb)=bt884 [Esch ( 622)	3396	751.0	8.2e-214
gi 22415751 gb AAM95162.1	insecticidal protein Cr ( 618)	4064	896.8	0	gi 155103227 gb ABT03519.1	Sequence 8 from patent ( 614)	3370	745.3	4.2e-212
gi 1669651 emb CAA70506.1	delta-endotoxin [Bacill (1173)	4058	895.6	0	gi 56579956 gb AAW01774.1	Sequence 8 from patent ( 614)	3370	745.3	4.2e-212
gi 22770982 gb AAN06817.1	insect toxin CryIA(c) [ ( 615)	4043	892.2	0	gi 10063046 gb AAE38035.1	Sequence 8 from patent ( 614)	3370	745.3	4.2e-212
gi 4090435 gb AAC98807.1	truncated CryIAc ( 613)	4033	890.0	0	gi 21517418 gb AAM60746.1	Sequence 13 from patent ( 614)	3370	745.3	4.2e-212
gi 56638319 gb AAW10622.1	Sequence 11 from patent ( 613)	4033	890.0	0	gi 56638320 gb AAW10623.1	Sequence 13 from patent ( 614)	3370	745.3	4.2e-212
gi 155103226 gb ABT03518.1	Sequence 6 from patent ( 613)	4033	890.0	0	gi 1297290 gb AAA98959.1	delta-endotoxin CryET1 (1170)	3353	741.7	9.3e-211
gi 56579955 gb AAW01773.1	Sequence 6 from patent ( 613)	4033	890.0	0	gi 15105605 gb AAE66199.1	Sequence 8 from patent (1193)	3339	738.7	7.8e-210
gi 10063045 gb AAE38034.1	Sequence 6 from patent ( 613)	4033	890.0	0	gi 2298890 emb CAA02752.1	unnamed protein product (1193)	3339	738.7	7.8e-210
gi 21517416 gb AAM60745.1	Sequence 11 from patent ( 613)	4033	890.0	0	gi 53984835 gb AAV26511.1	Sequence 8 from patent (1193)	3339	738.7	7.8e-210
gi 40275 emb CAA38098.1	unnamed protein product [ ( 618)	4033	890.0	0	gi 19700901 emb CAD29021.1	unnamed protein produc (1193)	3339	738.7	7.8e-210
gi 1850365 gb AAB82749.1	insecticidal crystal pro ( 911)	3999	882.7	0	gi 3990786 gb AAC84213.1	AR000636 Sequence 8 from (1193)	3339	738.7	7.8e-210
gi 2555147 gb AAC63055.1	CryIA(c) [synthetic cons ( 616)	3982	878.9	0	gi 19700905 emb CAD29023.1	unnamed protein produc (1193)	3336	738.0	1.2e-209
gi 70673280 gb AAZ06794.1	truncated insecticidal ( 716)	3975	877.4	0	gi 19700907 emb CAD29024.1	unnamed protein produc (1193)	3336	738.0	1.2e-209
gi 1171235 gb AAA86266.1	CryIA(c) ( 607)	3970	876.2	0	gi 19700909 emb CAD29025.1	unnamed protein produc ( 668)	3306	731.3	7.1e-208
gi 1022728 gb AAA79694.1	crystal toxin (1155)	3918	865.1	0	gi 19700903 emb CAD29022.1	unnamed protein produc ( 631)	3304	730.9	9.2e-208
gi 13173240 gb AAK14337.1	insecticidal crystal pr (1118)	3906	862.4	0	gi 40189707 gb AAR76447.1	Sequence 30 from patent (1193)	3301	730.4	2.5e-207
gi 34429675 gb AAQ72336.1	Sequence 3 from patent ( 595)	3892	859.2	0	gi 31688819 gb AAP60984.1	Sequence 30 from patent (1193)	3301	730.4	2.5e-207
gi 117518746 gb ABK35074.1	insecticidal delta end (1173)	3880	856.8	0	gi 47257346 gb AAT23509.1	Sequence 30 from patent (1193)	3301	730.4	2.5e-207
gi 1022696 gb AAB00376.1	CryIc (1215)	3827	845.2	0	gi 112061965 gb ABH98783.1	Sequence 30 from paten (1193)	3301	730.4	2.5e-207
gi 5916230 gb AAD55947.1	Cry IAc insecticidal tox ( 587)	3819	843.3	0	gi 29718514 gb AAP01238.1	Sequence 30 from patent (1193)	3301	730.4	2.5e-207
gi 13173242 gb AAK14338.1	insecticidal crystal pr (1118)	3817	843.0	0	gi 77376721 gb ABA70268.1	Sequence 30 from patent (1193)	3301	730.4	2.5e-207

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gi 20221576 gb AAE87149.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 436839 gb AAA21120.1	CryIII delta-endotoxin	(1138)	2588	574.8	1.7e-160
gi 12824342 gb AAE49248.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 565394 emb CAA86568.1	delta-endotoxin [Bacillu	(1233)	2550	566.5	5.6e-158
gi 16242913 gb AAE80143.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 1234884 emb CAA65457.1	delta-endotoxin [Bacill	(756)	2525	560.9	1.6e-156
gi 15126308 gb AAE73544.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 118628705 emb CAL85375.1	unnamed protein produ	(1102)	2517	559.3	7.5e-156
gi 83329856 gb ABC06985.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 10053904 gb AAE30811.1	Sequence 1 from patent	(718)	2321	516.4	4e-143
gi 162500743 gb ABY14167.1	Sequence 30 from paten	(1193)	3301	730.4	2.5e-207	gi 594012 gb AAA55619.1	Sequence 3 from Patent EP	(869)	2322	516.6	4e-143
gi 53937593 gb AAV01844.1	Sequence 30 from patent	(1193)	3301	730.4	2.5e-207	gi 15110439 gb AAE68103.1	Sequence 11 from patent	(547)	2289	509.3	4e-141
gi 1831476 gb AAB45930.1	Sequence 12 from patent	(1190)	3286	727.1	2.4e-206	gi 42682717 gb AAS28780.1	Sequence 11 from patent	(547)	2289	509.3	4e-141
gi 37993013 gb AAR06667.1	hybrid CryIAb-CryIcA pr	(640)	3278	725.2	4.8e-206	gi 1610952 gb AAB13931.1	Sequence 27 from patent	(1148)	2289	509.5	7.4e-141
gi 34429674 gb AAQ72335.1	Sequence 2 from patent	(593)	3222	713.0	2.1e-202	gi 15110436 gb AAE68100.1	Sequence 2 from patent	(1148)	2289	509.5	7.4e-141
gi 62548840 gb AAE86871.1	delta-endotoxin CryI-A3	(769)	3176	703.0	2.8e-199	gi 5973539 gb AAE12819.1	Sequence 23 from patent	(1148)	2289	509.5	7.4e-141
gi 10053905 gb AAE30812.1	Sequence 2 from patent	(452)	3084	682.8	2e-193	gi 5987871 gb AAE17036.1	Sequence 35 from patent	(1148)	2289	509.5	7.4e-141
gi 34422134 gb AAQ68245.1	Sequence 6 from patent	(1129)	2997	664.0	2.2e-187	gi 42682714 gb AAS28777.1	Sequence 2 from patent	(1148)	2289	509.5	7.4e-141
gi 1171233 gb AAA86265.1	CryIA(a)	(620)	2993	663.0	2.5e-187	gi 1608056 gb AAB11011.1	Sequence 23 from patent	(1148)	2289	509.5	7.4e-141
gi 112025965 gb ABH87582.1	Sequence 8 from patent	(609)	2942	661.9	5.5e-184	gi 5973541 gb AAE12821.1	Sequence 27 from patent	(1148)	2289	509.5	7.4e-141
gi 112025964 gb ABH87581.1	Sequence 7 from patent	(609)	2936	650.6	1.4e-183	gi 5987862 gb AAE17027.1	Sequence 23 from patent	(1148)	2289	509.5	7.4e-141
gi 112025963 gb ABH87580.1	Sequence 6 from patent	(609)	2935	650.3	1.6e-183	gi 1608058 gb AAB11013.1	Sequence 27 from patent	(1148)	2289	509.5	7.4e-141
gi 112025962 gb ABH87579.1	Sequence 5 from patent	(609)	2935	650.3	1.6e-183	gi 5973548 gb AAE12828.1	Sequence 35 from patent	(1148)	2289	509.5	7.4e-141
gi 112025960 gb ABH87577.1	Sequence 3 from patent	(609)	2926	648.4	6.1e-183	gi 5987864 gb AAE17029.1	Sequence 27 from patent	(1148)	2289	509.5	7.4e-141
gi 112025961 gb ABH87578.1	Sequence 4 from patent	(609)	2926	648.4	6.1e-183	gi 1610950 gb AAB13929.1	Sequence 23 from patent	(1148)	2289	509.5	7.4e-141
gi 34429673 gb AAQ72334.1	Sequence 1 from patent	(593)	2801	621.1	9.8e-175	gi 5987871 gb AAE17026.1	Sequence 21 from patent	(1150)	2289	509.5	7.4e-141
gi 77364098 gb ABA65394.1	Sequence 2 from patent	(823)	2711	601.5	1.1e-168	gi 5973538 gb AAE12818.1	Sequence 21 from patent	(1150)	2289	509.5	7.4e-141
gi 17918194 gb AAE85628.1	Sequence 2 from patent	(823)	2711	601.5	1.1e-168	gi 1608055 gb AAB11010.1	Sequence 21 from patent	(1150)	2289	509.5	7.4e-141
gi 40356 emb CAA31951.1	unnamed protein product [	(823)	2711	601.5	1.1e-168	gi 1610949 gb AAB13928.1	Sequence 21 from patent	(1150)	2289	509.5	7.4e-141
gi 4000303 gb AAC93735.1	AR023437 Sequence 2 from	(823)	2711	601.5	1.1e-168	gi 42682719 gb AAS28782.1	Sequence 21 from patent	(1163)	2289	509.5	7.5e-141
gi 42690552 gb AAS32607.1	Sequence 2 from patent	(823)	2711	601.5	1.1e-168	gi 15110441 gb AAE68105.1	Sequence 21 from patent	(1163)	2289	509.5	7.5e-141
gi 490199 emb CAA00882.1	lepidoptera larvicidal p	(823)	2709	601.1	1.4e-168	gi 1831475 gb AAB45929.1	Sequence 11 from patent	(1163)	2289	509.5	7.5e-141
gi 33765729 gb AAQ52380.1	Sequence 38 from patent	(1228)	2710	601.4	1.7e-168	gi 15110442 gb AAE68106.1	Sequence 23 from patent	(1186)	2289	509.5	7.6e-141
gi 13537913 emb CAC35766.1	unnamed protein produc	(1228)	2710	601.4	1.7e-168	gi 42682720 gb AAS28783.1	Sequence 23 from patent	(1186)	2289	509.5	7.6e-141
gi 112088054 gb ABI06961.1	Sequence 38 from paten	(1228)	2710	601.4	1.7e-168	gi 5987874 gb AAE17039.1	Sequence 38 from patent	(1148)	2282	508.0	2.1e-140
gi 125172653 gb ABN37586.1	Sequence 2 from patent	(1228)	2699	599.0	9e-168	gi 5973551 gb AAE12831.1	Sequence 38 from patent	(1148)	2282	508.0	2.1e-140
gi 15143039 emb CAC50778.1	unnamed protein produc	(1228)	2699	599.0	9e-168	gi 5973550 gb AAE12830.1	Sequence 37 from patent	(1148)	2282	508.0	2.1e-140
gi 37729016 gb AAO39720.1	insecticidal crystal pr	(1235)	2696	598.4	1.4e-167	gi 5987873 gb AAE17038.1	Sequence 37 from patent	(1148)	2282	508.0	2.1e-140
gi 33765736 gb AAQ52387.1	Sequence 63 from patent	(1227)	2681	595.1	1.4e-166	gi 81302556 gb ABB70817.1	insecticidal crystal pr	(1154)	2168	483.1	6.6e-133
gi 112088065 gb ABI06968.1	Sequence 63 from paten	(1227)	2681	595.1	1.4e-166	gi 3993437 gb AAC86865.1	AR006381 Sequence 2 from	(1149)	2094	466.9	4.8e-128
gi 3410671 gb AAC31093.1	I90731 Sequence 8 from pa	(1227)	2680	594.9	1.6e-166	gi 5972897 gb AAE12788.1	Sequence 2 from patent U	(1149)	2094	466.9	4.8e-128
gi 3360519 gb AAC32850.1	CryIbE1 delta-endotoxin	(1227)	2680	594.9	1.6e-166	gi 41056817 gb AAR98783.1	HBF-1 CryIII delta-endo	(1160)	2094	466.9	4.8e-128
gi 474894 gb AAA22344.1	crystal protein	(1229)	2667	592.0	1.1e-165	gi 532524 gb AAA21119.1	CryIII delta-endotoxin	(1160)	2094	466.9	4.8e-128
gi 2096163 gb AAB54995.1	Sequence 4 from patent U	(1229)	2667	592.0	1.1e-165	gi 118628703 emb CAL85374.1	unnamed protein produ	(1131)	2086	465.2	1.6e-127
gi 3006692 gb AAC09534.1	I70557 Sequence 4 from pa	(1229)	2667	592.0	1.1e-165	gi 125172656 gb ABN37588.1	Sequence 6 from patent	(1152)	2038	454.7	2.3e-124
gi 6001560 gb AAE22522.1	Sequence 4 from patent U	(1229)	2667	592.0	1.1e-165	gi 15143043 emb CAC50780.1	unnamed protein produc	(1152)	2038	454.7	2.3e-124
gi 5942793 gb AAE02325.1	Sequence 7 from patent U	(1207)	2661	590.7	2.8e-165	gi 33731258 gb AAQ37321.1	Sequence 72 from patent	(1156)	2019	450.6	4.1e-123
gi 21690363 emb CAD37454.1	unnamed protein produc	(1207)	2661	590.7	2.8e-165	gi 33765724 gb AAQ52375.1	Sequence 28 from patent	(1156)	2019	450.6	4.1e-123
gi 47270459 gb AAT27225.1	Sequence 7 from patent	(1207)	2661	590.7	2.8e-165	gi 21504423 gb AAM57117.1	Sequence 72 from patent	(1156)	2019	450.6	4.1e-123
gi 21713534 emb CAD38220.1	unnamed protein produc	(1207)	2661	590.7	2.8e-165	gi 53970041 gb AAV19134.1	Sequence 72 from patent	(1156)	2019	450.6	4.1e-123
gi 12808281 gb AAE43501.1	Sequence 7 from patent	(1207)	2661	590.7	2.8e-165	gi 112088045 gb ABI06956.1	Sequence 28 from paten	(1156)	2019	450.6	4.1e-123
gi 2095428 gb AAB57610.1	I42023 Sequence 7 from pa	(1207)	2661	590.7	2.8e-165	gi 150249714 gb ABR67863.1	pesticidal crystal pro	(1144)	2012	449.0	1.2e-122
gi 126566926 gb ABO20894.1	insecticidal protein C	(1228)	2661	590.7	2.8e-165	gi 71792200 emb CAV21127.1	unnamed protein produc	(1154)	1979	441.8	1.7e-120
gi 1200002 emb CAA65003.1	cryIbA2 [Bacillus thuri	(1228)	2661	590.7	2.8e-165	gi 62288329 gb AAX78440.1	crystal protein Cry9Ed1	(1154)	1979	441.8	1.7e-120
gi 580949 emb CAA29898.1	unnamed protein product	(1228)	2661	590.7	2.8e-165	gi 45593719 gb AAS68357.1	insecticidal protein Cr	(1154)	1963	438.4	2e-119
gi 14486714 gb AAK63251.1	AF368257_1 CryIbA [Bacil	(1228)	2661	590.7	2.8e-165	gi 38231198 gb AAR14533.1	CryIc [Chloroplast tran	(661)	1958	437.1	2.6e-119
gi 13959051 gb AAK51084.1	AF363025_1 delta-endotox	(1228)	2661	590.7	2.8e-165	gi 3986086 dbj BAA34908.1	Cry9 like protein [Baci	(1150)	1945	434.4	3e-118
gi 4097878 gb AAD10292.1	insecticidal crystal pro	(1231)	2652	588.7	1.1e-164	gi 27413810 gb AAO12908.1	AF358863_1 crystal endot	(1150)	1945	434.4	3e-118
gi 22213635 gb AAM93496.1	CryIBII [Bacillus thuri	(1231)	2652	588.7	1.1e-164	gi 53970042 gb AAV19135.1	Sequence 74 from patent	(1150)	1945	434.4	3e-118
gi 146335684 gb ABQ23438.1	CryIb [Bacillus thurin	(1228)	2642	586.6	5e-164	gi 33731259 gb AAQ37322.1	Sequence 74 from patent	(1150)	1945	434.4	3e-118
gi 119087867 gb ABL60921.1	CryIb [Bacillus thurin	(1228)	2632	584.4	2.3e-163	gi 120431604 gb ABM21765.1	cry9Ea3 insecticidal c	(1150)	1945	434.4	3e-118
gi 436841 gb AAA21121.1	CryIII delta-endotoxin	(1138)	2606	578.7	1.1e-161	gi 21504424 gb AAM57118.1	Sequence 74 from patent	(1150)	1945	434.4	3e-118
gi 490178 emb CAA00646.1	toxin [Bacillus thuringi	(1138)	2601	577.6	2.3e-161	gi 112025959 gb ABH87576.1	Sequence 1 from patent	(641)	1849	413.3	3.7e-112
gi 142761 gb AAA22351.1	crystal protein	(1138)	2601	577.6	2.3e-161	gi 79014094 gb ABB51653.1	crystal protein Cry28Aa	(1128)	1818	406.7	6.5e-110

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gi 9828610 gb AAG00235.1 AF285775_1 parasporal inc (1128) 1810 405.0 2.2e-109	gi 39653329 gb AAR29331.1 Cry1A [Bacillus thuring (196) 1279 288.6 3.9e-75
gi 114439356 gb ABI74753.1 Cry1Ab-like toxin [unc (373) 1800 402.5 3.9e-109	gi 29329419 emb CAP83752.1 unnamed protein produc (1386) 1285 290.4 8e-75
gi 110734449 gb ABG88858.1 Cry1Ab-like BT toxin O (373) 1796 401.6 7.2e-109	gi 111927190 gb ABH71842.1 Sequence 6 from patent (1386) 1285 290.4 8e-75
gi 1769867 emb CAA67557.1 delta-endotoxin [synthe (630) 1786 399.6 5e-108	gi 112088057 gb ABI06963.1 Sequence 42 from paten (710) 1280 289.2 9.8e-75
gi 12824438 gb AAE49344.1 Sequence 2 from patent (630) 1786 399.6 5e-108	gi 33765731 gb AAQ52382.1 Sequence 42 from patent (710) 1280 289.2 9.8e-75
gi 12578818 emb CAC27275.1 unnamed protein produc (629) 1771 396.3 4.9e-107	gi 21665941 gb AAM73516.1 Cry [Bacillus thuringie (719) 1277 288.5 1.6e-74
gi 53921983 gb AAU98442.1 Sequence 5 from patent (1157) 1724 386.2 9.9e-104	gi 1261624 gb AAB00958.1 CGCryV gene product (719) 1267 286.3 7.1e-74
gi 5945389 gb AAE03465.1 Sequence 5 from patent U (1157) 1724 386.2 9.9e-104	gi 55583756 gb AAV53390.1 delta endotoxin [Bacill (719) 1266 286.1 8.2e-74
gi 13619537 emb CAC36453.1 unnamed protein produc (1157) 1724 386.2 9.9e-104	gi 51998303 emb CAH33947.1 unnamed protein produc (601) 1263 285.4 1.1e-73
gi 6064160 emb CAB58495.1 unnamed protein product (1157) 1724 386.2 9.9e-104	gi 51998348 emb CAH33946.1 unnamed protein produc (629) 1263 285.4 1.2e-73
gi 547556 emb CAA85764.1 unnamed protein product (1157) 1724 386.2 9.9e-104	gi 32709126 gb AAP86782.1 Cry1I [Bacillus thuring (719) 1262 285.2 1.5e-73
gi 27268358 gb AAN89299.1 Sequence 5 from patent (1157) 1724 386.2 9.9e-104	gi 142768 gb AAA22354.1 insecticidal protein (719) 1262 285.2 1.5e-73
gi 6064240 emb CAB58501.1 unnamed protein product (1157) 1722 385.8 1.3e-103	gi 33326396 gb AAQ08616.1 Cry1Ia [Bacillus thurin (720) 1262 285.2 1.5e-73
gi 22122188 dbj BAC07226.1 cry8 [Bacillus thuring (1144) 1719 385.1 2.1e-103	gi 33325407 gb AAQ08233.1 Cry1Ia [Bacillus thurin (746) 1262 285.2 1.6e-73
gi 42682715 gb AAS28778.1 Sequence 4 from patent (605) 1702 381.2 1.6e-102	gi 467235 gb AAA82114.1 cryV465 gene product (719) 1261 285.0 1.8e-73
gi 15110437 gb AAE68101.1 Sequence 4 from patent (605) 1702 381.2 1.6e-102	gi 3329593 gb AAC26910.1 insecticidal protein [Ba (719) 1261 285.0 1.8e-73
gi 3410669 gb AAC31091.1 I90729 Sequence 4 from pa (725) 1657 371.4 1.7e-99	gi 1621216 emb CAA70124.1 Bt toxin [Bacillus thur (719) 1259 284.6 2.4e-73
gi 48880 emb CAA41425.1 crystal protein [Bacillus (1151) 1619 363.3 7.8e-97	gi 46359602 dbj BAH15303.1 parasporal crystal pro (1332) 1262 285.4 2.5e-73
gi 33731257 gb AAQ37320.1 Sequence 70 from patent (1156) 1619 363.3 7.8e-97	gi 111927193 gb ABH71845.1 Sequence 18 from paten (1332) 1262 285.4 2.5e-73
gi 53970040 gb AAV19133.1 Sequence 70 from patent (1156) 1619 363.3 7.8e-97	gi 29329431 emb CAP83755.1 unnamed protein produc (1332) 1262 285.4 2.5e-73
gi 21504422 gb AAM57116.1 Sequence 70 from patent (1156) 1619 363.3 7.8e-97	gi 14537812 gb AAK66742.1 AF373207_1 Cry1Ia [Bacil (719) 1257 284.1 3.2e-73
gi 15105606 gb AAE66200.1 Sequence 10 from patent (1156) 1619 363.3 7.8e-97	gi 106897084 gb ABF83202.1 Cry1Ia [Bacillus thuri (719) 1255 283.7 4.3e-73
gi 53984836 gb AAV26512.1 Sequence 10 from patent (1156) 1619 363.3 7.8e-97	gi 32260894 emb CAC85964.1 delta-endotoxin [Bacil (719) 1255 283.7 4.3e-73
gi 40271 emb CAA41122.1 delta-endotoxin CryIG pro (1156) 1619 363.3 7.8e-97	gi 159131958 gb ABW88019.1 Cry1Ib-type protein [B (719) 1255 283.7 4.3e-73
gi 162767653 emb CAP58830.1 unnamed protein produ (604) 1610 361.1 1.8e-96	gi 40290 emb CAA44633.1 delta-endotoxin [Bacillus (719) 1251 282.8 8e-73
gi 162767651 emb CAP58829.1 unnamed protein produ (726) 1610 361.2 2.1e-96	gi 39653331 gb AAR29332.1 Cry1A [Bacillus thuring (193) 1242 280.5 1e-72
gi 49035989 gb AAT48690.1 Cry8X [Bacillus thuring (1174) 1601 359.3 1.2e-95	gi 5531642 gb AAD44366.1 AF047579_1 insecticidal c (719) 1246 281.7 1.7e-72
gi 1612705 gb AAB15685.1 Sequence 4 from patent U (1169) 1584 355.6 1.6e-94	gi 540282 gb AAC36999.1 insecticidal protein (719) 1244 281.3 2.3e-72
gi 436835 gb AAA21118.1 CryIII delta-endotoxin (1169) 1584 355.6 1.6e-94	gi 12003323 gb AAG43526.1 AF211190_1 Cry1I [Bacill (719) 1238 280.0 5.7e-72
gi 58700647 gb AAW81032.1 Cry8 [Bacillus thuringi (739) 1579 354.4 2.3e-94	gi 436833 gb AAA21117.1 CryIII delta-endotoxin (1157) 1229 278.1 3.3e-71
gi 62126062 gb AA63901.1 crystal endotoxin [Baci (244) 1550 347.8 7.4e-93	gi 1612704 gb AAB15684.1 Sequence 2 from patent U (1157) 1229 278.1 3.3e-71
gi 33731260 gb AAQ37323.1 Sequence 76 from patent (1134) 1543 346.7 7.6e-92	gi 61891427 emb CAI72241.1 unnamed protein produc (712) 1214 274.8 2.1e-70
gi 53970043 gb AAV19136.1 Sequence 76 from patent (1134) 1543 346.7 7.6e-92	gi 61891425 emb CAI72240.1 unnamed protein produc (719) 1214 274.8 2.1e-70
gi 21504426 gb AAM57119.1 Sequence 76 from patent (1134) 1543 346.7 7.6e-92	gi 13173244 gb AAK14339.1 insecticidal crystal pr (1155) 1211 274.2 5e-70
gi 1334252 emb CAA52927.1 delta-endotoxin [Bacill (1144) 1543 346.7 7.6e-92	gi 71792204 emb CAJ21129.1 unnamed protein produc (765) 1200 271.7 1.9e-69
gi 2102642 dbj BAA19948.1 cry9Da1 [Bacillus thuri (1169) 1536 345.2 2.2e-91	gi 142738 gb AAA22337.1 mosquitocidal protein (1135) 1198 271.4 3.5e-69
gi 3991198 gb AAC84625.1 AR001048 Sequence 2 from (1169) 1536 345.2 2.2e-91	gi 908825 emb CAA34382.1 delta-endotoxin (AA 429- (297) 1157 262.1 5.7e-67
gi 5979668 gb AAE15488.1 Sequence 2 from patent U (1169) 1536 345.2 2.2e-91	gi 15119597 gb AAE71691.1 Sequence 2 from patent (719) 1142 259.0 1.2e-65
gi 5985341 gb AAE16149.1 Sequence 2 from patent U (1169) 1536 345.2 2.2e-91	gi 10061243 gb AAE37099.1 Sequence 2 from patent (719) 1142 259.0 1.2e-65
gi 33765712 gb AAQ52363.1 Sequence 4 from patent (243) 1525 342.4 3.2e-91	gi 3702807 gb AAC62933.1 crystal protein toxin [B (719) 1142 259.0 1.2e-65
gi 112088022 gb ABI06944.1 Sequence 4 from patent (243) 1525 342.4 3.2e-91	gi 21311715 gb AAM46818.1 AF490398_1 truncated Cry (210) 1111 252.0 4.5e-64
gi 62288327 gb AA78439.1 crystal protein Cry9Db1 (1169) 1523 342.3 1.6e-90	gi 216288 dbj BAA00178.1 130 kDa insecticidal pro (1135) 1118 253.9 6.4e-64
gi 71792198 emb CAJ21126.1 unnamed protein produc (1169) 1523 342.3 1.6e-90	gi 60459410 gb AA20050.1 130 kDa crystal protein (1136) 1118 253.9 6.4e-64
gi 153866164 gb ABS53003.1 crystal protein [Bacil (1157) 1511 339.7 9.8e-90	gi 21685442 emb CAD30095.1 pesticidal crystal pr (1136) 1118 253.9 6.4e-64
gi 61661422 gb AA51301.1 Cry7 delta-endotoxin [B (488) 1472 331.0 1.7e-87	gi 594241 gb AAA54408.1 Sequence 1 from Patent EP (1136) 1118 253.9 6.4e-64
gi 54112021 gb AAV28716.1 Cry9Bb delta-endotoxin (1163) 1467 330.1 7.6e-87	gi 40310 emb CAA30114.1 unnamed protein product [ (1136) 1118 253.9 6.4e-64
gi 29329417 emb CAD83751.1 unnamed protein produc (1316) 1466 329.9 9.8e-87	gi 40354 emb CAA30312.1 unnamed protein product [ (1136) 1118 253.9 6.4e-64
gi 111927189 gb ABH71841.1 Sequence 4 from patent (1316) 1466 329.9 9.8e-87	gi 592801 gb AAA54408.1 Sequence 3 from Patent WO (1136) 1118 253.9 6.4e-64
gi 46409863 gb AAS93799.1 cryl type crystal prote (782) 1453 326.9 4.6e-86	gi 592802 gb AAA54409.1 Sequence 4 from Patent WO (1136) 1118 253.9 6.4e-64
gi 4574730 gb AAD24189.1 AF132928_1 Cry28Aa1 delta (1109) 1450 326.4 9.6e-86	gi 216290 dbj BAA00179.1 130 kDa insecticidal pro (1180) 1112 252.6 1.6e-63
gi 161784134 gb ABX79555.1 crystal Cry7-like prot (490) 1420 319.6 4.6e-84	gi 21685485 emb CAD30148.1 pesticidal crystal pr (1180) 1112 252.6 1.6e-63
gi 71793184 emb CAJ21051.1 unnamed protein produc (1206) 1411 317.9 3.8e-83	gi 57639076 gb AAW55474.1 delta-endotoxin [Bacill (1136) 1107 251.5 3.4e-63
gi 115828938 gb ABJ38777.1 Sequence 2 from patent (1206) 1411 317.9 3.8e-83	gi 593736 gb AAA55343.1 Sequence 2 from Patent EP (1180) 1100 250.0 1e-62
gi 25277380 emb CAD57542.1 unnamed protein produc (1206) 1411 317.9 3.8e-83	gi 592588 gb AAA54195.1 Sequence 2 from Patent WO (1180) 1100 250.0 1e-62
gi 46409859 gb AAS93797.1 cry1B type crystal prot (849) 1377 310.4 4.8e-81	gi 40352 emb CAA68485.1 unnamed protein product [ (1180) 1100 250.0 1e-62
gi 62433238 dbj BAD95474.1 Cryhime1 [Paenibacillu (1340) 1344 303.3 1e-78	gi 52145404 gb AAU29411.1 Cry3Aa protein [Bacillu (652) 1094 248.5 1.5e-62
gi 46359600 dbj BAD15301.1 parasporal crystal pro (1344) 1314 296.7 9.7e-77	gi 124263655 gb ABM97547.1 Cry4A [Bacillus thurin (1180) 1096 249.1 1.8e-62
gi 29329433 emb CAD83756.1 unnamed protein produc (1344) 1314 296.7 9.7e-77	gi 29823396 emb CAD88617.1 unnamed protein produc (596) 1086 246.8 4.7e-62
gi 111927194 gb ABH71846.1 Sequence 20 from paten (1344) 1314 296.7 9.7e-77	gi 155689526 gb ABU29255.1 Sequence 7 from patent (596) 1086 246.8 4.7e-62

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gi	158496871	gb	ABW60288.1	Sequence 7 from patent	( 596)	1086	246.8	4.7e-62	gi	29823408	emb	CAD88623.1	unnamed protein produc	( 602)	1078	245.0	1.6e-61
gi	111920198	gb	ABH70473.1	Sequence 7 from patent	( 596)	1086	246.8	4.7e-62	gi	158496877	gb	ABW60294.1	Sequence 19 from paten	( 602)	1078	245.0	1.6e-61
gi	45934892	gb	AAS79487.1	insecticidal crystal pr	( 652)	1086	246.8	5.1e-62	gi	111920204	gb	ABH70479.1	Sequence 19 from paten	( 602)	1078	245.0	1.6e-61
gi	208153	gb	AAA73184.1	crystal toxin	( 597)	1084	246.3	6.4e-62	gi	155689532	gb	ABU29261.1	Sequence 19 from paten	( 602)	1078	245.0	1.6e-61
gi	111920197	gb	ABH70472.1	Sequence 4 from patent	( 597)	1084	246.3	6.4e-62	gi	2490715	gb	AAB78851.1	I26291 Sequence 4 from pa	( 645)	1077	244.8	2e-61
gi	158496870	gb	ABW60287.1	Sequence 4 from patent	( 597)	1084	246.3	6.4e-62	gi	593596	gb	AAA55203.1	Sequence 5 from Patent EP	( 610)	1075	244.4	2.5e-61
gi	312848	emb	CAA50310.1	cryIIIA insect control p	( 597)	1084	246.3	6.4e-62	gi	162767645	emb	CAP58826.1	unnamed protein produ	( 465)	1072	243.7	3.2e-61
gi	29823393	emb	CAD88616.1	unnamed protein produc	( 597)	1084	246.3	6.4e-62	gi	58826238	gb	AAW82872.1	Cry3 delta endotoxin [B	( 644)	1068	242.9	7.7e-61
gi	155689525	gb	ABU29254.1	Sequence 4 from patent	( 597)	1084	246.3	6.4e-62	gi	31698148	gb	AAP63846.1	Sequence 2 from patent	( 644)	1065	242.1	1.2e-60
gi	471281	emb	CAA51996.1	CryIIIA insecticidal cry	( 610)	1084	246.3	6.5e-62	gi	56626137	gb	AAW05659.1	Sequence 2 from patent	( 644)	1065	242.2	1.2e-60
gi	155689524	gb	ABU29253.1	Sequence 2 from patent	( 644)	1084	246.4	6.8e-62	gi	40145967	gb	AAR61472.1	Sequence 50 from patent	( 652)	1064	242.0	1.4e-60
gi	158496869	gb	ABW60286.1	Sequence 2 from patent	( 644)	1084	246.4	6.8e-62	gi	12810088	gb	AAE44003.1	Sequence 50 from patent	( 652)	1064	242.0	1.4e-60
gi	83322340	gb	ABC03740.1	Sequence 2 from patent	( 644)	1084	246.4	6.8e-62	gi	155684761	gb	ABU27016.1	Sequence 50 from paten	( 652)	1064	242.0	1.4e-60
gi	270236	gb	AAA01896.1	Sequence 2 from Patent US	( 644)	1084	246.4	6.8e-62	gi	40188401	gb	AAR75926.1	Sequence 50 from patent	( 652)	1064	242.0	1.4e-60
gi	143082	gb	AAA22541.1	insecticidal crystal prot	( 644)	1084	246.4	6.8e-62	gi	40188404	gb	AAR75929.1	Sequence 56 from patent	( 651)	1058	240.7	3.5e-60
gi	111920196	gb	ABH70471.1	Sequence 2 from patent	( 644)	1084	246.4	6.8e-62	gi	155684764	gb	ABU27019.1	Sequence 56 from paten	( 651)	1058	240.7	3.5e-60
gi	592649	gb	AAA54256.1	Sequence 2 from Patent WO	( 644)	1084	246.4	6.8e-62	gi	40145973	gb	AAR61475.1	Sequence 56 from patent	( 651)	1058	240.7	3.5e-60
gi	2490714	gb	AAB78850.1	I26290 Sequence 2 from pa	( 644)	1084	246.4	6.8e-62	gi	12810091	gb	AAE44006.1	Sequence 56 from patent	( 651)	1058	240.7	3.5e-60
gi	514312	gb	AAC43266.1	CryIIIA	( 644)	1084	246.4	6.8e-62	gi	40145965	gb	AAR61471.1	Sequence 48 from patent	( 652)	1054	239.8	6.5e-60
gi	269484	gb	AAA01454.1	Sequence 2 from Patent US	( 644)	1084	246.4	6.8e-62	gi	12810087	gb	AAE44002.1	Sequence 48 from patent	( 652)	1054	239.8	6.5e-60
gi	1607258	gb	AAB10214.1	Sequence 2 from patent US	( 644)	1084	246.4	6.8e-62	gi	40188400	gb	AAR75925.1	Sequence 48 from patent	( 652)	1054	239.8	6.5e-60
gi	142736	gb	AAA50255.1	crystal protein [Bacillus	( 644)	1084	246.4	6.8e-62	gi	155684760	gb	ABU27015.1	Sequence 48 from paten	( 652)	1054	239.8	6.5e-60
gi	14707	emb	CAA00116.1	66 kDa protein from B.thu	( 644)	1084	246.4	6.8e-62	gi	155684768	gb	ABU27023.1	Sequence 64 from paten	( 652)	1053	239.6	7.5e-60
gi	3995646	gb	AAC89074.1	AR013196 Sequence 2 from	( 644)	1084	246.4	6.8e-62	gi	40188408	gb	AAR75933.1	Sequence 64 from patent	( 652)	1053	239.6	7.5e-60
gi	40253	emb	CAA68482.1	unnamed protein product [	( 644)	1084	246.4	6.8e-62	gi	12810095	gb	AAE44010.1	Sequence 64 from patent	( 652)	1053	239.6	7.5e-60
gi	594203	gb	AAA55810.1	Sequence 9 from Patent EP	( 644)	1084	246.4	6.8e-62	gi	40145981	gb	AAR61479.1	Sequence 64 from patent	( 652)	1053	239.6	7.5e-60
gi	29823391	emb	CAD88615.1	unnamed protein produc	( 644)	1084	246.4	6.8e-62	gi	155684759	gb	ABU27014.1	Sequence 46 from paten	( 652)	1052	239.4	8.7e-60
gi	4688623	emb	CAB41411.1	Cry3Aa protein [Bacillu	( 652)	1084	246.4	6.9e-62	gi	12810086	gb	AAE44001.1	Sequence 46 from patent	( 652)	1052	239.4	8.7e-60
gi	12810107	gb	AAE44022.1	Sequence 113 from paten	( 652)	1084	246.4	6.9e-62	gi	40145963	gb	AAR61470.1	Sequence 46 from patent	( 652)	1052	239.4	8.7e-60
gi	40188420	gb	AAR75945.1	Sequence 113 from paten	( 652)	1084	246.4	6.9e-62	gi	40188399	gb	AAR75924.1	Sequence 46 from patent	( 652)	1052	239.4	8.7e-60
gi	155684780	gb	ABU27035.1	Sequence 113 from pate	( 652)	1084	246.4	6.9e-62	gi	12810089	gb	AAE44004.1	Sequence 52 from patent	( 651)	1048	238.5	1.6e-59
gi	142734	gb	AAA22336.1	delta-endotoxin	( 652)	1084	246.4	6.9e-62	gi	40188402	gb	AAR75927.1	Sequence 52 from patent	( 651)	1048	238.5	1.6e-59
gi	40146005	gb	AAR61491.1	Sequence 113 from paten	( 652)	1084	246.4	6.9e-62	gi	155684762	gb	ABU27017.1	Sequence 52 from paten	( 651)	1048	238.5	1.6e-59
gi	594327	gb	AAA55934.1	Sequence 14 from Patent E	( 644)	1083	246.1	7.9e-62	gi	40145969	gb	AAR61473.1	Sequence 52 from patent	( 651)	1048	238.5	1.6e-59
gi	155689527	gb	ABU29256.1	Sequence 9 from patent	( 598)	1082	245.9	8.7e-62	gi	40188409	gb	AAR75934.1	Sequence 66 from patent	( 652)	1045	237.8	2.5e-59
gi	29823398	emb	CAD88618.1	unnamed protein produc	( 598)	1082	245.9	8.7e-62	gi	40145932	gb	AAR61452.1	Sequence 10 from patent	( 652)	1045	237.8	2.5e-59
gi	111920199	gb	ABH70474.1	Sequence 9 from patent	( 598)	1082	245.9	8.7e-62	gi	40145983	gb	AAR61480.1	Sequence 66 from patent	( 652)	1045	237.8	2.5e-59
gi	158496872	gb	ABW60289.1	Sequence 9 from patent	( 598)	1082	245.9	8.7e-62	gi	155684741	gb	ABU26996.1	Sequence 10 from paten	( 652)	1045	237.8	2.5e-59
gi	111920203	gb	ABH70478.1	Sequence 17 from paten	( 600)	1082	245.9	8.7e-62	gi	155684769	gb	ABU27024.1	Sequence 66 from paten	( 652)	1045	237.8	2.5e-59
gi	29823406	emb	CAD88622.1	unnamed protein produc	( 600)	1082	245.9	8.7e-62	gi	12810068	gb	AAE43983.1	Sequence 10 from patent	( 652)	1045	237.8	2.5e-59
gi	158496876	gb	ABW60293.1	Sequence 17 from paten	( 600)	1082	245.9	8.7e-62	gi	40188381	gb	AAR75906.1	Sequence 10 from patent	( 652)	1045	237.8	2.5e-59
gi	155689531	gb	ABU29260.1	Sequence 17 from paten	( 600)	1082	245.9	8.7e-62	gi	12810096	gb	AAE44011.1	Sequence 66 from patent	( 652)	1045	237.8	2.5e-59
gi	158496873	gb	ABW60290.1	Sequence 11 from paten	( 606)	1082	245.9	8.8e-62	gi	155684766	gb	ABU27021.1	Sequence 60 from paten	( 652)	1044	237.6	2.9e-59
gi	155689528	gb	ABU29257.1	Sequence 11 from paten	( 606)	1082	245.9	8.8e-62	gi	40188406	gb	AAR75931.1	Sequence 60 from patent	( 652)	1044	237.6	2.9e-59
gi	111920200	gb	ABH70475.1	Sequence 11 from paten	( 606)	1082	245.9	8.8e-62	gi	40145977	gb	AAR61477.1	Sequence 60 from patent	( 652)	1044	237.6	2.9e-59
gi	29823400	emb	CAD88619.1	unnamed protein produc	( 606)	1082	245.9	8.8e-62	gi	12810093	gb	AAE44008.1	Sequence 60 from patent	( 652)	1044	237.6	2.9e-59
gi	155689529	gb	ABU29258.1	Sequence 13 from paten	( 597)	1081	245.7	1e-61	gi	155684758	gb	ABU27013.1	Sequence 44 from paten	( 652)	1043	237.4	3.4e-59
gi	111920201	gb	ABH70476.1	Sequence 13 from paten	( 597)	1081	245.7	1e-61	gi	40188389	gb	AAR75914.1	Sequence 26 from patent	( 652)	1043	237.4	3.4e-59
gi	29823402	emb	CAD88620.1	unnamed protein produc	( 597)	1081	245.7	1e-61	gi	40145947	gb	AAR61460.1	Sequence 26 from patent	( 652)	1043	237.4	3.4e-59
gi	158496874	gb	ABW60291.1	Sequence 13 from paten	( 597)	1081	245.7	1e-61	gi	40188398	gb	AAR75923.1	Sequence 44 from patent	( 652)	1043	237.4	3.4e-59
gi	155689530	gb	ABU29259.1	Sequence 15 from paten	( 601)	1080	245.5	1.2e-61	gi	40145961	gb	AAR61469.1	Sequence 44 from patent	( 652)	1043	237.4	3.4e-59
gi	29823404	emb	CAD88621.1	unnamed protein produc	( 601)	1080	245.5	1.2e-61	gi	155684749	gb	ABU27004.1	Sequence 26 from paten	( 652)	1043	237.4	3.4e-59
gi	158496875	gb	ABW60292.1	Sequence 15 from paten	( 601)	1080	245.5	1.2e-61	gi	12810085	gb	AAE44000.1	Sequence 44 from patent	( 652)	1043	237.4	3.4e-59
gi	111920202	gb	ABH70477.1	Sequence 15 from paten	( 601)	1080	245.5	1.2e-61	gi	12810076	gb	AAE43991.1	Sequence 26 from patent	( 652)	1043	237.4	3.4e-59
gi	143084	gb	AAA22542.1	insect control protein	( 644)	1080	245.5	1.3e-61	gi	40145971	gb	AAR61474.1	Sequence 54 from patent	( 652)	1042	237.2	4e-59
gi	111920205	gb	ABH70480.1	Sequence 21 from paten	( 597)	1079	245.2	1.4e-61	gi	155684778	gb	ABU27033.1	Sequence 111 from pate	( 652)	1042	237.2	4e-59
gi	29823410	emb	CAD88624.1	unnamed protein produc	( 597)	1079	245.2	1.4e-61	gi	40146001	gb	AAR61489.1	Sequence 111 from paten	( 652)	1042	237.2	4e-59
gi	158496878	gb	ABW60295.1	Sequence 21 from paten	( 597)	1079	245.2	1.4e-61	gi	40145979	gb	AAR61478.1	Sequence 62 from patent	( 652)	1042	237.2	4e-59
gi	155689533	gb	ABU29262.1	Sequence 21 from paten	( 597)	1079	245.2	1.4e-61	gi	12810105	gb	AAE44020.1	Sequence 111 from paten	( 652)	1042	237.2	4e-59

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gi	34423484	gb AAQ68937.1		Sequence 2 from patent	( 652)	1042	237.2	4e-59
gi	155684754	gb ABU27009.1		Sequence 36 from paten	( 652)	1042	237.2	4e-59
gi	40145950	gb AAR61462.1		Sequence 30 from patent	( 652)	1042	237.2	4e-59
gi	40188407	gb AAR75932.1		Sequence 62 from patent	( 652)	1042	237.2	4e-59
gi	12810081	gb AAE43996.1		Sequence 36 from patent	( 652)	1042	237.2	4e-59
gi	40145991	gb AAR61484.1		Sequence 98 from patent	( 652)	1042	237.2	4e-59
gi	40188391	gb AAR75916.1		Sequence 30 from patent	( 652)	1042	237.2	4e-59
gi	155684773	gb ABU27028.1		Sequence 98 from paten	( 652)	1042	237.2	4e-59
gi	155684767	gb ABU27022.1		Sequence 62 from paten	( 652)	1042	237.2	4e-59
gi	40145955	gb AAR61465.1		Sequence 36 from patent	( 652)	1042	237.2	4e-59
gi	40188394	gb AAR75919.1		Sequence 36 from patent	( 652)	1042	237.2	4e-59
gi	12810100	gb AAE44015.1		Sequence 98 from patent	( 652)	1042	237.2	4e-59
gi	40188418	gb AAR75943.1		Sequence 111 from paten	( 652)	1042	237.2	4e-59
gi	29702304	gb AAO96389.1		Sequence 2 from patent	( 652)	1042	237.2	4e-59
gi	1427230	gb AAA22334.1		cryIIIB2	( 652)	1042	237.2	4e-59
gi	12810090	gb AAE44005.1		Sequence 54 from patent	( 652)	1042	237.2	4e-59
gi	155684763	gb ABU27018.1		Sequence 54 from paten	( 652)	1042	237.2	4e-59
gi	77370837	gb ABA68333.1		Sequence 2 from patent	( 652)	1042	237.2	4e-59
gi	155684751	gb ABU27006.1		Sequence 30 from paten	( 652)	1042	237.2	4e-59
gi	12810078	gb AAE43993.1		Sequence 30 from patent	( 652)	1042	237.2	4e-59
gi	12810094	gb AAE44009.1		Sequence 62 from patent	( 652)	1042	237.2	4e-59
gi	114210119	emb CAL40964.1		unnamed protein produ	( 652)	1042	237.2	4e-59
gi	40188413	gb AAR75938.1		Sequence 98 from patent	( 652)	1042	237.2	4e-59
gi	40188403	gb AAR75928.1		Sequence 54 from patent	( 652)	1042	237.2	4e-59
gi	12810079	gb AAE43994.1		Sequence 32 from patent	( 652)	1041	237.0	4.6e-59
gi	12810097	gb AAE44012.1		Sequence 68 from patent	( 652)	1041	237.0	4.6e-59
gi	40188390	gb AAR75915.1		Sequence 28 from patent	( 652)	1041	237.0	4.6e-59
gi	40145949	gb AAR61461.1		Sequence 28 from patent	( 652)	1041	237.0	4.6e-59
gi	155684746	gb ABU27001.1		Sequence 20 from paten	( 652)	1041	237.0	4.6e-59
gi	155684750	gb ABU27005.1		Sequence 28 from paten	( 652)	1041	237.0	4.6e-59
gi	12810069	gb AAE43984.1		Sequence 12 from patent	( 652)	1041	237.0	4.6e-59
gi	40145952	gb AAR61463.1		Sequence 32 from patent	( 652)	1041	237.0	4.6e-59
gi	12810073	gb AAE43988.1		Sequence 20 from patent	( 652)	1041	237.0	4.6e-59
gi	155684752	gb ABU27007.1		Sequence 32 from paten	( 652)	1041	237.0	4.6e-59
gi	155684770	gb ABU27025.1		Sequence 68 from paten	( 652)	1041	237.0	4.6e-59
gi	40188410	gb AAR75935.1		Sequence 68 from patent	( 652)	1041	237.0	4.6e-59
gi	40145934	gb AAR61453.1		Sequence 12 from patent	( 652)	1041	237.0	4.6e-59
gi	40188392	gb AAR75917.1		Sequence 32 from patent	( 652)	1041	237.0	4.6e-59
gi	40145985	gb AAR61481.1		Sequence 68 from patent	( 652)	1041	237.0	4.6e-59
gi	12810077	gb AAE43992.1		Sequence 28 from patent	( 652)	1041	237.0	4.6e-59
gi	155684742	gb ABU26997.1		Sequence 12 from paten	( 652)	1041	237.0	4.6e-59
gi	40188386	gb AAR75911.1		Sequence 20 from patent	( 652)	1041	237.0	4.6e-59
gi	40145942	gb AAR61457.1		Sequence 20 from patent	( 652)	1041	237.0	4.6e-59
gi	40188382	gb AAR75907.1		Sequence 12 from patent	( 652)	1041	237.0	4.6e-59
gi	40188380	gb AAR75905.1		Sequence 8 from patent	( 652)	1040	236.8	5.4e-59
gi	40145930	gb AAR61451.1		Sequence 8 from patent	( 652)	1040	236.8	5.4e-59
gi	155684740	gb ABU26995.1		Sequence 8 from patent	( 652)	1040	236.8	5.4e-59
gi	12810067	gb AAE43982.1		Sequence 8 from patent	( 652)	1040	236.8	5.4e-59
gi	12810075	gb AAE43990.1		Sequence 24 from patent	( 652)	1040	236.8	5.4e-59
gi	155684748	gb ABU27003.1		Sequence 24 from paten	( 652)	1040	236.8	5.4e-59
gi	40145945	gb AAR61459.1		Sequence 24 from patent	( 652)	1040	236.8	5.4e-59
gi	40188388	gb AAR75913.1		Sequence 24 from patent	( 652)	1040	236.8	5.4e-59
gi	12810080	gb AAE43995.1		Sequence 34 from patent	( 652)	1038	236.3	7.3e-59
gi	29702305	gb AAO96390.1		Sequence 4 from patent	( 652)	1038	236.3	7.3e-59
gi	40188384	gb AAR75909.1		Sequence 16 from patent	( 652)	1038	236.3	7.3e-59
gi	40188393	gb AAR75918.1		Sequence 34 from patent	( 652)	1038	236.3	7.3e-59
gi	940200	gb AAA74198.1		Cry3Bb2	( 652)	1038	236.3	7.3e-59
gi	40145954	gb AAR61464.1		Sequence 34 from patent	( 652)	1038	236.3	7.3e-59
gi	40188417	gb AAR75942.1		Sequence 110 from paten	( 652)	1038	236.3	7.3e-59
gi	155684744	gb ABU26999.1		Sequence 16 from paten	( 652)	1038	236.3	7.3e-59
gi	114210121	emb CAL40965.1		unnamed protein produ	( 652)	1038	236.3	7.3e-59
gi	77370838	gb ABA68334.1		Sequence 4 from patent	( 652)	1038	236.3	7.3e-59
gi	40145938	gb AAR61455.1		Sequence 16 from patent	( 652)	1038	236.3	7.3e-59
gi	155684753	gb ABU27008.1		Sequence 34 from paten	( 652)	1038	236.3	7.3e-59
gi	155684777	gb ABU27032.1		Sequence 110 from pate	( 652)	1038	236.3	7.3e-59
gi	12810071	gb AAE43986.1		Sequence 16 from patent	( 652)	1038	236.3	7.3e-59
gi	12810104	gb AAE44019.1		Sequence 110 from paten	( 652)	1038	236.3	7.3e-59
gi	40145999	gb AAR61488.1		Sequence 110 from paten	( 652)	1038	236.3	7.3e-59
gi	40145975	gb AAR61476.1		Sequence 58 from patent	( 651)	1037	236.1	8.4e-59
gi	155684765	gb ABU27020.1		Sequence 58 from paten	( 651)	1037	236.1	8.4e-59
gi	12810092	gb AAE44007.1		Sequence 58 from patent	( 651)	1037	236.1	8.4e-59
gi	40188405	gb AAR75930.1		Sequence 58 from patent	( 651)	1037	236.1	8.4e-59
gi	155684755	gb ABU27010.1		Sequence 38 from paten	( 652)	1037	236.1	8.4e-59
gi	40145957	gb AAR61466.1		Sequence 38 from patent	( 652)	1037	236.1	8.4e-59
gi	12810082	gb AAE43997.1		Sequence 38 from patent	( 652)	1037	236.1	8.4e-59
gi	40145940	gb AAR61456.1		Sequence 18 from patent	( 652)	1037	236.1	8.4e-59
gi	40188415	gb AAR75940.1		Sequence 108 from paten	( 652)	1037	236.1	8.4e-59
gi	12810102	gb AAE44017.1		Sequence 108 from paten	( 652)	1037	236.1	8.4e-59
gi	12810072	gb AAE43987.1		Sequence 18 from patent	( 652)	1037	236.1	8.4e-59
gi	155684745	gb ABU27000.1		Sequence 18 from paten	( 652)	1037	236.1	8.4e-59
gi	40188385	gb AAR75910.1		Sequence 18 from patent	( 652)	1037	236.1	8.4e-59
gi	40145995	gb AAR61486.1		Sequence 108 from paten	( 652)	1037	236.1	8.4e-59
gi	40188395	gb AAR75920.1		Sequence 38 from patent	( 652)	1037	236.1	8.4e-59
gi	155684775	gb ABU27030.1		Sequence 108 from pate	( 652)	1037	236.1	8.4e-59
gi	490176	emb CAA00645.1		toxin [Bacillus thuringi	( 651)	1036	235.9	9.8e-59
gi	1612706	gb AAB15686.1		Sequence 6 from patent U	( 651)	1036	235.9	9.8e-59
gi	40145943	gb AAR61458.1		Sequence 22 from patent	( 652)	1036	235.9	9.8e-59
gi	155684747	gb ABU27002.1		Sequence 22 from paten	( 652)	1036	235.9	9.8e-59
gi	12810074	gb AAE43989.1		Sequence 22 from patent	( 652)	1036	235.9	9.8e-59
gi	40188387	gb AAR75912.1		Sequence 22 from patent	( 652)	1036	235.9	9.8e-59
gi	114210153	emb CAL40978.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	114210133	emb CAL40971.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	77370845	gb ABA68341.1		Sequence 18 from patent	( 653)	1036	235.9	9.8e-59
gi	114210131	emb CAL40970.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	29702320	gb AAO96405.1		Sequence 39 from patent	( 653)	1036	235.9	9.8e-59
gi	29702311	gb AAO96396.1		Sequence 16 from patent	( 653)	1036	235.9	9.8e-59
gi	77370853	gb ABA68349.1		Sequence 39 from patent	( 653)	1036	235.9	9.8e-59
gi	40145993	gb AAR61485.1		Sequence 100 from paten	( 653)	1036	235.9	9.8e-59
gi	114210155	emb CAL40979.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	77370852	gb ABA68348.1		Sequence 37 from patent	( 653)	1036	235.9	9.8e-59
gi	77370840	gb ABA68336.1		Sequence 8 from patent	( 653)	1036	235.9	9.8e-59
gi	114210125	emb CAL40967.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	29702308	gb AAO96393.1		Sequence 10 from patent	( 653)	1036	235.9	9.8e-59
gi	77370843	gb ABA68339.1		Sequence 14 from patent	( 653)	1036	235.9	9.8e-59
gi	12810101	gb AAE44016.1		Sequence 100 from paten	( 653)	1036	235.9	9.8e-59
gi	77370841	gb ABA68337.1		Sequence 10 from patent	( 653)	1036	235.9	9.8e-59
gi	77370844	gb ABA68340.1		Sequence 16 from patent	( 653)	1036	235.9	9.8e-59
gi	29702312	gb AAO96397.1		Sequence 18 from patent	( 653)	1036	235.9	9.8e-59
gi	114210135	emb CAL40972.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	29702310	gb AAO96395.1		Sequence 14 from patent	( 653)	1036	235.9	9.8e-59
gi	114210137	emb CAL40973.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	77370846	gb ABA68342.1		Sequence 20 from patent	( 653)	1036	235.9	9.8e-59
gi	114210127	emb CAL40968.1		unnamed protein produ	( 653)	1036	235.9	9.8e-59
gi	40188414	gb AAR75939.1		Sequence 100 from paten	( 653)	1036	235.9	9.8e-59
gi	29702319	gb AAO96404.1		Sequence 37 from patent	( 653)	1036	235.9	9.8e-59
gi	29702313	gb AAO96398.1		Sequence 20 from patent	( 653)	1036	235.9	9.8e-59
gi	29702307	gb AAO96392.1		Sequence 8 from patent	( 653)	1036	235.9	9.8e-59
gi	155684774	gb ABU27029.1		Sequence 100 from pate	( 653)	1036	235.9	9.8e-59



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gi	71793201	emb	CAJ21058.1	unnamed protein produc	( 620)	858	197.0	4.7e-47	gi	71793243	emb	CAJ21074.1	unnamed protein produc	( 673)	839	192.9	8.9e-46
gi	115828947	gb	ABJ38785.1	Sequence 20 from paten	( 620)	858	197.0	4.7e-47	gi	115828959	gb	ABJ38797.1	Sequence 54 from paten	( 673)	839	192.9	8.9e-46
gi	25277428	emb	CAD57553.1	unnamed protein produc	( 620)	858	197.0	4.7e-47	gi	115828980	gb	ABJ38817.1	Sequence 94 from paten	( 673)	839	192.9	8.9e-46
gi	71793215	emb	CAJ21062.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	71793267	emb	CAJ21086.1	unnamed protein produc	( 673)	839	192.9	8.9e-46
gi	71793249	emb	CAJ21077.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	110734455	gb	ABG88861.1	CryI-like Bt toxin 2 [ ( 144)	820	188.4	4.4e-45	
gi	71793211	emb	CAJ21061.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	15110444	gb	AAE68108.1	Sequence 27 from patent	( 655)	819	188.5	1.8e-44
gi	115828965	gb	ABJ38803.1	Sequence 66 from paten	( 673)	858	197.0	5e-47	gi	42682722	gb	AAS28785.1	Sequence 27 from patent	( 655)	819	188.5	1.8e-44
gi	115828950	gb	ABJ38788.1	Sequence 30 from paten	( 673)	858	197.0	5e-47	gi	19386614	dbj	BAB72016.2	mosquitocidal toxin [B ( 660)	809	186.3	8.2e-44	
gi	115828964	gb	ABJ38802.1	Sequence 64 from paten	( 673)	858	197.0	5e-47	gi	51998363	emb	CAH33953.1	unnamed protein produc	( 561)	807	185.9	9.6e-44
gi	71793271	emb	CAJ21088.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	62997562	gb	AAJ24695.1	Cry [Bacillus thuringie	(1134)	804	185.4	2.7e-43
gi	71793245	emb	CAJ21075.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	162767649	emb	CAP58828.1	unnamed protein produ	( 648)	788	181.8	1.9e-42
gi	115828967	gb	ABJ38805.1	Sequence 70 from paten	( 673)	858	197.0	5e-47	gi	162767647	emb	CAP58827.1	unnamed protein produ	( 770)	788	181.8	2.2e-42
gi	71793190	emb	CAJ21054.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	25897924	emb	CAD58214.1	unnamed protein produc	( 673)	786	181.3	2.7e-42
gi	115828942	gb	ABJ38780.1	Sequence 8 from patent	( 673)	858	197.0	5e-47	gi	3410672	gb	AAC31094.1	I90732 Sequence 10 from p	( 488)	777	179.3	8e-42
gi	71793203	emb	CAJ21059.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	14537815	gb	AAK66743.1	CryI-like protein [Baci	( 149)	764	176.2	2.1e-41
gi	76360363	emb	CAJ32199.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	15721993	gb	AAG36711.1	crystal protein [Bacill	(1236)	773	178.6	3.2e-41
gi	115828948	gb	ABJ38786.1	Sequence 22 from paten	( 673)	858	197.0	5e-47	gi	33765725	gb	AAQ52376.1	Sequence 30 from patent	( 802)	769	177.7	4.1e-41
gi	115828949	gb	ABJ38787.1	Sequence 26 from paten	( 673)	858	197.0	5e-47	gi	112088047	gb	ABT06957.1	Sequence 30 from paten	( 802)	769	177.7	4.1e-41
gi	71793207	emb	CAJ21060.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	40457464	gb	AAR86772.1	CRY9C [synthetic constr	( 387)	753	174.0	2.5e-40
gi	25277399	emb	CAD57547.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	21685445	emb	CAD30099.1	putative pesticidal c	( 489)	745	172.3	1e-39
gi	71793239	emb	CAJ21072.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	46359604	dbj	BAD15305.1	parasporal crystal pro	( 405)	739	170.9	2.2e-39
gi	76360359	emb	CAJ32197.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	118628707	emb	CAL85376.1	unnamed protein produ	( 629)	735	170.2	5.7e-39
gi	115828966	gb	ABJ38804.1	Sequence 68 from paten	( 673)	858	197.0	5e-47	gi	142759	gb	AAA22349.1	ORF	( 381)	714	165.5	9e-38
gi	71793247	emb	CAJ21076.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	160420050	dbj	BAF93483.1	Cry8Dlike [Bacillus t	(1174)	707	164.2	6.6e-37
gi	76360361	emb	CAJ32198.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	2624006	emb	CAA68876.1	unknown protein [Bacill	( 526)	696	161.6	1.8e-36
gi	71793251	emb	CAJ21078.1	unnamed protein produc	( 673)	858	197.0	5e-47	gi	31745045	dbj	BAC77649.1	hypothetical protein [	( 533)	693	161.0	2.9e-36
gi	115828978	gb	ABJ38815.1	Sequence 90 from paten	( 673)	858	197.0	5e-47	gi	16945770	dbj	BAB72017.1	Cry39ORF2 protein [Bac	( 558)	692	160.8	3.5e-36
gi	115828951	gb	ABJ38789.1	Sequence 34 from paten	( 673)	858	197.0	5e-47	gi	162767644	emb	CAP58825.1	unnamed protein produ	( 285)	686	159.3	4.9e-36
gi	115828961	gb	ABJ38799.1	Sequence 58 from paten	( 673)	858	197.0	5e-47	gi	41688284	dbj	BAD08533.1	hypothetical protein [	( 541)	689	160.1	5.3e-36
gi	17385648	dbj	BAB78602.1	crystal protein CryE6Q	(1254)	860	197.6	6.2e-47	gi	83336130	gb	ABC11712.1	Sequence 1 from patent	(1167)	691	160.7	4.4e-36
gi	25277431	emb	CAD57554.1	unnamed protein produc	( 620)	856	196.6	6.3e-47	gi	54695306	dbj	BAD67158.1	hypothetical protein [	( 486)	685	159.2	8.9e-36
gi	25277450	emb	CAD57557.1	unnamed protein produc	( 620)	856	196.6	6.3e-47	gi	50539656	dbj	BAD32658.1	hypothetical protein [	( 537)	685	159.2	9.6e-36
gi	25277446	emb	CAD57556.1	unnamed protein produc	( 673)	856	196.6	6.8e-47	gi	592659	gb	AAA54266.1	Sequence 2 from Patent	WO ( 103)	670	155.5	2.4e-35
gi	25277416	emb	CAD57551.1	unnamed protein produc	( 673)	856	196.6	6.8e-47	gi	3426160	dbj	BAA32397.1	insecticidal protein [B	( 682)	679	158.0	2.9e-35
gi	115828969	gb	ABJ38807.1	Sequence 74 from paten	( 675)	854	196.2	9.2e-47	gi	37999235	dbj	BAD00053.1	hypothetical protein [	( 545)	676	157.3	3.8e-35
gi	115828953	gb	ABJ38791.1	Sequence 42 from paten	( 675)	854	196.2	9.2e-47	gi	80975797	gb	ABB54494.1	Cry40 [Bacillus thuring	( 459)	673	156.6	5.2e-35
gi	71793255	emb	CAJ21080.1	unnamed protein produc	( 675)	854	196.2	9.2e-47	gi	89000902	dbj	BAE80089.1	C-terminal half of 130	( 559)	664	154.6	2.4e-34
gi	71793261	emb	CAJ21083.1	unnamed protein produc	( 675)	854	196.2	9.2e-47	gi	2624005	emb	CAA68875.1	mosquitocidal toxin [Ba	( 648)	652	152.1	1.7e-33
gi	71793229	emb	CAJ21067.1	unnamed protein produc	( 675)	854	196.2	9.2e-47	gi	17385646	dbj	BAB78601.1	crystal protein CryE6L	(1270)	653	152.5	2.5e-33
gi	115828972	gb	ABJ38810.1	Sequence 80 from paten	( 675)	854	196.2	9.2e-47	gi	17385650	dbj	BAB78603.1	crystal protein CryE6S	(1280)	645	150.7	8.4e-33
gi	115828956	gb	ABJ38794.1	Sequence 48 from paten	( 675)	854	196.2	9.2e-47	gi	51998374	emb	CAH33958.1	unnamed protein produc	( 669)	634	148.1	2.6e-32
gi	71793223	emb	CAJ21064.1	unnamed protein produc	( 675)	854	196.2	9.2e-47	gi	51998372	emb	CAH33957.1	unnamed protein produc	( 672)	634	148.1	2.6e-32
gi	115828960	gb	ABJ38798.1	Sequence 56 from paten	( 673)	850	195.3	1.7e-46	gi	16945773	dbj	BAB72019.1	Cry40ORF2 protein [Bac	( 558)	632	147.7	3e-32
gi	71793237	emb	CAJ21071.1	unnamed protein produc	( 673)	850	195.3	1.7e-46	gi	2815886	gb	AAB97923.1	delta-endotoxin [Bacillu	( 645)	603	141.4	2.7e-30
gi	71793269	emb	CAJ21087.1	unnamed protein produc	( 673)	850	195.3	1.7e-46	gi	71792192	emb	CAJ21125.1	unnamed protein produc	( 696)	599	140.5	5.4e-30
gi	115828977	gb	ABJ38814.1	Sequence 88 from paten	( 673)	850	195.3	1.7e-46	gi	71792202	emb	CAJ21128.1	unnamed protein produc	( 780)	599	140.5	5.9e-30
gi	115828962	gb	ABJ38800.1	Sequence 60 from paten	( 673)	847	194.6	2.6e-46	gi	156712245	emb	CAJ18351.1	Crystal toxin [Lysini	(1177)	593	139.3	2.1e-29
gi	71793273	emb	CAJ21089.1	unnamed protein produc	( 673)	847	194.6	2.6e-46	gi	156711548	emb	CAJ86546.1	Cry48Aa protein [Lysi	(1177)	593	139.3	2.1e-29
gi	115828979	gb	ABJ38816.1	Sequence 92 from paten	( 673)	847	194.6	2.6e-46	gi	156711546	emb	CAJ86545.1	Cry48Aa protein [Lysi	(1177)	593	139.3	2.1e-29
gi	71793241	emb	CAJ21073.1	unnamed protein produc	( 673)	847	194.6	2.6e-46	gi	632792	gb	AAC60477.1	delta-endotoxin CryIAb7	( 91)	578	135.4	2.4e-29
gi	110734457	gb	ABG88862.1	CryI-like Bt toxin 3 [ ( 144)	836	191.9	3.9e-46	gi	37999234	dbj	BAD00052.1	putative mosquitocidal	( 683)	583	137.0	5.9e-29	
gi	71793265	emb	CAJ21085.1	unnamed protein produc	( 677)	842	193.5	5.7e-46	gi	51090237	dbj	BAD35164.1	C-terminal half of Cry	( 735)	582	136.8	7.3e-29
gi	115828974	gb	ABJ38812.1	Sequence 84 from paten	( 677)	842	193.5	5.7e-46	gi	1246432	emb	CAA63860.1	cbm71 mosquitocidal tox	( 613)	580	136.3	8.5e-29
gi	71793233	emb	CAJ21069.1	unnamed protein produc	( 677)	842	193.5	5.7e-46	gi	2228580	gb	AAB93476.1	mosquitocidal toxin [Bac	( 753)	580	136.4	1e-28
gi	115828958	gb	ABJ38796.1	Sequence 52 from paten	( 677)	842	193.5	5.7e-46	gi	51090233	dbj	BAD35161.1	C-terminal half of Cry	( 737)	578	135.9	1.3e-28
gi	115828963	gb	ABJ38801.1	Sequence 62 from paten	( 673)	839	192.9	8.9e-46	gi	51090229	dbj	BAD35158.1	C-terminal half of Cry	( 737)	578	135.9	1.3e-28
gi	115828975	gb	ABJ38813.1	Sequence 86 from paten	( 673)	839	192.9	8.9e-46	gi	156711550	emb	CAJ86548.1	Cry48Aa protein [Lysi	(1129)	573	135.0	4.1e-28
gi	71793235	emb	CAJ21070.1	unnamed protein produc	( 673)	839	192.9	8.9e-46	gi	156711552	emb	CAJ86549.1	Cry48Aa protein [Lysi	(1129)	570	134.3	6.4e-28
gi	71793275	emb	CAJ21090.1	unnamed protein produc	( 673)	839	192.9	8.9e-46	gi	51998369	emb	CAH33956.1	unnamed protein produc	( 661)	566	133.3	7.6e-28

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gi	51998367	emb CAH33955.1	unnamed protein produc	( 671)	566	133.3	7.6e-28	gi	14112752	gb AAE58167.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12
gi	51998365	emb CAH33954.1	unnamed protein produc	( 682)	566	133.3	7.7e-28	gi	23325092	gb AAN23792.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12
gi	33765722	gb AAQ52373.1	Sequence 24 from patent	( 116)	543	127.9	5.8e-27	gi	56642280	gb AAW11998.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12
gi	112088041	gb ABI06954.1	Sequence 24 from paten	( 116)	543	127.9	5.8e-27	gi	56664645	gb AAW18070.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12
gi	6010670	gb AAF01213.1	endotoxin [Bacillus thur	( 140)	511	120.9	8.6e-25	gi	158456677	gb ABW41350.1	Sequence 30 from paten	( 50)	313	77.4	3.7e-12
gi	54695305	dbj BAD67157.1	Cry30-like [Bacillus t	( 688)	515	122.2	1.8e-24	gi	56642278	gb AAW11996.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12
gi	89885725	dbj BAE86999.1	pesticidal crystal pro	( 679)	512	121.5	2.7e-24	gi	17920881	gb AAE86501.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12
gi	41688283	dbj BAD08532.1	putative mosquitocidal	( 686)	511	121.3	3.2e-24	gi	158456679	gb ABW41352.1	Sequence 32 from paten	( 50)	313	77.4	3.7e-12
gi	46852037	gb AAT02712.1	Cry1Ab [Bacillus thurin	( 167)	492	116.8	1.8e-23	gi	17920883	gb AAE86503.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12
gi	145843784	gb ABP96899.1	cry4A [Bacillus thurin	( 255)	493	117.1	2.1e-23	gi	23325090	gb AAN23790.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12
gi	31745044	dbj BAC77648.1	putative mosquitocidal	( 666)	495	117.8	3.5e-23	gi	14103745	gb AAE55179.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12
gi	111927191	gb ABH71843.1	Sequence 8 from patent	( 265)	486	115.6	6.4e-23	gi	14103747	gb AAE55181.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12
gi	29329421	emb CAD83753.1	unnamed protein produc	( 265)	486	115.6	6.4e-23	gi	12810187	gb AAE44102.1	Sequence 2 from patent	( 1385)	326	81.1	8.2e-12
gi	5689049	dbj BAA82796.1	94kDa mosquitocidal tox	( 826)	490	116.8	8.9e-23	gi	142869	gb AAA67694.1	delta-endotoxin	( 1385)	326	81.1	8.2e-12
gi	46852035	gb AAT02711.1	Cry1E [Bacillus thuring	( 172)	479	114.0	1.3e-22	gi	1831841	gb AAB46299.1	Sequence 2 from patent U	( 1385)	326	81.1	8.2e-12
gi	46852039	gb AAT02713.1	Cry1Ba [Bacillus thurin	( 174)	473	112.7	3.2e-22	gi	34427717	gb AAQ71352.1	Sequence 1 from patent	( 1385)	326	81.1	8.2e-12
gi	29329423	emb CAD83754.1	unnamed protein produc	( 153)	464	110.7	1.1e-21	gi	5972712	gb AAE12603.1	Sequence 2 from patent U	( 1385)	326	81.1	8.2e-12
gi	111927192	gb ABH71844.1	Sequence 10 from paten	( 153)	464	110.7	1.1e-21	gi	40159628	gb AAR66712.1	Sequence 2 from patent	( 1385)	326	81.1	8.2e-12
gi	51998361	emb CAH33952.1	unnamed protein produc	( 690)	471	112.6	1.4e-21	gi	34427043	gb AAQ70970.1	Sequence 1 from patent	( 1385)	326	81.1	8.2e-12
gi	51998359	emb CAH33951.1	unnamed protein produc	( 693)	471	112.6	1.4e-21	gi	2096263	gb AAB55095.1	Sequence 2 from patent U	( 1385)	326	81.1	8.2e-12
gi	89000901	dbj BAE80088.1	delta-endotoxin [Bacil	( 684)	469	112.1	1.8e-21	gi	3994347	gb AAC87775.1	AR008749 Sequence 2 from	( 1385)	326	81.1	8.2e-12
gi	22121135	gb AAM92282.1	CryIA(b) protein [Zea m	( 68)	451	107.6	4.1e-21	gi	12810205	gb AAE44120.1	Sequence 43 from patent	( 1220)	325	80.9	8.6e-12
gi	50539655	dbj BAD32657.1	delta-endotoxin [Bacil	( 675)	462	110.6	5.2e-21	gi	1831859	gb AAB46313.1	Sequence 43 from patent	( 1220)	325	80.9	8.6e-12
gi	17977981	emb CAC80986.1	Cry30Aa protein [Bacil	( 688)	453	108.6	2.1e-20	gi	5972730	gb AAE12621.1	Sequence 43 from patent	( 1220)	325	80.9	8.6e-12
gi	51090240	dbj BAD35166.1	Cry protein [Bacillus	( 810)	451	108.3	3.2e-20	gi	14103743	gb AAE55177.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	51090236	dbj BAD35163.1	cancer cell-killing Cr	( 829)	449	107.8	4.4e-20	gi	14112748	gb AAE58163.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	87887911	dbj BAE79727.1	cry4A [Bacillus thurin	( 696)	445	106.9	7e-20	gi	56664643	gb AAW18068.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	23268634	gb AAN16462.1	insecticidal protein Cr	( 181)	431	103.5	1.9e-19	gi	56642276	gb AAW11994.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	51090228	dbj BAD35157.1	cancer cell-killing Cr	( 825)	439	105.6	2e-19	gi	23325088	gb AAN23788.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	51090232	dbj BAD35160.1	cancer cell-killing Cr	( 825)	439	105.6	2e-19	gi	158456675	gb ABW41348.1	Sequence 28 from paten	( 50)	306	75.9	1.1e-11
gi	16945772	dbj BAB72018.1	putative mosquitocidal	( 666)	437	105.1	2.3e-19	gi	17920879	gb AAE86499.1	Sequence 28 from patent	( 50)	306	75.9	1.1e-11
gi	17977979	emb CAC80985.1	Cry29Aa protein [Bacil	( 650)	425	102.5	1.4e-18	gi	10051730	gb AAE28637.1	Sequence 6 from patent	( 1167)	321	80.0	1.5e-11
gi	3668333	gb AAC61891.1	insecticidal protein Jeg	( 674)	419	101.2	3.5e-18	gi	5977359	gb AAE14769.1	Sequence 6 from patent U	( 1167)	321	80.0	1.5e-11
gi	3668335	gb AAC61892.1	insecticidal protein Jeg	( 675)	419	101.2	3.5e-18	gi	1830715	gb AAB45169.1	Sequence 6 from patent U	( 1167)	321	80.0	1.5e-11
gi	1922253	emb CAA67841.1	cbm72 mosquitocidal tox	( 618)	403	97.7	3.7e-17	gi	14112751	gb AAE58166.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	21685444	emb CAD30098.1	pesticidal crystal pr	( 675)	394	95.8	1.5e-16	gi	17920882	gb AAE86502.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	143229	gb AAA22614.1	insecticidal endotoxin (p	( 675)	394	95.8	1.5e-16	gi	23325091	gb AAN23791.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	110734451	gb ABG88859.1	CryII-like Bt toxin OL	( 381)	390	94.8	1.8e-16	gi	56642279	gb AAW11997.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	268659	gb AAA00893.1	Sequence 2 from Patent US	( 608)	375	91.6	2.5e-15	gi	14103746	gb AAE55180.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	29329415	emb CAD83750.1	unnamed protein produc	( 134)	361	88.2	5.9e-15	gi	158456678	gb ABW41351.1	Sequence 31 from paten	( 50)	303	75.3	1.7e-11
gi	111927188	gb ABH71840.1	Sequence 2 from patent	( 134)	361	88.2	5.9e-15	gi	56664646	gb AAW18071.1	Sequence 31 from patent	( 50)	303	75.3	1.7e-11
gi	152013905	gb ABS20059.1	dipterans toxic crysta	( 126)	349	85.5	3.5e-14	gi	33731246	gb AAQ37309.1	Sequence 41 from patent	( 137)	307	76.4	2.1e-11
gi	2725272	gb AAB92954.1	I67292 Sequence 9 from pa	( 1168)	361	88.7	3.6e-14	gi	53970029	gb AAV19122.1	Sequence 41 from patent	( 137)	307	76.4	2.1e-11
gi	152013909	gb ABS20061.1	dipterans toxic crysta	( 126)	345	84.7	6.3e-14	gi	16240180	gb AAE79628.1	Sequence 41 from patent	( 137)	307	76.4	2.1e-11
gi	22002424	dbj BAC06484.1	Cry21Ba [Bacillus thu	( 1286)	356	87.6	8.2e-14	gi	21504407	gb AAM57105.1	Sequence 41 from patent	( 137)	307	76.4	2.1e-11
gi	134274695	emb CAJ43600.1	pesticidal crystal pr	( 686)	352	86.6	9e-14	gi	56642277	gb AAW11995.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	152013911	gb ABS20062.1	dipterans toxic crysta	( 124)	341	83.8	1.1e-13	gi	17920880	gb AAE86500.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	152013903	gb ABS20058.1	dipterans toxic crysta	( 122)	336	82.7	2.4e-13	gi	14112749	gb AAE58164.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	3994348	gb AAC87776.1	AR008750 Sequence 4 from	( 1289)	338	83.7	1.3e-12	gi	56664644	gb AAW18069.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	2096264	gb AAB55096.1	Sequence 4 from patent U	( 1289)	338	83.7	1.3e-12	gi	23325089	gb AAN23789.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	34427718	gb AAQ71353.1	Sequence 4 from patent	( 1289)	338	83.7	1.3e-12	gi	158456676	gb ABW41349.1	Sequence 29 from paten	( 50)	300	74.6	2.7e-11
gi	40159629	gb AAR66713.1	Sequence 4 from patent	( 1289)	338	83.7	1.3e-12	gi	14103744	gb AAE55178.1	Sequence 29 from patent	( 50)	300	74.6	2.7e-11
gi	59727113	gb AAE12604.1	Sequence 4 from patent U	( 1289)	338	83.7	1.3e-12	gi	160724714	emb CAP40039.1	unnamed protein produ	( 693)	313	78.1	3.3e-11
gi	1831842	gb AAB46296.1	Sequence 4 from patent U	( 1289)	338	83.7	1.3e-12	gi	33731233	gb AAQ37296.1	Sequence 15 from patent	( 137)	304	75.7	3.4e-11
gi	12810188	gb AAE44103.1	Sequence 4 from patent	( 1289)	338	83.7	1.3e-12	gi	53970027	gb AAV19120.1	Sequence 37 from patent	( 137)	304	75.7	3.4e-11
gi	34427044	gb AAQ70971.1	Sequence 3 from patent	( 1289)	338	83.7	1.3e-12	gi	16240162	gb AAE79615.1	Sequence 15 from patent	( 137)	304	75.7	3.4e-11
gi	142770	gb AAA67693.1	delta-endotoxin	( 1289)	338	83.7	1.3e-12	gi	53970016	gb AAV19109.1	Sequence 15 from patent	( 137)	304	75.7	3.4e-11
gi	56664647	gb AAW18072.1	Sequence 32 from patent	( 50)	313	77.4	3.7e-12	gi	16240178	gb AAE79626.1	Sequence 37 from patent	( 137)	304	75.7	3.4e-11
gi	14112750	gb AAE58165.1	Sequence 30 from patent	( 50)	313	77.4	3.7e-12	gi	33731244	gb AAQ37307.1	Sequence 37 from patent	( 137)	304	75.7	3.4e-11

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gi 21504404 gb AAM57103.1	Sequence 37 from patent ( 137)	304	75.7	3.4e-11	gi 4239728 emb CAA10671.1	Cry2Aa protein [Bacillu ( 633)	267	68.0	3.2e-08
gi 21504390 gb AAM57092.1	Sequence 15 from patent ( 137)	304	75.7	3.4e-11	gi 114848912 gb ABT83671.1	insecticidal crystal p ( 633)	267	68.0	3.2e-08
gi 148529680 gb ABQ82088.1	Cry5A-like protein 1 [ ( 502)	310	77.4	4e-11	gi 4239730 emb CAA10672.1	Cry2Aa protein [Bacillu ( 633)	267	68.0	3.2e-08
gi 23325099 gb AAN23799.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 9622200 gb AAF89668.1	AF169251_1 parasporal cry ( 695)	266	67.8	4e-08
gi 56642287 gb AAW12005.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 2921832 gb AAC04867.1	insecticidal crystal pro ( 633)	265	67.6	4.4e-08
gi 17920890 gb AAE86510.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 142732 gb AAA22335.1	P2 crystal protein ( 633)	265	67.6	4.4e-08
gi 14103754 gb AAE55188.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 27447976 gb AAO13750.1	AF273218_1 Cry2Aa [Bacil ( 633)	265	67.6	4.4e-08
gi 56664654 gb AAW18079.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 142746 gb AAA83516.1	insecticidal crystal prot ( 633)	265	67.6	4.4e-08
gi 14112759 gb AAE58174.1	Sequence 39 from patent ( 50)	296	73.7	4.9e-11	gi 45685586 gb AAS75548.1	Cry2Aa [Bacillus thurin ( 633)	265	67.6	4.4e-08
gi 158456686 gb ABW41359.1	Sequence 39 from paten ( 50)	296	73.7	4.9e-11	gi 33314185 gb AAQ04263.1	AF433645_3 Cry2Aa [Bacil ( 633)	265	67.6	4.4e-08
gi 160724710 emb CAP40037.1	unnamed protein produ (1224)	313	78.2	5.3e-11	gi 47678765 emb CAD32378.1	insecticidal crystal p ( 633)	265	67.6	4.4e-08
gi 538378 gb AAA21516.1	delta endotoxin (1186)	308	77.1	1.1e-10	gi 67811088 gb AAAY82083.1	Cry2Aa [Bacillus thurin ( 633)	265	67.6	4.4e-08
gi 5977358 gb AAE14768.1	Sequence 4 from patent U (1186)	307	76.9	1.3e-10	gi 27311150 gb AAO00678.1	Sequence 12 from patent ( 634)	265	67.6	4.4e-08
gi 10051729 gb AAE28636.1	Sequence 4 from patent (1186)	307	76.9	1.3e-10	gi 3716488 emb CAA03661.1	unnamed protein product ( 706)	265	67.6	4.8e-08
gi 1830714 gb AAB45168.1	Sequence 4 from patent U (1186)	307	76.9	1.3e-10	gi 152013907 gb ABS20060.1	dipterans toxic crysta ( 99)	254	64.7	4.9e-08
gi 2484896 gb AAB73032.1	I44121 Sequence 6 from pa (1186)	307	76.9	1.3e-10	gi 27447952 gb AAO13734.1	AF252262_3 insecticidal ( 633)	263	67.2	5.9e-08
gi 160724712 emb CAP40038.1	unnamed protein produ (1235)	306	76.7	1.5e-10	gi 3994349 gb AAC87777.1	AR008751 Sequence 6 from (1257)	266	68.0	6.6e-08
gi 21504393 gb AAM57094.1	Sequence 19 from patent ( 137)	293	73.3	1.8e-10	gi 5972714 gb AAE12605.1	Cry2Aa 6 from patent U (1257)	266	68.0	6.6e-08
gi 33731235 gb AAQ37298.1	Sequence 19 from patent ( 137)	293	73.3	1.8e-10	gi 142772 gb AAA22355.1	delta-endotoxin (1257)	266	68.0	6.6e-08
gi 53970018 gb AAV19111.1	Sequence 19 from patent ( 137)	293	73.3	1.8e-10	gi 1831843 gb AAB46297.1	Sequence 6 from patent U (1257)	266	68.0	6.6e-08
gi 16240166 gb AAE79617.1	Sequence 19 from patent ( 137)	293	73.3	1.8e-10	gi 997763 gb AAA76064.1	Sequence 2 from patent US (1257)	266	68.0	6.6e-08
gi 14103753 gb AAE55187.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 12810189 gb AAE44104.1	Sequence 6 from patent (1257)	266	68.0	6.6e-08
gi 56642286 gb AAW12004.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 40159630 gb AAR66714.1	Sequence 6 from patent (1257)	266	68.0	6.6e-08
gi 17920889 gb AAE86509.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 2096265 gb AAB55097.1	Sequence 6 from patent U (1257)	266	68.0	6.6e-08
gi 14112758 gb AAE58173.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 1429252 emb CAA67506.1	parasporal crystal prot ( 706)	262	67.0	7.5e-08
gi 158456685 gb ABW41358.1	Sequence 38 from paten ( 50)	284	71.1	3e-10	gi 15105505 gb AAE66099.1	Sequence 2 from patent ( 706)	262	67.0	7.5e-08
gi 23325098 gb AAN23798.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 158478175 gb ABW49932.1	Sequence 6 from patent ( 627)	259	66.3	1.1e-07
gi 56664653 gb AAW18078.1	Sequence 38 from patent ( 50)	284	71.1	3e-10	gi 155718052 gb ABU37568.1	Sequence 6 from patent ( 627)	259	66.3	1.1e-07
gi 23325100 gb AAN23800.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 23559628 emb CAD52949.1	unnamed protein produc ( 627)	259	66.3	1.1e-07
gi 14112760 gb AAE58175.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 158456688 gb ABW41361.1	Sequence 41 from paten ( 50)	245	62.6	1.1e-07
gi 56664655 gb AAW18080.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 17920892 gb AAE86512.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 56642288 gb AAW12006.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 56642289 gb AAW12007.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 17920891 gb AAE86511.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 14103756 gb AAE55190.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 158456687 gb ABW41360.1	Sequence 40 from paten ( 50)	283	70.9	3.5e-10	gi 23325101 gb AAN23801.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 14103755 gb AAE55189.1	Sequence 40 from patent ( 50)	283	70.9	3.5e-10	gi 56664656 gb AAW18081.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 152013913 gb ABS20063.1	dipterans toxic crysta ( 108)	287	72.0	3.6e-10	gi 14112761 gb AAE58176.1	Sequence 41 from patent ( 50)	245	62.6	1.1e-07
gi 1831844 gb AAB46298.1	Sequence 8 from patent U (1245)	293	73.9	1.1e-09	gi 16240156 gb AAE79611.1	Sequence 7 from patent ( 137)	250	63.9	1.2e-07
gi 12810190 gb AAE44105.1	Sequence 8 from patent (1245)	293	73.9	1.1e-09	gi 21504385 gb AAM57088.1	Sequence 7 from patent ( 137)	250	63.9	1.2e-07
gi 2096266 gb AAB55098.1	Sequence 8 from patent U (1245)	293	73.9	1.1e-09	gi 53970012 gb AAV19105.1	Sequence 7 from patent ( 137)	250	63.9	1.2e-07
gi 5972715 gb AAE12606.1	Sequence 8 from patent U (1245)	293	73.9	1.1e-09	gi 33731229 gb AAQ37292.1	Sequence 7 from patent ( 137)	250	63.9	1.2e-07
gi 862637 gb AAA68598.1	delta endotoxin (1245)	293	73.9	1.1e-09	gi 155097691 gb ABT00622.1	Sequence 212 from pate ( 634)	257	65.8	1.5e-07
gi 152013915 gb ABS20064.1	dipterans toxic crysta ( 118)	272	68.7	3.8e-09	gi 33731254 gb AAQ37317.1	Sequence 57 from patent ( 137)	246	63.1	2.2e-07
gi 9622198 gb AAF89667.1	AF169250_2 parasporal cry ( 675)	281	71.1	4.1e-09	gi 21504418 gb AAM57113.1	Sequence 57 from patent ( 137)	246	63.1	2.2e-07
gi 155097716 gb ABT00647.1	Sequence 261 from pate ( 632)	276	70.0	8.2e-09	gi 16240190 gb AAE79636.1	Sequence 57 from patent ( 137)	246	63.1	2.2e-07
gi 112088020 gb ABT06943.1	Sequence 2 from patent ( 632)	276	70.0	8.2e-09	gi 53970037 gb AAV19130.1	Sequence 57 from patent ( 137)	246	63.1	2.2e-07
gi 158478173 gb ABW49930.1	Sequence 2 from patent ( 632)	276	70.0	8.2e-09	gi 116808704 emb CAL64717.1	unnamed protein produ ( 717)	255	65.4	2.2e-07
gi 155718050 gb ABU37566.1	Sequence 2 from patent ( 632)	276	70.0	8.2e-09	gi 155097701 gb ABT00632.1	Sequence 232 from pate ( 634)	253	65.0	2.7e-07
gi 33765711 gb AAQ52362.1	Sequence 2 from patent ( 632)	276	70.0	8.2e-09	gi 155097654 gb ABT00585.1	Sequence 138 from pate ( 634)	252	64.8	3.1e-07
gi 13537893 emb CAC35761.1	unnamed protein produc ( 632)	276	70.0	8.2e-09	gi 155097589 gb ABT00520.1	Sequence 8 from patent ( 634)	251	64.5	3.6e-07
gi 23559624 emb CAD52947.1	unnamed protein produc ( 632)	276	70.0	8.2e-09	gi 155097693 gb ABT00624.1	Sequence 216 from pate ( 634)	250	64.3	4.2e-07
gi 155718053 gb ABU37569.1	Sequence 8 from patent ( 633)	276	70.0	8.2e-09	gi 155097640 gb ABT00571.1	Sequence 110 from pate ( 634)	249	64.1	4.9e-07
gi 158478176 gb ABW49933.1	Sequence 8 from patent ( 633)	276	70.0	8.2e-09	gi 155097616 gb ABT00547.1	Sequence 62 from paten ( 634)	249	64.1	4.9e-07
gi 23559631 emb CAD52950.1	unnamed protein produc ( 633)	276	70.0	8.2e-09	gi 155097674 gb ABT00605.1	Sequence 178 from pate ( 634)	249	64.1	4.9e-07
gi 13537919 emb CAC35768.1	unnamed protein produc ( 635)	275	69.8	9.6e-09	gi 155097617 gb ABT00548.1	Sequence 64 from paten ( 634)	249	64.1	4.9e-07
gi 112088060 gb ABT06965.1	Sequence 46 from paten ( 635)	275	69.8	9.6e-09	gi 155097647 gb ABT00578.1	Sequence 124 from pate ( 634)	249	64.1	4.9e-07
gi 12822553 gb AAE48994.1	Sequence 4 from patent ( 635)	275	69.8	9.6e-09	gi 155097614 gb ABT00545.1	Sequence 58 from paten ( 634)	249	64.1	4.9e-07
gi 33765733 gb AAQ52384.1	Sequence 46 from patent ( 635)	275	69.8	9.6e-09	gi 21504415 gb AAM57111.1	Sequence 53 from patent ( 137)	240	61.8	5.4e-07
gi 5834516 emb CAA10670.2	Cry2A protein [Bacillus ( 551)	267	68.0	2.9e-08	gi 53970035 gb AAV19128.1	Sequence 53 from patent ( 137)	240	61.8	5.4e-07
gi 129307220 gb ABO30519.1	Cry2Afl1 [Bacillus thur ( 626)	267	68.0	3.2e-08	gi 16240188 gb AAE79634.1	Sequence 53 from patent ( 137)	240	61.8	5.4e-07

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gi	33731252	gb	AAQ37315.1	Sequence 53 from patent ( 137)	240	61.8	5.4e-07	gi	85717888	gb	ABC74968.1	crystal delta-endotoxin ( 633)	240	62.1	1.9e-06
gi	155097628	gb	ABT00559.1	Sequence 86 from patent ( 634)	248	63.9	5.7e-07	gi	155097665	gb	ABT00596.1	Sequence 160 from pate ( 634)	240	62.1	1.9e-06
gi	86440157	gb	ABC95997.1	Cry2Ac [Bacillus thurin ( 623)	247	63.7	6.5e-07	gi	155097669	gb	ABT00600.1	Sequence 168 from pate ( 634)	240	62.1	1.9e-06
gi	120431602	gb	ABM21764.1	cry2A-type insecticida ( 633)	246	63.4	7.7e-07	gi	155097637	gb	ABT00568.1	Sequence 104 from pate ( 634)	240	62.1	1.9e-06
gi	155097657	gb	ABT00588.1	Sequence 144 from pate ( 634)	246	63.4	7.7e-07	gi	155097660	gb	ABT00591.1	Sequence 150 from pate ( 634)	240	62.1	1.9e-06
gi	155097671	gb	ABT00602.1	Sequence 172 from pate ( 634)	246	63.4	7.7e-07	gi	155097652	gb	ABT00583.1	Sequence 134 from pate ( 634)	240	62.1	1.9e-06
gi	155097622	gb	ABT00553.1	Sequence 74 from paten ( 634)	246	63.4	7.7e-07	gi	155097659	gb	ABT00590.1	Sequence 148 from pate ( 634)	240	62.1	1.9e-06
gi	155097646	gb	ABT00577.1	Sequence 122 from pate ( 634)	246	63.4	7.7e-07	gi	33731242	gb	AAQ37305.1	Sequence 33 from patent ( 136)	231	59.8	2.1e-06
gi	155097655	gb	ABT00586.1	Sequence 140 from pate ( 634)	246	63.4	7.7e-07	gi	33731250	gb	AAQ37313.1	Sequence 49 from patent ( 136)	231	59.8	2.1e-06
gi	155097663	gb	ABT00594.1	Sequence 156 from pate ( 634)	246	63.4	7.7e-07	gi	21504402	gb	AAM57101.1	Sequence 33 from patent ( 136)	231	59.8	2.1e-06
gi	155097690	gb	ABT00621.1	Sequence 210 from pate ( 634)	246	63.4	7.7e-07	gi	33731256	gb	AAQ37319.1	Sequence 61 from patent ( 136)	231	59.8	2.1e-06
gi	155097685	gb	ABT00616.1	Sequence 200 from pate ( 634)	246	63.4	7.7e-07	gi	16240172	gb	AAE79622.1	Sequence 29 from patent ( 136)	231	59.8	2.1e-06
gi	155097588	gb	ABT00519.1	Sequence 6 from patent ( 634)	246	63.4	7.7e-07	gi	33731240	gb	AAQ37303.1	Sequence 29 from patent ( 136)	231	59.8	2.1e-06
gi	155097658	gb	ABT00597.1	Sequence 162 from pate ( 634)	245	63.2	9e-07	gi	53970033	gb	AAV19126.1	Sequence 49 from patent ( 136)	231	59.8	2.1e-06
gi	155097680	gb	ABT00611.1	Sequence 190 from pate ( 634)	245	63.2	9e-07	gi	53970023	gb	AAV19116.1	Sequence 29 from patent ( 136)	231	59.8	2.1e-06
gi	155097620	gb	ABT00551.1	Sequence 70 from paten ( 634)	245	63.2	9e-07	gi	53970025	gb	AAV19118.1	Sequence 33 from patent ( 136)	231	59.8	2.1e-06
gi	85717890	gb	ABC74969.1	crystal delta-endotoxin ( 623)	244	63.0	1e-06	gi	21504412	gb	AAM57109.1	Sequence 49 from patent ( 136)	231	59.8	2.1e-06
gi	124841305	gb	ABN15104.1	insecticidal crystal p ( 623)	244	63.0	1e-06	gi	16240399	gb	AAM57099.1	Sequence 29 from patent ( 136)	231	59.8	2.1e-06
gi	155097687	gb	ABT00618.1	Sequence 204 from pate ( 634)	244	63.0	1e-06	gi	16240176	gb	AAE79624.1	Sequence 33 from patent ( 136)	231	59.8	2.1e-06
gi	155097658	gb	ABT00589.1	Sequence 146 from pate ( 634)	244	63.0	1e-06	gi	21504420	gb	AAM57115.1	Sequence 61 from patent ( 136)	231	59.8	2.1e-06
gi	155097594	gb	ABT00525.1	Sequence 18 from paten ( 634)	244	63.0	1e-06	gi	16240039	gb	AAV19132.1	Sequence 61 from patent ( 136)	231	59.8	2.1e-06
gi	155097625	gb	ABT00556.1	Sequence 80 from paten ( 634)	244	63.0	1e-06	gi	16240184	gb	AAE79632.1	Sequence 49 from patent ( 136)	231	59.8	2.1e-06
gi	155097648	gb	ABT00579.1	Sequence 126 from pate ( 634)	244	63.0	1e-06	gi	16240192	gb	AAE79638.1	Sequence 61 from patent ( 136)	231	59.8	2.1e-06
gi	155097668	gb	ABT00599.1	Sequence 166 from pate ( 634)	244	63.0	1e-06	gi	155097590	gb	ABT00521.1	Sequence 10 from paten ( 634)	239	61.9	2.2e-06
gi	155097670	gb	ABT00601.1	Sequence 170 from pate ( 634)	244	63.0	1e-06	gi	155097694	gb	ABT00625.1	Sequence 218 from pate ( 634)	239	61.9	2.2e-06
gi	155097624	gb	ABT00555.1	Sequence 78 from paten ( 634)	244	63.0	1e-06	gi	155097610	gb	ABT00541.1	Sequence 50 from paten ( 634)	239	61.9	2.2e-06
gi	155097656	gb	ABT00587.1	Sequence 142 from pate ( 634)	244	63.0	1e-06	gi	21504391	gb	AAM57093.1	Sequence 17 from patent ( 136)	230	59.6	2.4e-06
gi	155097697	gb	ABT00628.1	Sequence 224 from pate ( 634)	244	63.0	1e-06	gi	16240164	gb	AAE79616.1	Sequence 17 from patent ( 136)	230	59.6	2.4e-06
gi	155097638	gb	ABT00569.1	Sequence 106 from pate ( 634)	244	63.0	1e-06	gi	33731234	gb	AAQ37297.1	Sequence 17 from patent ( 136)	230	59.6	2.4e-06
gi	155097612	gb	ABT00543.1	Sequence 54 from paten ( 634)	244	63.0	1e-06	gi	53970017	gb	AAV19110.1	Sequence 17 from patent ( 136)	230	59.6	2.4e-06
gi	155097615	gb	ABT00546.1	Sequence 60 from paten ( 634)	244	63.0	1e-06	gi	86161588	gb	ABC86927.1	crystal protein Cry2Ad ( 633)	238	61.7	2.6e-06
gi	155097662	gb	ABT00593.1	Sequence 154 from pate ( 634)	244	63.0	1e-06	gi	81051716	gb	ABB55273.1	crystal protein Cry2Ad2 ( 633)	238	61.7	2.6e-06
gi	155097672	gb	ABT00603.1	Sequence 174 from pate ( 634)	244	63.0	1e-06	gi	6457578	gb	AAF09583.1	AF200816_1 crystal protei ( 633)	238	61.7	2.6e-06
gi	155097678	gb	ABT00609.1	Sequence 186 from pate ( 634)	244	63.0	1e-06	gi	12822555	gb	AAE48996.1	Sequence 8 from patent ( 633)	238	61.7	2.6e-06
gi	155097621	gb	ABT00552.1	Sequence 72 from paten ( 634)	244	63.0	1e-06	gi	118566336	gb	ABL01536.1	crystal protein [Bacil ( 633)	238	61.7	2.6e-06
gi	155097618	gb	ABT00549.1	Sequence 66 from paten ( 634)	243	62.8	1.2e-06	gi	155097704	gb	ABT00635.1	Sequence 238 from pate ( 634)	238	61.7	2.6e-06
gi	155097630	gb	ABT00561.1	Sequence 90 from paten ( 634)	243	62.8	1.2e-06	gi	155097613	gb	ABT00544.1	Sequence 56 from paten ( 634)	238	61.7	2.6e-06
gi	72117495	gb	AAZ59758.1	Twin-arginine transloca ( 493)	241	62.3	1.3e-06	gi	155097675	gb	ABT00606.1	Sequence 180 from pate ( 634)	238	61.7	2.6e-06
gi	66734543	gb	AAZ53629.1	Cry2Ac [Bacillus thurin ( 623)	242	62.6	1.4e-06	gi	155097688	gb	ABT00619.1	Sequence 206 from pate ( 634)	238	61.7	2.6e-06
gi	37540131	gb	AAG35410.1	insecticidal crystal pr ( 623)	242	62.6	1.4e-06	gi	21504398	gb	AAM57098.1	Sequence 27 from patent ( 136)	229	59.4	2.8e-06
gi	85700968	gb	ABC74793.1	insecticidal crystal pr ( 623)	242	62.6	1.4e-06	gi	53970022	gb	AAV19115.1	Sequence 27 from patent ( 136)	229	59.4	2.8e-06
gi	12822554	gb	AAE48995.1	Sequence 6 from patent ( 623)	242	62.6	1.4e-06	gi	16240170	gb	AAE79621.1	Sequence 27 from patent ( 136)	229	59.4	2.8e-06
gi	112088062	gb	ABI06966.1	Sequence 48 from paten ( 625)	242	62.6	1.4e-06	gi	33731239	gb	AAQ37302.1	Sequence 27 from patent ( 136)	229	59.4	2.8e-06
gi	33765734	gb	AAQ52385.1	Sequence 48 from patent ( 625)	242	62.6	1.4e-06	gi	72133015	gb	AAZ66347.1	delta endotoxin [Bacill ( 633)	237	61.5	3e-06
gi	13537921	emb	CAC35769.1	unnamed protein produc ( 625)	242	62.6	1.4e-06	gi	142748	gb	AAA22342.1	crystal protein B2 ( 633)	237	61.5	3e-06
gi	155097707	gb	ABT00638.1	Sequence 244 from pate ( 634)	242	62.6	1.4e-06	gi	86440155	gb	ABC95996.1	Cry2Ab [Bacillus thurin ( 633)	237	61.5	3e-06
gi	155097626	gb	ABT00557.1	Sequence 82 from paten ( 634)	242	62.6	1.4e-06	gi	11526737	gb	AAG36762.1	Cry2Ab [Bacillus thurin ( 633)	237	61.5	3e-06
gi	155097683	gb	ABT00614.1	Sequence 196 from pate ( 634)	242	62.6	1.4e-06	gi	27311151	gb	AAO00679.1	Sequence 18 from patent ( 633)	237	61.5	3e-06
gi	155097703	gb	ABT00634.1	Sequence 236 from pate ( 634)	242	62.6	1.4e-06	gi	40312	emb	CAA39075.1	crystal protein CryIIB [B ( 633)	237	61.5	3e-06
gi	155097715	gb	ABT00646.1	Sequence 260 from pate ( 634)	242	62.6	1.4e-06	gi	31872007	gb	AAP59457.1	crystal delta-endotoxin ( 633)	237	61.5	3e-06
gi	155097689	gb	ABT00620.1	Sequence 208 from pate ( 634)	242	62.6	1.4e-06	gi	27436036	gb	AAO13296.1	AF336115_1 crystal delta ( 633)	237	61.5	3e-06
gi	155097702	gb	ABT00633.1	Sequence 234 from pate ( 634)	242	62.6	1.4e-06	gi	155097708	gb	ABT00639.1	Sequence 246 from pate ( 634)	237	61.5	3e-06
gi	155097700	gb	ABT00631.1	Sequence 230 from pate ( 634)	242	62.6	1.4e-06	gi	155097714	gb	ABT00645.1	Sequence 258 from pate ( 634)	237	61.5	3e-06
gi	155097591	gb	ABT00522.1	Sequence 12 from paten ( 634)	241	62.4	1.6e-06	gi	155097619	gb	ABT00550.1	Sequence 68 from paten ( 634)	237	61.5	3e-06
gi	155097623	gb	ABT00554.1	Sequence 76 from paten ( 634)	241	62.4	1.6e-06	gi	27311145	gb	AAO00673.1	Sequence 2 from patent ( 634)	237	61.5	3e-06
gi	155097684	gb	ABT00615.1	Sequence 198 from pate ( 634)	241	62.4	1.6e-06	gi	155097664	gb	ABT00595.1	Sequence 158 from pate ( 634)	237	61.5	3e-06
gi	155097592	gb	ABT00523.1	Sequence 14 from paten ( 634)	241	62.4	1.6e-06	gi	155097696	gb	ABT00627.1	Sequence 222 from pate ( 634)	237	61.5	3e-06
gi	155097593	gb	ABT00524.1	Sequence 16 from paten ( 634)	241	62.4	1.6e-06	gi	155097633	gb	ABT00564.1	Sequence 96 from paten ( 634)	237	61.5	3e-06
gi	155097603	gb	ABT00534.1	Sequence 36 from paten ( 634)	241	62.4	1.6e-06	gi	155097695	gb	ABT00626.1	Sequence 220 from pate ( 634)	237	61.5	3e-06

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gi	155097677	gb	ABT00608.1	Sequence 184 from pate ( 634)	237	61.5	3e-06
gi	155097635	gb	ABT00566.1	Sequence 100 from pate ( 634)	237	61.5	3e-06
gi	120431606	gb	ABM21766.1	cry2Ab-type insecticid ( 633)	236	61.3	3.5e-06
gi	155097641	gb	ABT00572.1	Sequence 112 from pate ( 634)	236	61.3	3.5e-06
gi	155097712	gb	ABT00643.1	Sequence 254 from pate ( 634)	236	61.3	3.5e-06
gi	155097699	gb	ABT00630.1	Sequence 228 from pate ( 634)	236	61.3	3.5e-06
gi	155097636	gb	ABT00567.1	Sequence 102 from pate ( 634)	236	61.3	3.5e-06
gi	155097649	gb	ABT00580.1	Sequence 128 from pate ( 634)	236	61.3	3.5e-06
gi	155097679	gb	ABT00610.1	Sequence 188 from pate ( 634)	236	61.3	3.5e-06
gi	155097629	gb	ABT00560.1	Sequence 88 from paten ( 634)	236	61.3	3.5e-06
gi	116248655	gb	ABT90464.1	Cry2Ad [Bacillus thuri ( 432)	233	60.5	4e-06
gi	155718051	gb	ABU37567.1	Sequence 4 from patent ( 632)	235	61.0	4.1e-06
gi	155097586	gb	ABT00517.1	Sequence 2 from patent ( 632)	235	61.0	4.1e-06
gi	23559626	emb	CAD52948.1	unnamed protein produc ( 632)	235	61.0	4.1e-06
gi	158478174	gb	ABW49931.1	Sequence 4 from patent ( 632)	235	61.0	4.1e-06
gi	155097604	gb	ABT00535.1	Sequence 38 from paten ( 633)	235	61.0	4.1e-06
gi	155097601	gb	ABT00532.1	Sequence 32 from paten ( 633)	235	61.0	4.1e-06
gi	33316454	gb	AAQ04609.1	AF441855_1 Cry2Ab [Bacil ( 633)	235	61.0	4.1e-06
gi	12822556	gb	AAE48997.1	Sequence 10 from patent ( 633)	235	61.0	4.1e-06
gi	155097609	gb	ABT00540.1	Sequence 48 from paten ( 634)	235	61.0	4.1e-06
gi	155097608	gb	ABT00539.1	Sequence 46 from paten ( 634)	235	61.0	4.1e-06
gi	155097599	gb	ABT00530.1	Sequence 28 from paten ( 634)	235	61.0	4.1e-06
gi	155097713	gb	ABT00644.1	Sequence 256 from pate ( 634)	235	61.0	4.1e-06
gi	155097605	gb	ABT00536.1	Sequence 40 from paten ( 634)	235	61.0	4.1e-06
gi	155097676	gb	ABT00607.1	Sequence 182 from pate ( 634)	235	61.0	4.1e-06
gi	155097611	gb	ABT00542.1	Sequence 52 from paten ( 634)	235	61.0	4.1e-06
gi	155097595	gb	ABT00526.1	Sequence 20 from paten ( 634)	235	61.0	4.1e-06
gi	155097607	gb	ABT00538.1	Sequence 44 from paten ( 634)	235	61.0	4.1e-06
gi	155097606	gb	ABT00537.1	Sequence 42 from paten ( 634)	235	61.0	4.1e-06
gi	155097709	gb	ABT00640.1	Sequence 248 from pate ( 634)	235	61.0	4.1e-06
gi	155097600	gb	ABT00531.1	Sequence 30 from paten ( 634)	235	61.0	4.1e-06
gi	155097686	gb	ABT00617.1	Sequence 202 from pate ( 634)	235	61.0	4.1e-06
gi	155097651	gb	ABT00582.1	Sequence 132 from pate ( 634)	235	61.0	4.1e-06
gi	155097642	gb	ABT00573.1	Sequence 114 from pate ( 634)	235	61.0	4.1e-06
gi	155097667	gb	ABT00598.1	Sequence 164 from pate ( 634)	235	61.0	4.1e-06
gi	155097645	gb	ABT00576.1	Sequence 120 from pate ( 634)	235	61.0	4.1e-06
gi	155097634	gb	ABT00565.1	Sequence 98 from paten ( 634)	235	61.0	4.1e-06
gi	155097602	gb	ABT00533.1	Sequence 34 from paten ( 634)	235	61.0	4.1e-06
gi	155097596	gb	ABT00527.1	Sequence 22 from paten ( 634)	235	61.0	4.1e-06
gi	155097710	gb	ABT00641.1	Sequence 250 from pate ( 634)	235	61.0	4.1e-06
gi	155097673	gb	ABT00604.1	Sequence 176 from pate ( 634)	235	61.0	4.1e-06
gi	155097698	gb	ABT00629.1	Sequence 226 from pate ( 634)	235	61.0	4.1e-06
gi	155097653	gb	ABT00584.1	Sequence 136 from pate ( 634)	235	61.0	4.1e-06
gi	155097639	gb	ABT00570.1	Sequence 108 from pate ( 634)	235	61.0	4.1e-06
gi	155097632	gb	ABT00563.1	Sequence 94 from paten ( 634)	234	60.8	4.7e-06
gi	155097705	gb	ABT00636.1	Sequence 240 from pate ( 634)	234	60.8	4.7e-06
gi	16240189	gb	AAE79635.1	Sequence 55 from patent ( 136)	225	58.5	5.2e-06
gi	53970036	gb	AAV19129.1	Sequence 55 from patent ( 136)	225	58.5	5.2e-06
gi	33731253	gb	AAQ37316.1	Sequence 55 from patent ( 136)	225	58.5	5.2e-06
gi	21504416	gb	AAM57112.1	Sequence 55 from patent ( 136)	225	58.5	5.2e-06
gi	155097631	gb	ABT00562.1	Sequence 92 from paten ( 634)	233	60.6	5.5e-06
gi	155097597	gb	ABT00528.1	Sequence 24 from paten ( 634)	233	60.6	5.5e-06
gi	155097644	gb	ABT00575.1	Sequence 118 from pate ( 634)	233	60.6	5.5e-06
gi	155097627	gb	ABT00558.1	Sequence 84 from paten ( 634)	233	60.6	5.5e-06
gi	155097706	gb	ABT00637.1	Sequence 242 from pate ( 634)	233	60.6	5.5e-06
gi	53970030	gb	AAV19123.1	Sequence 43 from patent ( 136)	224	58.3	6e-06
gi	21504408	gb	AAM57106.1	Sequence 43 from patent ( 136)	224	58.3	6e-06
gi	33731247	gb	AAQ37310.1	Sequence 43 from patent ( 136)	224	58.3	6e-06
gi	16240181	gb	AAE79629.1	Sequence 43 from patent ( 136)	224	58.3	6e-06
gi	155097650	gb	ABT00581.1	Sequence 130 from pate ( 634)	232	60.4	6.4e-06
gi	155097692	gb	ABT00623.1	Sequence 214 from pate ( 634)	231	60.2	7.5e-06
gi	155097587	gb	ABT00518.1	Sequence 4 from patent ( 634)	230	60.0	8.7e-06
gi	155097598	gb	ABT00529.1	Sequence 26 from paten ( 634)	230	60.0	8.7e-06
gi	53970013	gb	AAV19106.1	Sequence 9 from patent ( 136)	221	57.6	9.5e-06
gi	16240157	gb	AAE79612.1	Sequence 9 from patent ( 136)	221	57.6	9.5e-06
gi	21504386	gb	AAM57089.1	Sequence 9 from patent ( 136)	221	57.6	9.5e-06
gi	33731230	gb	AAQ37293.1	Sequence 9 from patent ( 136)	221	57.6	9.5e-06
gi	53970032	gb	AAV19125.1	Sequence 47 from patent ( 142)	221	57.6	9.8e-06
gi	21504411	gb	AAM57108.1	Sequence 47 from patent ( 142)	221	57.6	9.8e-06
gi	16240183	gb	AAE79631.1	Sequence 47 from patent ( 142)	221	57.6	9.8e-06
gi	33731249	gb	AAQ37312.1	Sequence 47 from patent ( 142)	221	57.6	9.8e-06
gi	155097711	gb	ABT00642.1	Sequence 252 from pate ( 634)	228	59.5	1.2e-05
gi	155097643	gb	ABT00574.1	Sequence 116 from pate ( 634)	227	59.3	1.4e-05
gi	21504410	gb	AAM57107.1	Sequence 45 from patent ( 137)	218	57.0	1.5e-05
gi	53970031	gb	AAV19124.1	Sequence 45 from patent ( 137)	218	57.0	1.5e-05
gi	33731248	gb	AAQ37311.1	Sequence 45 from patent ( 137)	218	57.0	1.5e-05
gi	16240182	gb	AAE79630.1	Sequence 45 from patent ( 137)	218	57.0	1.5e-05
gi	155097682	gb	ABT00613.1	Sequence 194 from pate ( 634)	226	59.1	1.6e-05
gi	16240191	gb	AAE79637.1	Sequence 59 from patent ( 142)	216	56.5	2.1e-05
gi	33731255	gb	AAQ37318.1	Sequence 59 from patent ( 142)	216	56.5	2.1e-05
gi	53970038	gb	AAV19131.1	Sequence 59 from patent ( 142)	216	56.5	2.1e-05
gi	33731241	gb	AAQ37304.1	Sequence 31 from patent ( 142)	216	56.5	2.1e-05
gi	21504419	gb	AAM57114.1	Sequence 59 from patent ( 142)	216	56.5	2.1e-05
gi	16240174	gb	AAE79623.1	Sequence 31 from patent ( 142)	216	56.5	2.1e-05
gi	53970024	gb	AAV19117.1	Sequence 31 from patent ( 142)	216	56.5	2.1e-05
gi	21504400	gb	AAM57100.1	Sequence 31 from patent ( 142)	216	56.5	2.1e-05
gi	112088035	gb	ABT06950.1	Sequence 16 from paten ( 132)	215	56.3	2.3e-05
gi	33765718	gb	AAQ52369.1	Sequence 16 from patent ( 132)	215	56.3	2.3e-05
gi	155097681	gb	ABT00612.1	Sequence 192 from pate ( 634)	222	58.2	2.9e-05
gi	16240177	gb	AAE79625.1	Sequence 35 from patent ( 137)	213	55.9	3.2e-05
gi	16240179	gb	AAE79627.1	Sequence 39 from patent ( 137)	213	55.9	3.2e-05
gi	53970034	gb	AAV19127.1	Sequence 51 from patent ( 137)	213	55.9	3.2e-05
gi	33731251	gb	AAQ37314.1	Sequence 51 from patent ( 137)	213	55.9	3.2e-05
gi	21504406	gb	AAM57104.1	Sequence 39 from patent ( 137)	213	55.9	3.2e-05
gi	53970028	gb	AAV19121.1	Sequence 39 from patent ( 137)	213	55.9	3.2e-05
gi	53970026	gb	AAV19119.1	Sequence 35 from patent ( 137)	213	55.9	3.2e-05
gi	21504414	gb	AAM57110.1	Sequence 51 from patent ( 137)	213	55.9	3.2e-05
gi	16240186	gb	AAE79633.1	Sequence 51 from patent ( 137)	213	55.9	3.2e-05
gi	33731245	gb	AAQ37308.1	Sequence 39 from patent ( 137)	213	55.9	3.2e-05
gi	21504403	gb	AAM57102.1	Sequence 35 from patent ( 137)	213	55.9	3.2e-05
gi	33731243	gb	AAQ37306.1	Sequence 35 from patent ( 137)	213	55.9	3.2e-05
gi	155097661	gb	ABT00592.1	Sequence 152 from pate ( 633)	221	58.0	3.4e-05
gi	40286	emb	CAA40536.1	CryIIC delta-endotoxin [B ( 622)	217	57.1	6.1e-05
gi	53970015	gb	AAV19108.1	Sequence 13 from patent ( 135)	207	54.6	7.8e-05
gi	33731232	gb	AAQ37295.1	Sequence 13 from patent ( 135)	207	54.6	7.8e-05
gi	21504389	gb	AAM57091.1	Sequence 13 from patent ( 135)	207	54.6	7.8e-05
gi	16240160	gb	AAE79614.1	Sequence 13 from patent ( 135)	207	54.6	7.8e-05
gi	53970014	gb	AAV19107.1	Sequence 11 from patent ( 137)	202	53.5	0.00017
gi	16240158	gb	AAE79613.1	Sequence 11 from patent ( 137)	202	53.5	0.00017
gi	21504388	gb	AAM57090.1	Sequence 11 from patent ( 137)	202	53.5	0.00017
gi	33731231	gb	AAQ37294.1	Sequence 11 from patent ( 137)	202	53.5	0.00017
gi	592658	gb	AA54265.1	Sequence 1 from Patent WO ( 99)	197	52.3	0.00027
gi	19916590	gb	AAM06002.1	hypothetical protein MA ( 171)	191	51.1	0.0011
gi	19916590	gb	AAM06002.1	hypothetical protein MA ( 171)	191	51.1	0.0011
gi	33765717	gb	AAQ52368.1	Sequence 14 from patent ( 93)	186	49.9	0.0014
gi	112088034	gb	ABI06949.1	Sequence 14 from paten ( 93)	186	49.9	0.0014
gi	14112762	gb	AAE58177.1	Sequence 42 from patent ( 50)	182	48.9	0.0015
gi	17920893	gb	AAE86513.1	Sequence 42 from patent ( 50)	182	48.9	0.0015

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gi	158456689 gb ABW41362.1	Sequence 42 from paten	( 50)	182	48.9	0.0015
gi	23325102 gb AAN23802.1	Sequence 42 from patent	( 50)	182	48.9	0.0015
gi	56664657 gb AAW18082.1	Sequence 42 from patent	( 50)	182	48.9	0.0015
gi	56642290 gb AAW12008.1	Sequence 42 from patent	( 50)	182	48.9	0.0015
gi	14103757 gb AAE55191.1	Sequence 42 from patent	( 50)	182	48.9	0.0015
gi	116808700 emb CAL64715.1	unnamed protein produ	( 700)	194	52.1	0.0022
gi	17920885 gb AAE86505.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	23325094 gb AAN23794.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	56642282 gb AAW12000.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	56642281 gb AAW11999.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	158456680 gb ABW41353.1	Sequence 33 from paten	( 50)	179	48.2	0.0024
gi	14103749 gb AAE55183.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	56664648 gb AAW18073.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	56664649 gb AAW18074.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	17920884 gb AAE86504.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	14112754 gb AAE58169.1	Sequence 34 from patent	( 50)	179	48.2	0.0024
gi	23325093 gb AAN23793.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	14112753 gb AAE58168.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	158456681 gb ABW41354.1	Sequence 34 from paten	( 50)	179	48.2	0.0024
gi	14103748 gb AAE55182.1	Sequence 33 from patent	( 50)	179	48.2	0.0024
gi	112088032 gb ABI06948.1	Sequence 12 from paten	( 102)	182	49.0	0.0027
gi	33765716 gb AAQ52367.1	Sequence 12 from patent	( 102)	182	49.0	0.0027
gi	23325103 gb AAN23803.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	56642291 gb AAW12009.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	158456690 gb ABW41363.1	Sequence 43 from paten	( 50)	175	47.3	0.0043
gi	17920894 gb AAE86514.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	56664658 gb AAW18083.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	14103758 gb AAE55192.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	14112763 gb AAE58178.1	Sequence 43 from patent	( 50)	175	47.3	0.0043
gi	112088031 gb ABI06947.1	Sequence 10 from paten	( 113)	179	48.4	0.0047
gi	33765715 gb AAQ52366.1	Sequence 10 from patent	( 113)	179	48.4	0.0047
gi	51998352 emb CAH33948.1	unnamed protein produc	( 735)	187	50.6	0.0066
gi	33765714 gb AAQ52365.1	Sequence 8 from patent	( 109)	174	47.3	0.0096
gi	112088030 gb ABI06946.1	Sequence 8 from patent	( 109)	174	47.3	0.0096
gi	2302646 emb CAA03156.1	unnamed protein product	( 312)	177	48.2	0.015
gi	12806992 gb AAE42889.1	Sequence 2 from patent	( 312)	177	48.2	0.015
gi	51998356 emb CAH33950.1	unnamed protein produc	( 694)	181	49.3	0.016
gi	51998354 emb CAH33949.1	unnamed protein produc	( 744)	181	49.3	0.016
gi	33765723 gb AAQ52374.1	Sequence 26 from patent	( 62)	165	45.2	0.024
gi	112088043 gb ABI06955.1	Sequence 26 from paten	( 62)	165	45.2	0.024
gi	971347 emb CAA60504.1	mosquitocidal toxin [Bac	( 724)	178	48.6	0.025
gi	2302648 emb CAA03157.1	unnamed protein product	( 724)	178	48.6	0.025
gi	12806993 gb AAE42890.1	Sequence 4 from patent	( 724)	178	48.6	0.025
gi	12806994 gb AAE42891.1	Sequence 6 from patent	( 725)	178	48.6	0.025
gi	21685428 emb CAD30081.1	pesticidal crystal pr	( 643)	175	48.0	0.036
gi	592275 gb AAA53882.1	Sequence 2 from Patent WO	( 643)	175	48.0	0.036
gi	142763 gb AAA22352.1	mosquito-toxic crystal pr	( 643)	175	48.0	0.036
gi	12806995 gb AAE42892.1	Sequence 7 from patent	( 644)	175	48.0	0.036
gi	88687362 dbj BAE79809.1	Cry31-like 82-kDa prot	( 726)	169	46.7	0.099
gi	1612048 gb AAB15028.1	Sequence 3 from patent U	( 19)	147	41.0	0.13
gi	34426439 gb AAQ70692.1	Sequence 1 from patent	( 19)	147	41.0	0.13
gi	23325095 gb AAN23795.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	56664650 gb AAW18075.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	158456682 gb ABW41355.1	Sequence 35 from paten	( 50)	151	42.1	0.16
gi	56642283 gb AAW12001.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	17920886 gb AAE86506.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	14103750 gb AAE55184.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	14112755 gb AAE58170.1	Sequence 35 from patent	( 50)	151	42.1	0.16
gi	114842165 dbj BAF32570.1	hypothetical protein	( 726)	163	45.4	0.25

gi	4033727 gb AAC97162.1	d-endotoxin [Bacillus th	( 750)	163	45.4	0.25
gi	136352573 gb EBN58813.1	hypothetical protein G	( 416)	159	44.4	0.28
gi	112088059 gb ABI06964.1	Sequence 44 from paten	( 72)	149	41.7	0.3
gi	33765732 gb AAQ52383.1	Sequence 44 from patent	( 72)	149	41.7	0.3
gi	33731238 gb AAQ37301.1	Sequence 25 from patent	( 108)	150	42.1	0.36
gi	53970021 gb AAV19114.1	Sequence 25 from patent	( 108)	150	42.1	0.36
gi	21504396 gb AAM57097.1	Sequence 25 from patent	( 108)	150	42.1	0.36
gi	16240169 gb BAE79620.1	Sequence 25 from patent	( 108)	150	42.1	0.36
gi	75812162 dbj BAE44985.1	hypothetical protein [	( 378)	155	43.5	0.48
gi	145843786 gb ABP96900.1	cry4B [Bacillus thurin	( 94)	147	41.4	0.51
gi	118640569 gb ABL09855.1	Cry4B [Bacillus thurin	( 95)	147	41.4	0.51
gi	68348789 gb AAV96321.1	cry4A insecticidal prot	( 145)	149	41.9	0.54
gi	56642285 gb AAW12003.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	17920888 gb AAE86508.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	14103752 gb AAE55186.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	56664652 gb AAW18077.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	56642297 gb AAW12015.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	23325097 gb AAN23797.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	158456684 gb ABW41357.1	Sequence 37 from paten	( 50)	143	40.3	0.55
gi	14112757 gb AAE58172.1	Sequence 37 from patent	( 50)	143	40.3	0.55
gi	17920900 gb AAE86520.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	14103764 gb AAE55198.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	14112769 gb AAE58184.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	23325109 gb AAN23809.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	56664664 gb AAW18089.1	Sequence 49 from patent	( 50)	143	40.3	0.55
gi	158456696 gb ABW41369.1	Sequence 49 from paten	( 50)	143	40.3	0.55
gi	75812164 dbj BAE44986.1	hypothetical protein [	( 397)	154	43.3	0.58
gi	14112756 gb AAE58171.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	56642284 gb AAW12002.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	23325096 gb AAN23796.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	56664651 gb AAW18076.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	14103751 gb AAE55185.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	158456683 gb ABW41356.1	Sequence 36 from paten	( 50)	142	40.1	0.64
gi	17920887 gb AAE86507.1	Sequence 36 from patent	( 50)	142	40.1	0.64
gi	75812158 dbj BAE44983.1	hypothetical protein [	( 397)	152	42.8	0.79
gi	88687360 dbj BAE79808.1	Cry31-like 81-kDa prot	( 723)	155	43.6	0.82
gi	9798640 dbj BAB11757.1	81-kDa leukemia toxin [	( 723)	155	43.6	0.82
gi	114842169 dbj BAF32572.1	hypothetical protein	( 723)	154	43.4	0.96
gi	114842167 dbj BAF32571.1	hypothetical protein	( 723)	154	43.4	0.96

>>gi|142722|gb|AAA22331.1| crystal protein (1178 aa)  
 initn: 7849 init1: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0  
 Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap  
 (5-1182:1-1178)

		10	20	30	40	50	60
Cry1Ac	CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF						
	.....						
gi 142	MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF						
		10	20	30	40	50	
		70	80	90	100	110	120
Cry1Ac	VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFRE						
	.....						
gi 142	VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFRE						
		60	70	80	90	100	110
		130	140	150	160	170	180

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGIIEGSIIRSPHL  
 gi|142 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGIIEGSIIRSPHL  
 240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 gi|142 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
 GVYRRLSSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQVSDLEIIPPQ  
 gi|142 GVYRRLSSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQVSDLEIIPPQ  
 360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 gi|142 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540  
 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 gi|142 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600  
 TPIHLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 gi|142 TPIHLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 540 550 560 570 580 590

Cry1Ac 610 620 630 640 650 660  
 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 gi|142 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 600 610 620 630 640 650

Cry1Ac 670 680 690 700 710 720  
 SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKIDINRQPERGWGGSTGITIQGGDDVF  
 gi|142 SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKIDINRQPERGWGGSTGITIQGGDDVF  
 660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780  
 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAKHETV  
 gi|142 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAKHETV  
 720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840  
 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG  
 gi|142 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG  
 780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900  
 CTDLNEGLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 gi|142 CTDLNEGLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960  
 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNA  
 gi|142 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNA  
 900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020  
 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHVDVEEQNNQRSVLVPEWEA  
 gi|142 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHVDVEEQNNQRSVLVPEWEA  
 960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080  
 EVSQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNNVTVC  
 gi|142 EVSQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNNVTVC  
 1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140  
 NDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRRGYRDYTP  
 gi|142 NDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRRGYRDYTP  
 1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180  
 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 gi|142 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 1140 1150 1160 1170

>>gi|1839246|gb|AAB46989.1| insecticidal delta-endotoxin (1178 aa)  
 initn: 7849 init1: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0  
 Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap  
 (5-1182:1-1178)

Cry1Ac 10 20 30 40 50 60  
 CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 gi|183 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

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Cry1Ac 70 80 90 100 110 120
VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|183 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|183 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|183 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGI EGSIRSPHL
gi|183 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGI ERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRI VAQLGQ
gi|183 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRI VAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
gi|183 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFN NIIASDSITQIPA
gi|183 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFN NIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASV
gi|183 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASV
480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWGNS SIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|183 TPIHLNVNWGNS SIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540 550 560 570 580 590

Cry1Ac 610 620 630 640 650 660
GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|183 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

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Cry1Ac 670 680 690 700 710 720
SDEFCLDEKRELS EKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSGITIQGGDDVVF
gi|183 SDEFCLDEKRELS EKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSGITIQGGDDVVF
660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780
KENYVTLSGTTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|183 KENYVTLSGTTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLDIDVG
gi|183 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLDIDVG
780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900
CTDLNEDLGWVVI FKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|183 CTDLNEDLGWVVI FKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPELSVIPGVNA
gi|183 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVVPEWEA
gi|183 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVVPEWEA
960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080
EVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTTIHEIENNTDELKFSNCVEE E IYPNNTVTC
gi|183 EVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTTIHEIENNTDELKFSNCVEE E IYPNNTVTC
1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140
NDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPC EFN RGYRDTYP
gi|183 NDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPC EFN RGYRDTYP
1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180
LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|183 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

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>>gi|2584729|emb|CAA05505.1| insecticidal crystal protei (1178 aa)
initn: 7849 initl: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0
Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap
(5-1182:1-1178)

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Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|258 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|258 VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|258 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWVRYNQFRREL  
gi|258 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWVRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL  
gi|258 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ  
gi|258 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ  
gi|258 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ

Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|258 NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
gi|258 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
gi|258 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
gi|258 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF  
gi|258 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF

Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYIRYNAKHETV  
gi|258 KENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYIRYNAKHETV

Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG  
gi|258 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG

Cry1Ac CTDLNEDELGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
gi|258 CTDLNEDELGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW

Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNA  
gi|258 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNA

Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQRSVLVPEWEA  
gi|258 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQRSVLVPEWEA

Cry1Ac EVSQEVRVCPGRGYLLRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEIYPNNTVTC  
gi|258 EVSQEVRVCPGRGYLLRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEIYPNNTVTC

Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRGRYDYTP  
gi|258 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRGRYDYTP

Cry1Ac LPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|258 LPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE

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gi|258 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|1888559|gb|AAB49768.1| Cry1Ac delta-endotoxin [Baci (1178 aa)  
 initn: 7849 initl: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0  
 Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap  
 (5-1182:1-1178)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 .....  
 gi|188 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 .....  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 .....  
 gi|188 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 .....  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi|188 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 .....  
 gi|188 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 .....  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGI EGSIRSPHL  
 .....  
 gi|188 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGI EGSIRSPHL  
 .....  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi|188 MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
 .....  
 gi|188 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
 .....  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 .....  
 gi|188 NNNVPPRQGF SHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 .....  
 420 430 440 450 460 470

490 500 510 520 530 540  
 Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....

gi|188 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

550 560 570 580 590 600  
 Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 .....

gi|188 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 540 550 560 570 580 590

610 620 630 640 650 660  
 Cry1Ac GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 .....

gi|188 GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 600 610 620 630 640 650

670 680 690 700 710 720  
 Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF  
 .....

gi|188 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF  
 660 670 680 690 700 710

730 740 750 760 770 780  
 Cry1Ac KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAKHETV  
 .....

gi|188 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAKHETV  
 720 730 740 750 760 770

790 800 810 820 830 840  
 Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG  
 .....

gi|188 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG  
 780 790 800 810 820 830

850 860 870 880 890 900  
 Cry1Ac CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 .....

gi|188 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 840 850 860 870 880 890

910 920 930 940 950 960  
 Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPPELSPVPGVNA  
 .....

gi|188 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPPELSPVPGVNA  
 900 910 920 930 940 950

970 980 990 1000 1010 1020  
 Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA  
 .....

gi|188 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA  
 960 970 980 990 1000 1010

1030 1040 1050 1060 1070 1080  
 Cry1Ac EVSQEVRVCPGRGYLLRVTA YKEGYGEGCVT IHEIENNTDELKFSNCV EEEIYPNNTVTC  
 .....

gi|188 EVSQEVRVCPGRGYLLRVTA YKEGYGEGCVT IHEIENNTDELKFSNCV EEEIYPNNTVTC  
 1020 1030 1040 1050 1060 1070

1090 1100 1110 1120 1130 1140  
 Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRYGRDYTP

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gi|188 NDYTVNQEEYGGAYTSRNRGYNAPSPADYASVVEEKSYPDGRRENPCFNRRGYRDTYP
1080 1090 1100 1110 1120 1130

Cry1Ac LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE

gi|188 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170

>>gi|1842095|gb|AAC44841.1| crystal protein [Bacillus th (1178 aa)
initn: 7849 initl: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0
Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap
(5-1182:1-1178)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

gi|184 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi|184 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|184 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL

gi|184 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
TLTVLDIVALFPNYSRTPYIRTVSQTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL

gi|184 TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi|184 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GVTVDLDEIPPQ
GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GVTVDLDEIPPQ

gi|184 GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GVTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi|184 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVYASV
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVYASV

gi|184 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVYASV
480 490 500 510 520 530

Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI VGVRFSGTA
TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI VGVRFSGTA

gi|184 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI VGVRFSGTA
540 550 560 570 580 590

Cry1Ac GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

gi|184 GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF

gi|184 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
660 670 680 690 700 710

Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV

gi|184 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
720 730 740 750 760 770

Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG

gi|184 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
780 790 800 810 820 830

Cry1Ac CTDLNEEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
CTDLNEEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW

gi|184 CTDLNEEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840 850 860 870 880 890

Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA

gi|184 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSNWNKGVHVDVEEQNNQSRVLPVPEWEA
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSNWNKGVHVDVEEQNNQSRVLPVPEWEA

gi|184 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSNWNKGVHVDVEEQNNQSRVLPVPEWEA
960 970 980 990 1000 1010

Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSNWNKGVHVDVEEQNNQSRVLPVPEWEA
1030 1040 1050 1060 1070 1080

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Cry1Ac EVSQEVRVCPGRGYILRVTA...
gi|184 EVSQEVRVCPGRGYILRVTA...

Cry1Ac NDYTVNQEEYGGAYTSRNR...
gi|184 NDYTVNQEEYGGAYTSRNR...

Cry1Ac LPVG YVTKELEYFPETDK...
gi|184 LPVG YVTKELEYFPETDK...

>>gi|29293657|gb|AAO72077.1| Cry1Ac [Bacillus thuringien (1178 aa)
initn: 7849 initl: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0
Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap
(5-1182:1-1178)

Cry1Ac CMQAMDNPNINCEIPYNCL...
gi|292 MDNPNINCEIPYNCL...

Cry1Ac VLGLVDI IWGIFGPSQWDA...
gi|292 VLGLVDI IWGIFGPSQWDA...

Cry1Ac WEADPTNPALREEMRIQFN...
gi|292 WEADPTNPALREEMRIQFN...

Cry1Ac VFGQRWGFDAATINSRYNDL...
gi|292 VFGQRWGFDAATINSRYNDL...

Cry1Ac TLTVLDIVSLFPNYDSRTP...
gi|292 TLTVLDIVSLFPNYDSRTP...

Cry1Ac MDILNSITTYDHRGEYYWS...
gi|292 MDILNSITTYDHRGEYYWS...

Cry1Ac MDILNSITTYDHRGEYYWS...
gi|292 MDILNSITTYDHRGEYYWS...

Cry1Ac GYVRTLSSTLYRRFPNIGINN...
gi|292 GYVRTLSSTLYRRFPNIGINN...

Cry1Ac NNNVPPRQGFSHRLSHVSM...
gi|292 NNNVPPRQGFSHRLSHVSM...

Cry1Ac VKGNFLFNGSVISGPGFTGG...
gi|292 VKGNFLFNGSVISGPGFTGG...

Cry1Ac TPIHLNVNWGNSSIFSNTPA...
gi|292 TPIHLNVNWGNSSIFSNTPA...

Cry1Ac GVIIDRFEPFIPVTATLEAE...
gi|292 GVIIDRFEPFIPVTATLEAE...

Cry1Ac SDEFCLDEKRELSEKVKHAK...
gi|292 SDEFCLDEKRELSEKVKHAK...

Cry1Ac KENYVTLSGTFDECYPTYLY...
gi|292 KENYVTLSGTFDECYPTYLY...

Cry1Ac NVPGTGSLWPLSAQSPIGK...
gi|292 NVPGTGSLWPLSAQSPIGK...

Cry1Ac CTDLNE DLG VVIFKIKTQD...
gi|292 CTDLNE DLG VVIFKIKTQD...

Cry1Ac ETNIVYKEAKESVDALFVNS...
gi|292 ETNIVYKEAKESVDALFVNS...

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          970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSVLVPEWEA
gi|292 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSVLVPEWEA
          960      970      980      990      1000      1010

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          1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNNTVTC
gi|292 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNNTVTC
          1020      1030      1040      1050      1060      1070

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          1090      1100      1110      1120      1130      1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYRDYTP
gi|292 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYRDYTP
          1080      1090      1100      1110      1120      1130

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          1150      1160      1170      1180
Cry1Ac LPVGyVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|292 LPVGyVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
          1140      1150      1160      1170

```

>>gi|1612050|gb|AAB15030.1| Sequence 5 from patent US 55 (1178 aa)  
 in1tn: 7849 in1tl: 7849 opt: 7849 Z-score: 9247.3 bits: 1723.1 E(): 0  
 Smith-Waterman score: 7849; 99.406% identity (99.660% similar) in 1178 aa overlap  
 (5-1182:1-1178)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|161 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

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          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|161 VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

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          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|161 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

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          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWRYNQFRREL
gi|161 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWRYNQFRREL
          180      190      200      210      220      230

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          250      260      270      280      290      300
Cry1Ac TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGIERSIRSPHL
gi|161 TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGIERSIRSPHL
          240      250      260      270      280      290

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          310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrGEYyWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|161 MDILNSITIIYTDahrGEYyWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

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          370      380      390      400      410      420
Cry1Ac GvyRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSgtVDSLDEIPPQ
gi|161 GvyRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSgtVDSLDEIPPQ
          360      370      380      390      400      410

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          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|161 NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          420      430      440      450      460      470

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          490      500      510      520      530      540
Cry1Ac VKGNFLFNgsVIsGPGFTGGDLVRLNssGNNIQNRgyIEVPIHFPSTSTRYRVRVRYASV
gi|161 VKGNFLFNgsVIsGPGFTGGDLVRLNssGNNIQNRgyIEVPIHFPSTSTRYRVRVRYASV
          480      490      500      510      520      530

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          550      560      570      580      590      600
Cry1Ac TPIHLNVNwGNSsIFsNTVPATATSLDNLQSSDFGyFESANAFtSSLGNIVGVRNfSGTA
gi|161 TPIHLNVNwGNSsIFsNTVPATATSLDNLQSSDFGyFESANAFtSSLGNIVGVRNfSGTA
          540      550      560      570      580      590

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          610      620      630      640      650      660
Cry1Ac GVIIDRFefIPVtATLEAEYNLERAQKAVNALFTSTNQLGLKtNVDYHIDQVSNLVtYL
gi|161 GVIIDRFefIPVtATLEAEYNLERAQKAVNALFTSTNQLGLKtNVDYHIDQVSNLVtYL
          600      610      620      630      640      650

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          670      680      690      700      710      720
Cry1Ac SDFeCLDEKRElSEKvKHAKRLSDERNLLQDSNfKdINRQPERGWGGStGITIQGGDDVf
gi|161 SDFeCLDEKRElSEKvKHAKRLSDERNLLQDSNfKdINRQPERGWGGStGITIQGGDDVf
          660      670      680      690      700      710

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          730      740      750      760      770      780
Cry1Ac KENyVtLSGtFDEcYPTyLYQKIDESKlKAFtRYQLRGyIEDSODLEIySIRyNAKHETV
gi|161 KENyVtLSGtFDEcYPTyLYQKIDESKlKAFtRYQLRGyIEDSODLEIySIRyNAKHETV
          720      730      740      750      760      770

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          790      800      810      820      830      840
Cry1Ac NVPGtGSLwPLsAQSPiGKCGEPNRCAPHLEWNPDLDCScRDGEKCAHSHHFSLDIDVg
gi|161 NVPGtGSLwPLsAQSPiGKCGEPNRCAPHLEWNPDLDCScRDGEKCAHSHHFSLDIDVg
          780      790      800      810      820      830

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          850      860      870      880      890      900
Cry1Ac CTDLNEdLgVwVIFKIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKREKLEW
gi|161 CTDLNEdLgVwVIFKIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKREKLEW
          840      850      860      870      880      890

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Cry1Ac 910 920 930 940 950 960
ETNIVYKKAKEASVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|161 ETNIVYKKAKEASVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQRSVLVPEWEA
gi|161 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQRSVLVPEWEA
960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080
EVSQEVVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
gi|161 EVSQEVVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140
NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRRGYRDTYP
gi|161 NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRRGYRDTYP
1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180
LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|161 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

>>gi|52783575|gb|AAU87037.1| Cry1Ac [Bacillus thuringien (1178 aa)
initn: 7844 initl: 7844 opt: 7844 Z-score: 9241.4 bits: 1722.0 E(): 0
Smith-Waterman score: 7844; 99.321% identity (99.660% similar) in 1178 aa overlap
(5-1182:1-1178)

Cry1Ac 10 20 30 40 50 60
CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|527 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|527 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|527 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVYQFRREL
gi|527 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVYQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLIDIVLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
gi|527 TLTVLIDIVLFPNYSRRYPRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ
gi|527 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRRLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|527 GVYRRLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|527 NNVVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|527 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|527 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540 550 560 570 580 590

Cry1Ac 610 620 630 640 650 660
GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|527 GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

Cry1Ac 670 680 690 700 710 720
SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|527 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780
KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
gi|527 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG
gi|527 NVPGTGSLWPLSTQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG

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780      790      800      810      820      830
Cry1Ac      850      860      870      880      890      900
CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|527      840      850      860      870      880      890
CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW

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910      920      930      940      950      960
Cry1Ac      910      920      930      940      950      960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|527      900      910      920      930      940      950
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA

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970      980      990      1000      1010      1020
Cry1Ac      970      980      990      1000      1010      1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVPEWEA
gi|527      960      970      980      990      1000      1010
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVPEWEA

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1030     1040     1050     1060     1070     1080
Cry1Ac      1030     1040     1050     1060     1070     1080
EVSQEVVRCVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
gi|527      1020     1030     1040     1050     1060     1070
EVSQEVVRCVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC

```

```

1090     1100     1110     1120     1130     1140
Cry1Ac      1090     1100     1110     1120     1130     1140
NDYTYNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGRYDYTP
gi|527      1080     1090     1100     1110     1120     1130
NDYTYNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGRYDYTP

```

```

1150     1160     1170     1180
Cry1Ac      1150     1160     1170     1180
LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|527      1140     1150     1160     1170
LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE

```

>>gi|143126|gb|AAA73077.1| [Bacillus thuringiensis gene, (1178 aa)  
 in1n: 7842 in1l: 7842 opt: 7842 Z-score: 9239.1 bits: 1721.5 E(): 0  
 Smith-Waterman score: 7842; 99.321% identity (99.660% similar) in 1178 aa overlap  
 (5-1182:1-1178)

```

10      20      30      40      50      60
Cry1Ac      10      20      30      40      50      60
CMQAMNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|143      10      20      30      40      50
MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

```

```

70      80      90      100     110     120
Cry1Ac      70      80      90      100     110     120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|143      60      70      80      90      100     110
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

```

```

130     140     150     160     170     180
Cry1Ac      130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPFLAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|143      130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS

```

```

120      130      140      150      160      170
Cry1Ac      190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|143      180      190      200      210      220      230
VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL

```

```

250      260      270      280      290      300
Cry1Ac      250      260      270      280      290      300
TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQIEGSIIRSPHL
gi|143      240      250      260      270      280      290
TLTVLDIVSLFPNYSRRYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQIEGSIIRSPHL

```

```

310      320      330      340      350      360
Cry1Ac      310      320      330      340      350      360
MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|143      300      310      320      330      340      350
MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

```

```

370      380      390      400      410      420
Cry1Ac      370      380      390      400      410      420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|143      360      370      380      390      400      410
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ

```

```

430      440      450      460      470      480
Cry1Ac      430      440      450      460      470      480
NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|143      420      430      440      450      460      470
NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

```

```

490      500      510      520      530      540
Cry1Ac      490      500      510      520      530      540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|143      480      490      500      510      520      530
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

```

```

550      560      570      580      590      600
Cry1Ac      550      560      570      580      590      600
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIIVGRNFSGTA
gi|143      540      550      560      570      580      590
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIIVGRNFSGTA

```

```

610      620      630      640      650      660
Cry1Ac      610      620      630      640      650      660
GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|143      600      610      620      630      640      650
GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

```

```

670      680      690      700      710      720
Cry1Ac      670      680      690      700      710      720
SDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|143      660      670      680      690      700      710
SDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF

```

```

730      740      750      760      770      780
Cry1Ac      730      740      750      760      770      780
KENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV

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gi|143 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAKHETV
      720      730      740      750      760      770
          790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDV
      .....
gi|143 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDV
      780      790      800      810      820      830
          850      860      870      880      890      900
Cry1Ac CTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      .....
gi|143 CTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      840      850      860      870      880      890
          910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
      .....
gi|143 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
      900      910      920      930      940      950
          970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGVHDVVEEQNNQRSLVVPWEWA
      .....
gi|143 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGVHDVVEEQNNQRSLVVPWEWA
      960      970      980      990      1000      1010
          1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
      .....
gi|143 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
      1020      1030      1040      1050      1060      1070
          1090      1100      1110      1120      1130      1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYRDYTP
      .....
gi|143 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYRDYTP
      1080      1090      1100      1110      1120      1130
          1150      1160      1170      1180
Cry1Ac LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|143 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|87298907|gb|ABD37053.1| insecticidal crystal protei (1178 aa)
  initn: 7830 initl: 7830 opt: 7830 Z-score: 9224.9 bits: 1718.9 E(): 0
Smith-Waterman score: 7830; 99.236% identity (99.576% similar) in 1178 aa overlap
(5-1182:1-1178)
          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|872 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
          10      20      30      40      50
          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
      .....

```

```

gi|872 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|872 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      .....
gi|872 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
          250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      .....
gi|872 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290
          310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|872 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
          370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      .....
gi|872 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      360      370      380      390      400      410
          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
      .....
gi|872 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
      420      430      440      450      460      470
          490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
      .....
gi|872 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
      480      490      500      510      520      530
          550      560      570      580      590      600
Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      .....
gi|872 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590
          610      620      630      640      650      660
Cry1Ac GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      .....
gi|872 GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      600      610      620      630      640      650
          670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDV

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gi | 872 SDEFCLDEKRELSEVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSTGITIQGGDDVF
660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780
KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV

gi | 872 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNKHEV
720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVG

gi | 872 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVG
780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900
CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW

gi | 872 CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA

gi | 872 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA

gi | 872 AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA
960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080
EVSQEVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTC

gi | 872 EVSQEVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTC
1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140
NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRDYTP

gi | 872 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRDYTP
1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180
LPVGVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi | 872 LPVGVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

>>gi|3979717|emb|CAA10270.1| crystal toxin protein [Baci (1178 aa)
initn: 7827 initl: 7827 opt: 7827 Z-score: 9221.4 bits: 1718.2 E(): 0
Smith-Waterman score: 7827; 99.151% identity (99.576% similar) in 1178 aa overlap
(5-1182:1-1178)

Cry1Ac 10 20 30 40 50 60
CMQAMNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

gi | 397 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE

gi | 397 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi | 397 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYQFREL

gi | 397 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYQFREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

gi | 397 TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi | 397 MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQ

gi | 397 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi | 397 NNVVPPRQGFSHRLSHVSMFRSGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

gi | 397 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

gi | 397 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540 550 560 570 580 590

610 620 630 640 650 660

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Cry1Ac GVIIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 .....  
 gi | 397 GVIIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 600 610 620 630 640 650

Cry1Ac 670 680 690 700 710 720  
 SDEFCLDEKREKLESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF  
 .....  
 gi | 397 SDEFCLDEKREKLESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF  
 660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780  
 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV  
 .....  
 gi | 397 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRNAKHETV  
 720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840  
 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFLDIDVDF  
 .....  
 gi | 397 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFLDIDVDF  
 780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900  
 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 .....  
 gi | 397 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960  
 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA  
 .....  
 gi | 397 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA  
 900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020  
 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNQRSVLVPEWEA  
 .....  
 gi | 397 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNQRSVLVPEWEA  
 960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080  
 EVSQEVRVCPGRGYLLRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEIIYPNNTVTC  
 .....  
 gi | 397 EVSQEVRVCPGRGYLLRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEIIYPNNTVTC  
 1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140  
 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRDYTP  
 .....  
 gi | 397 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRDYTP  
 1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180  
 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 .....  
 gi | 397 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 1140 1150 1160 1170

>>gi|23344760|gb|AAN07788.1| insecticidal crystal protei (1177 aa)  
 initn: 4926 init1: 4926 opt: 7819 Z-score: 9212.0 bits: 1716.5 E(): 0  
 Smith-Waterman score: 7819; 99.151% identity (99.576% similar) in 1178 aa overlap  
 (5-1182:1-1177)

Cry1Ac 10 20 30 40 50 60  
 CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 .....  
 gi | 233 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50

Cry1Ac 70 80 90 100 110 120  
 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
 .....  
 gi | 233 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180  
 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi | 233 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
 VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 .....  
 gi | 233 VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHL  
 .....  
 gi | 233 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHL  
 240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi | 233 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ  
 .....  
 gi | 233 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ  
 360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
 NNNVPRQGFSHRSLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 .....  
 gi | 233 NNNVPRQGFSHRSLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540  
 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....  
 gi | 233 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

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550      560      570      580      590      600
Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVRNFSGTA
gi|233 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVRNFSGTA
540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|233 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600      610      620      630      640      650

670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|233 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
660      670      680      690      700      710

730      740      750      760      770      780
Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|233 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAKHETV
720      730      740      750      760      770

790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLDIDVGV
gi|233 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLDIDVGV
780      790      800      810      820      830

850      860      870      880      890      900
Cry1Ac CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|233 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840      850      860      870      880      890

910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|233 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
900      910      920      930      940      950

970      980      990      1000     1010     1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA
gi|233 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA
960      970      980      990      1000     1010

1030     1040     1050     1060     1070     1080
Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNNTVTC
gi|233 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNNTVTC
1020     1030     1040     1050     1060     1070

1090     1100     1110     1120     1130     1140
Cry1Ac NDYTYNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRRGYRDTYP
gi|233 NDYTYNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRRGYRDTYP
1080     1090     1100     1110     1120     1130

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1150     1160     1170     1180
Cry1Ac LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|233 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170

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>>gi|593570|gb|AAA55177.1| Sequence 1 from Patent EP 036 (1177 aa)  
 initn: 4926 init1: 4926 opt: 7812 Z-score: 9203.7 bits: 1715.0 E(): 0  
 Smith-Waterman score: 7812; 99.066% identity (99.576% similar) in 1178 aa overlap  
 (5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|593 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISREGLSNLYQIYAESFRE
gi|593 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISREGLSNLYQIYAESFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|593 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFREL
gi|593 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFREL
180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|593 TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLQG
gi|593 MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLQG
300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac GVYRTLSSITLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|593 GVYRTLSSITLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360     370     380     390     400     410

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430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|593 NNNVPRQGFSHRLSHVSMFRSG-FSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420     430     440     450     460     470

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          490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVLSGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|593 VKGNFLFNGSVLSGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
          480      490      500      510      520      530

          550      560      570      580      590      600
Cry1Ac TPIHLNVNWGNSISFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|593 TPIHLNVNWGNSISFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
          540      550      560      570      580      590

          610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|593 GVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
          600      610      620      630      640      650

          670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGSGTGTITIQGGDDVF
gi|593 SDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGSGTGTITIQGGDDVF
          660      670      680      690      700      710

          730      740      750      760      770      780
Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
gi|593 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV
          720      730      740      750      760      770

          790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG
gi|593 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVG
          780      790      800      810      820      830

          850      860      870      880      890      900
Cry1Ac CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|593 CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
          840      850      860      870      880      890

          910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
gi|593 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
          900      910      920      930      940      950

          970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVVPWEWA
gi|593 AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVVPWEWA
          960      970      980      990      1000      1010

          1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
gi|593 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC

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          1020      1030      1040      1050      1060      1070
Cry1Ac          1090      1100      1110      1120      1130      1140
NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDYTP
gi|593 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDYTP
          1080      1090      1100      1110      1120      1130

          1150      1160      1170      1180
Cry1Ac LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|593 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140      1150      1160      1170

>>gi|142742|gb|AAA22339.1| cryIA(c)3 (1177 aa)
initn: 4926 init1: 4926 opt: 7812 Z-score: 9203.7 bits: 1715.0 E(): 0
Smith-Waterman score: 7812; 99.066% identity (99.576% similar) in 1178 aa overlap
(5-1182:1-1177)

          10      20      30      40      50      60
Cry1Ac CMQAMNPNINCEPIYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|142 MDNPNINCEPIYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|142 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL
          180      190      200      210      220      230

          250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRYPVRTVSQTLREIYTNPVLNFDGSRGSAQGIERSIRSPHL
gi|142 TLTVLDIVSLFPNYDSRYPVRTVSQTLREIYTNPVLNFDGSRGSAQGIERSIRSPHL
          240      250      260      270      280      290

          310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|142 MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

          370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|142 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ

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360      370      380      390      400      410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      430      440      450      460      470      480
gi|142  NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      420      430      440      450      460      470

      490      500      510      520      530      540
Cry1Ac  VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTSTRYRVRVRYASV
      480      490      500      510      520      530
gi|142  VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTSTRYRVRVRYASV
      480      490      500      510      520      530

      550      560      570      580      590      600
Cry1Ac  TPIHLNVNWGNSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590
gi|142  TPIHLNVNWGNSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590

      610      620      630      640      650      660
Cry1Ac  GVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      600      610      620      630      640      650
gi|142  GVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      600      610      620      630      640      650

      670      680      690      700      710      720
Cry1Ac  SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
      660      670      680      690      700      710
gi|142  SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
      660      670      680      690      700      710

      730      740      750      760      770      780
Cry1Ac  KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
      720      730      740      750      760      770
gi|142  KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNKAKHETV
      720      730      740      750      760      770

      790      800      810      820      830      840
Cry1Ac  NVPGTGSLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
      780      790      800      810      820      830
gi|142  NVPGTGSLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
      780      790      800      810      820      830

      850      860      870      880      890      900
Cry1Ac  CTDLNEGLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      840      850      860      870      880      890
gi|142  CTDLNEGLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      840      850      860      870      880      890

      910      920      930      940      950      960
Cry1Ac  ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
      900      910      920      930      940      950
gi|142  ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
      900      910      920      930      940      950

      970      980      990      1000      1010      1020
Cry1Ac  AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSLVLPVEWEA
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gi|142  AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSLVLPVEWEA
      960      970      980      990      1000      1010

      1030      1040      1050      1060      1070      1080
Cry1Ac  EVSQEVRVPCPRGYILRVYTAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEEYIPNNTVTC
      .....
gi|142  EVSQEVRVPCPRGYILRVYTAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEEYIPNNTVTC
      1020      1030      1040      1050      1060      1070

      1090      1100      1110      1120      1130      1140
Cry1Ac  NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYRDYTP
      .....
gi|142  NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYRDYTP
      1080      1090      1100      1110      1120      1130

      1150      1160      1170      1180
Cry1Ac  LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|142  LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170

>>gi|157394690|gb|AA18704.2| Cry1Ac [Bacillus thuringie (1177 aa)
      initn: 4926 initl: 4926 opt: 7812 Z-score: 9203.7 bits: 1715.0 E(): 0
      Smith-Waterman score: 7812; 99.066% identity (99.576% similar) in 1178 aa overlap
      (5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac  CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|157  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      .....
gi|157  VLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|157  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL
      .....
gi|157  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      .....
gi|157  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac  MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....

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gi|157 MDILNSITYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ
gi|157 GYVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|157 NNVVPPRQGFSHRSLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530      540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|157 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
      480      490      500      510      520      530
Cry1Ac 550      560      570      580      590      600
TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|157 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590
Cry1Ac 610      620      630      640      650      660
GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|157 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      600      610      620      630      640      650
Cry1Ac 670      680      690      700      710      720
SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
gi|157 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
      660      670      680      690      700      710
Cry1Ac 730      740      750      760      770      780
KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYSIRYNAKHETV
gi|157 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYLIRYNAKHETV
      720      730      740      750      760      770
Cry1Ac 790      800      810      820      830      840
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG
gi|157 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVG
      780      790      800      810      820      830
Cry1Ac 850      860      870      880      890      900
CTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|157 CTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      840      850      860      870      880      890
Cry1Ac 910      920      930      940      950      960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIPGVNA

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gi|157 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIPGVNA
      900      910      920      930      940      950
Cry1Ac 970      980      990      1000      1010      1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVVEEQNNQRSVLVPEWEA
gi|157 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVVEEQNNQRSVLVPEWEA
      960      970      980      990      1000      1010
Cry1Ac 1030      1040      1050      1060      1070      1080
EVSQEVRCVCPGRGYLLRVTAKEGYGEGCVTTIHEIENNTDELKFSNCVVEEIEYPNNTVTC
gi|157 EVSQEVRCVCPGRGYLLRVTAKEGYGEGCVTTIHEIENNTDELKFSNCVVEEIEYPNNTVTC
      1020      1030      1040      1050      1060      1070
Cry1Ac 1090      1100      1110      1120      1130      1140
NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYDYTP
gi|157 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYDYTP
      1080      1090      1100      1110      1120      1130
Cry1Ac 1150      1160      1170      1180
LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|157 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170
>>gi|82698017|gb|ABB89046.1| delta-endocytotoxin [Bacillus (1177 aa)
      initn: 4926 init1: 4926 opt: 7806 Z-score: 9196.6 bits: 1713.7 E(): 0
Smith-Waterman score: 7806; 98.981% identity (99.491% similar) in 1178 aa overlap
(5-1182:1-1177)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|826 MDNPNPTNECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100      110      120
VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|826 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|826 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|826 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHL

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gi|826 240 250 260 270 280 290
      310 320 330 340 350 360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQLGQ
gi|826 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQLGQ
      300 310 320 330 340 350
      370 380 390 400 410 420
Cry1Ac GvYrTLsStLYRRPFNIGInnQQLsVLDGTEfAYGTSSnLPSAVYrKSGTVDsLDEIppQ
gi|826 GvYrTLsStLYRRPFNIGInnQQLsVLDGTEfAYGTSSnLPSAVYrKSGTVDsLDEIppQ
      360 370 380 390 400 410
      430 440 450 460 470 480
Cry1Ac NNNVPPRQGFsHrLShVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNNIIASDSITQIPA
gi|826 NNNVPPRQGFsHrLShVSMFRSG-SSSSVSIIRAPMfSWIHRSAEFNNIIASDSITQIPA
      420 430 440 450 460 470
      490 500 510 520 530 540
Cry1Ac VKGNfLNGSVISGPGfTGdDLVrLNSsGNNIQNRGYIEVPIHfPSTsTRyRVRVRYASV
gi|826 VKGNfLNGSVISGPGfTGdDLVrLNSsGNNIQNRGYIEVPIHfPSTsTRyRVRVRYASV
      480 490 500 510 520 530
      550 560 570 580 590 600
Cry1Ac TPIHLNVNwGNSsIFsNTVPATATsLDNLQSSDFGyFESANAFtSSLGNIVGVRNfSGTA
gi|826 TPIHLNVNwGNSsIFsNTVPATATsLDNLQSSDFGyFESANAFtSSLGNIVGVRNfSGTA
      540 550 560 570 580 590
      610 620 630 640 650 660
Cry1Ac GvIIdRfEFIPVtATLEAEYnLERAQKAVNALFtSTnQLGLKtNVTdYHIDQVSNLVtYL
gi|826 GvIIdRfEFIPVtATLEAEYnLERAQKAVNALFtSTnQLGLKtNVTdYHIDQVSNLVtYL
      600 610 620 630 640 650
      670 680 690 700 710 720
Cry1Ac SDEfCLDEKRElSEKvKHAKRLSDERNLLQDSNfKdINRQPERGwGGStGItIQGGdDVf
gi|826 SDEfCLDEKRElSEKvKHAKRLSDERNLLQDSNfKdINRQPERGwGGStGItIQGGdDVf
      660 670 680 690 700 710
      730 740 750 760 770 780
Cry1Ac KENyVtLSGtFDEcYpTYLYQKIDESKLKAFTRyQLRGYIEDsQDLIEIYsIRYNAKHETV
gi|826 KENyVtLSGtFDEcYpTYLYQKIDESKLKAFTRyQLRGYIEDsQDLIEIYsIRYNAKHETV
      720 730 740 750 760 770
      790 800 810 820 830 840
Cry1Ac NVPGtGSLwPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLDIDVg
gi|826 NVPGtGSLwPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLDIDVg
      780 790 800 810 820 830
      850 860 870 880 890 900

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Cry1Ac CTDLNEdlGVWvIFkIKtQdGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKREKLEW
gi|826 CTDLNEdlGVWvIFkIKtQdGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKREKLEW
      840 850 860 870 880 890
      910 920 930 940 950 960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|826 ETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRVHSIREAYLPELSVIPGVNA
      900 910 920 930 940 950
      970 980 990 1000 1010 1020
Cry1Ac AIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKghVDVEEQNNQRsVLVPEWEA
gi|826 AIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKghVDVEEQNNQRsVLVPEWEA
      960 970 980 990 1000 1010
      1030 1040 1050 1060 1070 1080
Cry1Ac EVsQEVrVcPGRGYILrVtAYKEGYGEGcVtIHEIENNTDELKfSNCVEEIYpNNTVtC
gi|826 EVsQEVrVcPGRGYILrVtAYKEGYGEGcVtIHEIENNTDELKfSNCVEEIYpNNTVtC
      1020 1030 1040 1050 1060 1070
      1090 1100 1110 1120 1130 1140
Cry1Ac NDYtVNQEEYGGAYtSRNRGYNEAPsVPADYASVYEEKsYtDGRRENpCFNrgYRDYtP
gi|826 NDYtVNQEEYGGAYtSRNRGYNEAPsVPADYASVYEEKsYtDGRRENpCFNrgYRDYtP
      1080 1090 1100 1110 1120 1130
      1150 1160 1170 1180
Cry1Ac LPVGYVtKELEyFPETDKVWIEIGETEGtFIVDSVELLMEE
gi|826 LPVGYVtKELEyFPETDKVWIEIGETEGtFIVDSVELLMEE
      1140 1150 1160 1170
>>gi|142740|gb|AAA22338.1| delta-endotoxin (1177 aa)
  initn: 4900 initl: 4900 opt: 7794 Z-score: 9182.5 bits: 1711.0 E(): 0
Smith-Waterman score: 7794; 98.981% identity (99.406% similar) in 1178 aa overlap
(5-1182:1-1177)
      10 20 30 40 50 60
Cry1Ac CMQAMDNPNINeCIPYnCLSNPEVEVLGGERIETGYtPIDISLSLTQfLLSEfVPGAGf
gi|142 MDNPNINeCIPYnCLSNPEVEVLGGERIETGYtPIDISLSLTQfLLSEfVPGAGf
      10 20 30 40 50
      70 80 90 100 110 120
Cry1Ac VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAIrSLEGLSNLYQIYAESfRE
gi|142 VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAIrSLEGLSNLYQIYAESfRE
      60 70 80 90 100 110
      130 140 150 160 170 180
Cry1Ac WEADpTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|142 WEADpTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120 130 140 150 160 170
      190 200 210 220 230 240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|142 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|142 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
gi|142 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|142 NNVVPPRQGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|142 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|142 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540 550 560 570 580 590

Cry1Ac 610 620 630 640 650 660
GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|142 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

Cry1Ac 670 680 690 700 710 720
SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTITIQGGDDVF
gi|142 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTITIQGGDDVF
660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780
KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAKHETV
gi|142 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAKHETV
720 730 740 750 760 770

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Cry1Ac 790 800 810 820 830 840
NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLDIDVG
gi|142 NVPGTGSLWPLSAQSPIGKCGEPNRFAPHLEWNPDLDCSCRDEKCAHSHHFFSLDIDVG
780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900
CTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|142 CTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
gi|142 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020
AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA
gi|142 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEA
960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080
EVSQEVRCVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIIYPNNTVTC
gi|142 EVSQEVRCVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIIYPNNTVTC
1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130 1140
NDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGRDYTP
gi|142 NDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGRDYTP
1080 1090 1100 1110 1120 1130

Cry1Ac 1150 1160 1170 1180
LPVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|142 LPVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170

>>gi|118566334|gb|ABL01535.1| crystal protein [Bacillus (1177 aa)
initn: 4921 init1: 4921 opt: 7788 Z-score: 9175.4 bits: 1709.7 E(): 0
Smith-Waterman score: 7788; 98.812% identity (99.406% similar) in 1178 aa overlap
(5-1182:1-1177)

Cry1Ac 10 20 30 40 50 60
CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|118 MDNPNINECNPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISRLEGLSNLYQIYAESFRE
gi|118 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

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130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|118 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
gi|118 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRWVRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVLSLFPNYDSRTYPIRTVSQTLREIYTNPVLENFDGFSFRGSAQGIIEGSIRSPHL
gi|118 TLTVLDIVALFSNYDSRRYPVRTVSQTLREIYTNPVLENFDGFSFRGSAQGIERSIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|118 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
gi|118 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|118 NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420      430      440      450      460      470

490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASV
gi|118 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASV
480      490      500      510      520      530

550      560      570      580      590      600
Cry1Ac TPIHLNVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGSFTA
gi|118 TPIHLNVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGSFTA
540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac GVIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|118 GVIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600      610      620      630      640      650

670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|118 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
660      670      680      690      700      710

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730      740      750      760      770      780
Cry1Ac KENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGIYEDSQDLEIYSIRYNAKHETV
gi|118 KENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGIYEDSQDLEIYLIRYNAKHETV
720      730      740      750      760      770

790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
gi|118 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
780      790      800      810      820      830

850      860      870      880      890      900
Cry1Ac CTDLNEIDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|118 CTDLNEIDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840      850      860      870      880      890

910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|118 ETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIPGVNA
900      910      920      930      940      950

970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSLVLPVEWEA
gi|118 AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSLVLPVEWEA
960      970      980      990      1000      1010

1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYILRVTAKEGYGEGCVTIIHEIENNTDELKFSNCVEEIIYPNNTVTC
gi|118 EVSQEVRVCPGRGYILRVTAKEGYGEGCVTIIHEIENNTDELKFSNCVEEIIYPNNTVTC
1020      1030      1040      1050      1060      1070

1090      1100      1110      1120      1130      1140
Cry1Ac NDYTVNQEEYGGAYTSRNRNGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYRDYTP
gi|118 NDYTVNQEEYGGAYTSRNRNGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYRDYTP
1080      1090      1100      1110      1120      1130

1150      1160      1170      1180
Cry1Ac LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|118 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170

>>gi|34422369|gb|AAQ68348.1| Sequence 2 from patent US 5 (1177 aa)
initn: 4915 initl: 4915 opt: 7782 Z-score: 9168.3 bits: 1708.4 E(): 0
Smith-Waterman score: 7782; 98.727% identity (99.406% similar) in 1178 aa overlap
(5-1182:1-1177)

10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|344 MDNPNINECIPYNCLSNPEVEVLGGERIETAYTPIDISLSLTQPLLTFVPGAGF
10      20      30      40      50

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          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|344 VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|344 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|344 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          180     190     200     210     220     230

          250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIEGSIRSPLH
gi|344 TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPLH
          240     250     260     270     280     290

          310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|344 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
          300     310     320     330     340     350

          370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
gi|344 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
          360     370     380     390     400     410

          430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|344 NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
          420     430     440     450     460     470

          490     500     510     520     530     540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|344 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
          480     490     500     510     520     530

          550     560     570     580     590     600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|344 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
          540     550     560     570     580     590

          610     620     630     640     650     660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|344 GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

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          600     610     620     630     640     650
          670     680     690     700     710     720
Cry1Ac SDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
gi|344 SDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGRDDVDF
          660     670     680     690     700     710

          730     740     750     760     770     780
Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNKAKHETV
gi|344 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNKAKHETV
          720     730     740     750     760     770

          790     800     810     820     830     840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLDIDVG
gi|344 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLDIDVG
          780     790     800     810     820     830

          850     860     870     880     890     900
Cry1Ac CTDLNEEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|344 CTDLNEEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
          840     850     860     870     880     890

          910     920     930     940     950     960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIRIAYLPELSVIPGVNA
gi|344 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIRIAYLPELSVIPGVNA
          900     910     920     930     940     950

          970     980     990     1000    1010    1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDVEEQNNQRSVLVPEWEA
gi|344 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDVEEQNNQRSVLVPEWEA
          960     970     980     990     1000    1010

          1030    1040    1050    1060    1070    1080
Cry1Ac EVSQEVRVCPGRGYLLRVTAIYKGEYEGCVTTIHEIENNTDELKFSNCVEEIEYPNNTVTC
gi|344 EVSQEVRVCPGRGYLLRVTAIYKGEYEGCVTTIHEIENNTDELKFSNCVEEIEYPNNTVTC
          1020    1030    1040    1050    1060    1070

          1090    1100    1110    1120    1130    1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRGRYDYTP
gi|344 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRGRYDYTP
          1080    1090    1100    1110    1120    1130

          1150    1160    1170    1180
Cry1Ac LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|344 LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
          1140    1150    1160    1170

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>>gi|68236022|gb|AA88347.1| Cry [Bacillus thuringiensis (1177 aa)
initn: 4883 init1: 4883 opt: 7777 Z-score: 9162.4 bits: 1707.3 E(): 0

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Smith-Waterman score: 7777; 98.812% identity (99.236% similar) in 1178 aa overlap (5-1182:1-1177)

Sequence alignment for Cry1Ac and gi|682. The alignment shows high identity between the two sequences, with positions 10-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, 430-480, 490-540, and 550-600 aligned. The sequences are: Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF... and gi|682 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF...

Continuation of sequence alignment for Cry1Ac and gi|682. The alignment shows high identity between the two sequences, with positions 540-590, 600-660, 670-720, 730-780, 790-840, 850-900, 910-960, 970-1020, 1030-1080, 1090-1140, and 1150-1180 aligned. The sequences are: Cry1Ac GVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL... and gi|682 GVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTCL...

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Cry1Ac LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 .....  
 gi|682 LPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVESLLMEE  
 1140 1150 1160 1170

>>gi|33321716|gb|AAQ06607.1| Cry1Ac [Bacillus thuringien (1177 aa)  
 initn: 4889 initl: 4889 opt: 7775 Z-score: 9160.1 bits: 1706.9 E(): 0  
 Smith-Waterman score: 7775; 98.727% identity (99.406% similar) in 1178 aa overlap  
 (5-1182:1-1177)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 .....  
 gi|333 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50 60

Cry1Ac VLGLVDIWIWIFGSPQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 .....  
 gi|333 VLGLVDIWIWIFGSPQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi|333 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYNQFRREL  
 .....  
 gi|333 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVYNQFRREL  
 180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL  
 .....  
 gi|333 TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi|333 MDILNSITIIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPPQ  
 .....  
 gi|333 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPPQ  
 360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA  
 .....  
 gi|333 NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA  
 420 430 440 450 460 470 480

Cry1Ac .....  
 gi|333 .....  
 490 500 510 520 530 540

Cry1Ac VKGNFLFNNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....  
 gi|333 VKGNFLFNNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

Cry1Ac .....  
 gi|333 .....  
 540 550 560 570 580 590 600

Cry1Ac .....  
 gi|333 .....  
 610 620 630 640 650 660

Cry1Ac .....  
 gi|333 .....  
 670 680 690 700 710 720

Cry1Ac .....  
 gi|333 .....  
 730 740 750 760 770 780

Cry1Ac .....  
 gi|333 .....  
 790 800 810 820 830 840

Cry1Ac .....  
 gi|333 .....  
 850 860 870 880 890 900

Cry1Ac .....  
 gi|333 .....  
 910 920 930 940 950 960

Cry1Ac .....  
 gi|333 .....  
 970 980 990 1000 1010 1020

Cry1Ac .....  
 gi|333 .....  
 1030 1040 1050 1060 1070 1080

Cry1Ac .....  
 gi|333 .....  
 1090 1100 1110 1120 1130 1140

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1090      1100      1110      1120      1130      1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRRGYRDYTP
gi|333 NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRRGYRDHTP
1080      1090      1100      1110      1120      1130

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1150      1160      1170      1180
Cry1Ac LPVGyVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|333 LPVGyVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140      1150      1160      1170

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>>gi|1610958|gb|AAB13937.1| Sequence 34 from patent US 5 (1188 aa)  
 in1tn: 7338 in1tl: 7272 opt: 7743 Z-score: 9122.2 bits: 1699.9 E(): 0  
 Smith-Waterman score: 7743; 97.555% identity (98.735% similar) in 1186 aa overlap  
 (1-1182:3-1188)

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10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGA
gi|161 ABCPEPMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGA
10      20      30      40      50      60

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60      70      80      90      100      110
Cry1Ac GFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESF
gi|161 GFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESF
70      80      90      100      110      120

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```

120     130     140     150     160     170
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|161 REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
130     140     150     160     170     180

```

```

180     190     200     210     220     230
Cry1Ac VSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRR
gi|161 VSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRR
190     200     210     220     230     240

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```

240     250     260     270     280     290
Cry1Ac ELTLTVLDIVLSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSIIRSP
gi|161 ELTLTVLDIVLSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSIIRSP
250     260     270     280     290     300

```

```

300     310     320     330     340     350
Cry1Ac HLMIDLNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQL
gi|161 HLMIDLNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQL
310     320     330     340     350     360

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```

360     370     380     390     400     410
Cry1Ac GQGVYRTLSSLTLYRRPFNIGINNQLSVLDGTEFAYGTSNLPASVYRKSQGTVDLSLDEIP
gi|161 GQGVYRTLSSLTLYRRPFNIGINNQLSVLDGTEFAYGTSNLPASVYRKSQGTVDLSLDEIP
370     380     390     400     410     420

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```

420      430      440      450      460      470
Cry1Ac PQNNNVPPRQGFHSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|161 PQNNNVPPRQGFHSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
430      440      450      460      470      480

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```

480      490      500      510      520      530
Cry1Ac PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA
gi|161 PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA
490      500      510      520      530      540

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540      550      560      570      580      590
Cry1Ac SVTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFSG
gi|161 SVTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFSG
550      560      570      580      590      600

```

```

600      610      620      630      640      650
Cry1Ac TAGVIIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
gi|161 TAGVIIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
610      620      630      640      650      660

```

```

660      670      680      690      700      710
Cry1Ac YLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDD
gi|161 YLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDD
670      680      690      700      710      720

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```

720      730      740      750      760      770
Cry1Ac VFKENYVTLSGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHE
gi|161 VFKENYVTLSGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHE
730      740      750      760      770      780

```

```

780      790      800      810      820      830
Cry1Ac TVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID
gi|161 TVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID
790      800      810      820      830      840

```

```

840      850      860      870      880      890
Cry1Ac VGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL
gi|161 VGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL
850      860      870      880      890      900

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900      910      920      930      940      950
Cry1Ac EWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIPGV
gi|161 EWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIPGV
910      920      930      940      950      960

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960      970      980      990      1000     1010
Cry1Ac NAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNRQSVLVVPEW
gi|161 NAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNRQSVLVVPEW
970      980      990      1000     1010     1020

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1020 1030 1040 1050 1060 1070
Cry1Ac EAEVSVQEVVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYVNNVT
gi|161 EAEVSVQEVVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYVNNVT

1080 1090 1100 1110 1120 1130
Cry1Ac TCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEFNRG
gi|161 TCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEFNRG

1140 1150 1160 1170 1180
Cry1Ac YRDYTPPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|161 YRDYTPPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE

>>gi|5987870|gb|AAE17035.1| Sequence 34 from patent US 5 (1188 aa)
initn: 7338 initl: 7272 opt: 7743 Z-score: 9122.2 bits: 1699.9 E(): 0
Smith-Waterman score: 7743; 97.555% identity (98.735% similar) in 1186 aa overlap
(1-1182:3-1188)

10 20 30 40 50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGA
gi|598 ABCPEPMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGA

60 70 80 90 100 110
Cry1Ac GFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESF
gi|598 GFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESF

120 130 140 150 160 170
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|598 REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD

180 190 200 210 220 230
Cry1Ac VSVFQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRR
gi|598 VSVFQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRR

240 250 260 270 280 290
Cry1Ac ELTLTVLDIVLFPNYDSRRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSP
gi|598 ELTLTVLDIVLFPNYDSRRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSP

300 310 320 330 340 350
Cry1Ac HLMIDLNSITIIYTDHARGBYWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|598 HLMIDLNSITIIYTDHARGBYWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL

360 370 380 390 400 410
Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQLSVLDGTFEYAGTSSNLPASVYRKSQVDSLDEIP
gi|598 GQGVYRTLSTLYRRPFNIGINNQQLSVLDGTFEYAGTSSNLPASVYRKSQVDSLDEIP

420 430 440 450 460 470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|598 PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI

480 490 500 510 520 530
Cry1Ac PAVKGNFLNFGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYA
gi|598 PAVKGNFLNFGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYA

540 550 560 570 580 590
Cry1Ac SVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVRNFSG
gi|598 SVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVRNFSG

600 610 620 630 640 650
Cry1Ac TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
gi|598 TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT

660 670 680 690 700 710
Cry1Ac YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD
gi|598 YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD

720 730 740 750 760 770
Cry1Ac VFKENYVTLSTGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHE
gi|598 VFKENYVTLSTGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHE

780 790 800 810 820 830
Cry1Ac TVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID
gi|598 TVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID

840 850 860 870 880 890
Cry1Ac VGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL
gi|598 VGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL

900 910 920 930 940 950
Cry1Ac EWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGV
gi|598 EWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGV

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          910      920      930      940      950      960
Cry1Ac  960      970      980      990      1000     1010
NAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGHV DVEEQNNQRSLVLPVPEW
gi|598  NAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGHV DVEEQNNHRSLVLPVPEW
          970      980      990      1000     1010     1020
Cry1Ac  1020     1030     1040     1050     1060     1070
EAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEE EIIYPNNTV
gi|598  EAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEE EIVPNNTV
          1030     1040     1050     1060     1070     1080
Cry1Ac  1080     1090     1100     1110     1120     1130
TCNDYTVNQEEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFENRG
gi|598  TCNDYTATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCEENRG
          1090     1100     1110     1120     1130     1140
Cry1Ac  1140     1150     1160     1170     1180
YRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|598  YGDYTPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1150     1160     1170     1180
>>gi|5973547|gb|AAE12827.1| Sequence 34 from patent US 5 (1182 aa)
  initn: 7338 initl: 7272 opt: 7732 Z-score: 9109.3 bits: 1697.5 E(): 0
Smith-Waterman score: 7732; 97.800% identity (98.900% similar) in 1182 aa overlap
(5-1182:1-1182)
          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
gi|597  MDNNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
          10      20      30      40      50
Cry1Ac  70      80      90      100     110     120
VLGLVDIIWGIFG PSQLWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|597  VLGLVDIIWGIFG PSQLWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110
Cry1Ac  130     140     150     160     170     180
WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|597  WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
Cry1Ac  190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDH AVRWYNTGLERVWGPDSRDWRIRYNQFRREL
gi|597  VFGQRWGFDAATINSRYNDLTRLIGNYTDY AVRWYNTGLERVWGPDSRDWRIRYNQFRREL
          180     190     200     210     220     230
Cry1Ac  250     260     270     280     290     300
TLTVLDIVSLFPNYSRTPYIRTVS QLTREIYTNPVLENFDGSRFGSAQGI EGSIIRSPHL
gi|597  TLTVLDIVSLFPNYSRTPYIRTVS QLTREIYTNPVLENFDGSRFGSAQGI ERSIIRSPHL

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          240      250      260      270      280      290
Cry1Ac  310      320      330      340      350      360
MDILNSITIIYTD AHRGYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIVAQLGQ
gi|597  MDILNSITIIYTD AHRGYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350
Cry1Ac  370      380      390      400      410      420
GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
gi|597  GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
          360      370      380      390      400      410
Cry1Ac  430      440      450      460      470      480
NNNVPPRQGFSHR LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
gi|597  NNVVPPRQGFSHR LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
          420      430      440      450      460      470
Cry1Ac  490      500      510      520      530      540
VKGNFLFNGSVIS GPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP STSTRYRVRVRYASV
gi|597  VKGNFLFNGSVIS GPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP STSTRYRVRVRYASV
          480      490      500      510      520      530
Cry1Ac  550      560      570      580      590      600
TPIHLNVNWGNS SIFSNTPATATSLDNLQSSDFGYFESANAFTS SGLNIVGVRNFSGTA
gi|597  TPIHLNVNWGNS SIFSNTPATATSLDNLQSSDFGYFESANAFTS SGLNIVGVRNFSGTA
          540      550      560      570      580      590
Cry1Ac  610      620      630      640      650      660
GVIIDRFEP I PVTATLEAEYNLERAQKAVNALFTSTNQLGLK TNVTDYHIDQVSNLVTYL
gi|597  GVIIDRFEP I PVTATLEAEYNLERAQKAVNALFTSTNQLGLK TNVTDYHIDQVSNLVTYL
          600      610      620      630      640      650
Cry1Ac  670      680      690      700      710      720
SDEFCLDEKREL SEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG ITIQGGDDVDF
gi|597  SDEFCLDEKREL SEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG ITIQGGDDVDF
          660      670      680      690      700      710
Cry1Ac  730      740      750      760      770      780
KENYVTLSGTF DECYPTYLYQKIDESKLLKAFTRYQLRGYIED SQDLEIYIIRYNAKHETV
gi|597  KENYVTLSGTF DECYPTYLYQKIDESKLLKAFTRYQLRGYIED SQDLEIYIIRYNAKHETV
          720      730      740      750      760      770
Cry1Ac  790      800      810      820      830      840
NVPGTGSLWPLS AQSPIGKCGEPNRCAPHLEWNPDLDCS CRDGEKCAHSHHFSLDIDVGV
gi|597  NVPGTGSLWPLS AQSPIGKCGEPNRCAPHLEWNPDLDCS CRDGEKCAHSHHFSLDIDVGV
          780      790      800      810      820      830
Cry1Ac  850      860      870      880      890      900
CTDLNEDLVGVV I FKIKTQDGHARLGNLEFLEEKPLVGBALARVKRAEKKWRDKREKLEW
gi|597  CTDLNEDLVGVV I FKIKTQDGHARLGNLEFLEEKPLVGBALARVKRAEKKWRDKREKLEW

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gi|597 CTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
840 850 860 870 880 890

Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
910 920 930 940 950 960

gi|597 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
900 910 920 930 940 950

Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQSRVSLVPEWEA
970 980 990 1000 1010 1020

gi|597 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVSLVPEWEA
960 970 980 990 1000 1010

Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYEGECVTIHEIENNTDELKFSNCVEEIIYPNNTVTC
1030 1040 1050 1060 1070 1080

gi|597 EVSQEVRVCPGRGYILRVTAAYKEGYEGECVTIHEIENNTDELKFSNCVEEIVPNNTVTC
1020 1030 1040 1050 1060 1070

Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFNRGYR
1090 1100 1110 1120 1130

gi|597 NDYTVNQEEYGGAYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESTRGYG
1080 1090 1100 1110 1120 1130

Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170 1180

gi|597 DYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170 1180

>>gi|1608064|gb|AAB11019.1| Sequence 34 from patent US 5 (1182 aa)
initn: 7338 initl: 7272 opt: 7732 Z-score: 9109.3 bits: 1697.5 E(): 0
Smith-Waterman score: 7732; 97.800% identity (98.900% similar) in 1182 aa overlap
(5-1182:1-1182)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

gi|160 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|160 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|160 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|160 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

gi|160 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
250 260 270 280 290 300

gi|160 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360

gi|160 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSSTVDSLEIPPQ
370 380 390 400 410 420

gi|160 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSSTVDSLEIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|160 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac VKGNFLFNQSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
490 500 510 520 530 540

gi|160 VKGNFLFNQSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480 490 500 510 520 530

Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
550 560 570 580 590 600

gi|160 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540 550 560 570 580 590

Cry1Ac GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
610 620 630 640 650 660

gi|160 GVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650

Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
670 680 690 700 710 720

gi|160 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
660 670 680 690 700 710

Cry1Ac KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
730 740 750 760 770 780

gi|160 KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAKHETV
720 730 740 750 760 770

Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
790 800 810 820 830 840

gi|160 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
780 790 800 810 820 830

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gi|160 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVG
      780   790   800   810   820   830
Cry1Ac      850   860   870   880   890   900
CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|160 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      840   850   860   870   880   890
Cry1Ac      910   920   930   940   950   960
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA
gi|160 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNA
      900   910   920   930   940   950
Cry1Ac      970   980   990  1000  1010  1020
AIFEELEGRIFTFASFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA
gi|160 AIFEELEGRIFTFASFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA
      960   970   980   990  1000  1010
Cry1Ac     1030  1040  1050  1060  1070  1080
EVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNNTVTC
gi|160 EVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNNTVTC
      1020  1030  1040  1050  1060  1070
Cry1Ac     1090  1100  1110  1120  1130
NDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPECFNRRGYR
gi|160 NDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPECFNRRGYR
      1080  1090  1100  1110  1120  1130
Cry1Ac     1140  1150  1160  1170  1180
DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|160 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140  1150  1160  1170  1180
>>gi|90568470|gb|ABD94160.1| insecticidal crystal protei (1164 aa)
  initn: 4892 initl: 4892 opt: 7727 Z-score: 9103.5 bits: 1696.4 E(): 0
Smith-Waterman score: 7727; 99.056% identity (99.571% similar) in 1165 aa overlap
(12-1176:1-1164)
Cry1Ac      10   20   30   40   50   60
CMQAMNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|905      10   20   30   40
NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
Cry1Ac      70   80   90  100  110  120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNAQAI SRLEGLSNLYQIYAESFRE
gi|905      50   60   70   80   90  100
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNAQAI SRLEGLSNLYQIYAESFRE
Cry1Ac     130  140  150  160  170  180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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gi|905 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      110   120   130   140   150   160
Cry1Ac      190   200   210   220   230   240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
gi|905 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
      170   180   190   200   210   220
Cry1Ac      250   260   270   280   290   300
TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL
gi|905 TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL
      230   240   250   260   270   280
Cry1Ac      310   320   330   340   350   360
MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|905 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      290   300   310   320   330   340
Cry1Ac      370   380   390   400   410   420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|905 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      350   360   370   380   390   400
Cry1Ac      430   440   450   460   470   480
NNNVPPRQGFSHRSLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|905 NNVVPPRQGFSHRSLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      410   420   430   440   450   460
Cry1Ac      490   500   510   520   530   540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|905 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
      470   480   490   500   510   520
Cry1Ac      550   560   570   580   590   600
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI VGVNRFSGTA
gi|905 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI VGVNRFSGTA
      530   540   550   560   570   580
Cry1Ac      610   620   630   640   650   660
GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|905 GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
      590   600   610   620   630   640
Cry1Ac      670   680   690   700   710   720
SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|905 SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
      650   660   670   680   690   700
Cry1Ac      730   740   750   760   770   780

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Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|905 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAKHETV
710 720 730 740 750 760

790 800 810 820 830 840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVVG
gi|905 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVVG
770 780 790 800 810 820

850 860 870 880 890 900
Cry1Ac CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|905 CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
830 840 850 860 870 880

910 920 930 940 950 960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSPVPGVNA
gi|905 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSPVPGVNA
890 900 910 920 930 940

970 980 990 1000 1010 1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA
gi|905 AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVPEWEA
950 960 970 980 990 1000

1030 1040 1050 1060 1070 1080
Cry1Ac EVSQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTC
gi|905 EVSQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTC
1010 1020 1030 1040 1050 1060

1090 1100 1110 1120 1130 1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYTP
gi|905 NDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYTP
1070 1080 1090 1100 1110 1120

1150 1160 1170 1180
Cry1Ac LPVGVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|905 LPVGVTKELEYFPETDKVWIEIGETEGTFIVDSVE
1130 1140 1150 1160

>>gi|67089175|gb|AAY66992.1| Cry1Ac [Bacillus thuringien (1164 aa)
  initn: 4892 initl: 4892 opt: 7727 Z-score: 9103.5 bits: 1696.4 E(): 0
  Smith-Waterman score: 7727; 99.056% identity (99.571% similar) in 1165 aa overlap
  (12-1176:1-1164)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|670 NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40

70 80 90 100 110 120

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Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|670 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
50 60 70 80 90 100

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|670 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
110 120 130 140 150 160

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWRVYRQFRREL
gi|670 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVYRQFRREL
170 180 190 200 210 220

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|670 TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
230 240 250 260 270 280

310 320 330 340 350 360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|670 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
290 300 310 320 330 340

370 380 390 400 410 420
Cry1Ac GVYRSLSSFTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|670 GVYRSLSSFTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
350 360 370 380 390 400

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|670 NNNVPPRQGFSHRLSHVSMFRSG-SSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
410 420 430 440 450 460

490 500 510 520 530 540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVYASV
gi|670 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVYASV
470 480 490 500 510 520

550 560 570 580 590 600
Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFSGTA
gi|670 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFSGTA
530 540 550 560 570 580

610 620 630 640 650 660
Cry1Ac GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|670 GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
590 600 610 620 630 640

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        670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
gi|670 SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
        650      660      670      680      690      700

        730      740      750      760      770      780
Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|670 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAKHETV
        710      720      730      740      750      760

        790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVGV
gi|670 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDVGV
        770      780      790      800      810      820

        850      860      870      880      890      900
Cry1Ac CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|670 CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
        830      840      850      860      870      880

        910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRHVSIREAYLPELSVIPGVNA
gi|670 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRHVSIREAYLPELSVIPGVNA
        890      900      910      920      930      940

        970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSVLVPEWEA
gi|670 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSVLVPEWEA
        950      960      970      980      990      1000

        1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
gi|670 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTC
        1010      1020      1030      1040      1050      1060

        1090      1100      1110      1120      1130      1140
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYRDYTP
gi|670 NDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYRDYTP
        1070      1080      1090      1100      1110      1120

        1150      1160      1170      1180
Cry1Ac LPVGYYTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|670 LPVGYYTKELEYFPETDKVWIEIGETEGTFIVDSVE
        1130      1140      1150      1160

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>>gi|594153|gb|AAA55760.1| Sequence 1 from Patent EP 032 (1182 aa)
  initn: 7322 initl: 7256 opt: 7716 Z-score: 9090.4 bits: 1694.0 E(): 0
Smith-Waterman score: 7716; 97.631% identity (98.900% similar) in 1182 aa overlap
(5-1182:1-1182)

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        10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
        10      20      30      40      50

        70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|594 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
        60      70      80      90      100      110

        130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        120      130      140      150      160      170

        190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
        180      190      200      210      220      230

        250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
gi|594 TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
        240      250      260      270      280      290

        310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|594 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
        300      310      320      330      340      350

        370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|594 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
        360      370      380      390      400      410

        430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|594 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
        420      430      440      450      460      470

        490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|594 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
        480      490      500      510      520      530

        550      560      570      580      590      600
Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIIVGVRNFSGTA
gi|594 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIIVGVRNFSGTA
        540      550      560      570      580      590

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Cry1Ac 610 620 630 640 650 660  
 GVIIIDRFEFIPVATLEAEYNLERAKAVNALFTSTNLGLKTNVTDYHIDQVSNLVTYL  
 .....  
 gi | 594 GVIIIDRFEFIPVATLEAEYNLERAKAVNALFTSTNLGLKTNVTDYHIDQVSNLVTYL  
 600 610 620 630 640 650

Cry1Ac 670 680 690 700 710 720  
 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF  
 .....  
 gi | 594 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF  
 660 670 680 690 700 710

Cry1Ac 730 740 750 760 770 780  
 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV  
 .....  
 gi | 594 KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAKHETV  
 720 730 740 750 760 770

Cry1Ac 790 800 810 820 830 840  
 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGV  
 .....  
 gi | 594 NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGV  
 780 790 800 810 820 830

Cry1Ac 850 860 870 880 890 900  
 CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 .....  
 gi | 594 CTDLNEGLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW  
 840 850 860 870 880 890

Cry1Ac 910 920 930 940 950 960  
 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA  
 .....  
 gi | 594 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPAVNA  
 900 910 920 930 940 950

Cry1Ac 970 980 990 1000 1010 1020  
 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVVEEQNQRSVLVPEWEA  
 .....  
 gi | 594 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVVEEQNHRSVLVVPEWEA  
 960 970 980 990 1000 1010

Cry1Ac 1030 1040 1050 1060 1070 1080  
 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVEEVIYNNVTVC  
 .....  
 gi | 594 EVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVEEVIYNNVTVC  
 1020 1030 1040 1050 1060 1070

Cry1Ac 1090 1100 1110 1120 1130  
 NDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPCEFNRGYR  
 .....  
 gi | 594 NDYTATQEEYATYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRDNPCESTRNGYR  
 1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180  
 DYTPLPVGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 .....  
 gi | 594 DYTPLPAGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

1140 1150 1160 1170 1180  
 >>gi|34426442|gb|AAQ70695.1| Sequence 5 from patent US 5 (1178 aa)  
 initn: 6770 initl: 6770 opt: 7687 Z-score: 9056.2 bits: 1687.7 E(): 0  
 Smith-Waterman score: 7687; 98.051% identity (98.559% similar) in 1180 aa overlap  
 (5-1182:1-1178)

Cry1Ac 10 20 30 40 50 60  
 CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 .....  
 gi | 344 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50

Cry1Ac 70 80 90 100 110 120  
 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
 .....  
 gi | 344 VLGLVDIIWIGIFGPSQWDAFPVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180  
 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi | 344 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAQVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 .....  
 gi | 344 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL  
 180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
 TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL  
 .....  
 gi | 344 TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
 MDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi | 344 MDILNSITIIYTDHARGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ  
 .....  
 gi | 344 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ  
 360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL  
 .....  
 gi | 344 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL  
 420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540  
 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....  
 gi | 344 AVGNFLFNGSVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYASV

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480      490      500      510      520      530
Cry1Ac  TPIHLNVNWNSSIFSNTVPAATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|344  TPIHLMVNWGNSIFSNTVPA-ATSLDNLQSSDF-YFESANAFTSSLGNIVGVRNFSGTA
540      550      560      570      580      590
Cry1Ac  GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTMVTDYHIDQVSNLVTYL
gi|344  GVIIDRIFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTMVTDYHIDQVSNLVTYL
600      610      620      630      640      650
Cry1Ac  SDEFCLDEKRELSKVKHAKRLSDERNLLQDSNF-KD-INRQPERGWGGSTGITIQGGDD
gi|344  SDEFCLDEKRELSKVKHAKRLSDERNLLQDSMFKRDGINRQPERGWGGSTGITIQGGDD
660      670      680      690      700      710
Cry1Ac  VFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|344  VFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAKHE
720      730      740      750      760      770
Cry1Ac  TVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID
gi|344  TVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDID
780      790      800      810      820      830
Cry1Ac  VGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL
gi|344  VGCTHLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKL
840      850      860      870      880      890
Cry1Ac  EWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIPGV
gi|344  EWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIPGV
900      910      920      930      940      950
Cry1Ac  NAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWVWKGVDVVEEQNQRSLVIVVPEW
gi|344  NAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWVWKGVDVVEEQNQRSLVIVVPEW
960      970      980      990      1000     1010
Cry1Ac  EAEVQSQEVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTV
gi|344  EAEVQSQEVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTV
1020     1030     1040     1050     1060     1070
Cry1Ac  TCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRGYRDY
gi|344  TCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRGYRDY

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gi|344  TCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRGYRDY
1080     1090     1100     1110     1120     1130
Cry1Ac  TPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|344  TPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140     1150     1160     1170
>>gi|594598|gb|AAA56205.1| Sequence 8 from Patent EP 022 (1178 aa)
initn: 5098 init1: 5098 opt: 7401 Z-score: 8718.9 bits: 1625.3 E(): 0
Smith-Waterman score: 7401; 93.993% identity (96.954% similar) in 1182 aa overlap
(5-1182:1-1178)
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|594  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-TQFLLSEFVPGAGF
10      20      30      40      50      60
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|594  VLGLVDIIWIGIFGPSQWDAFPVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
70      80      90      100     110     120
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAAANLHLSVLRDVS
130     140     150     160     170     180
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190     200     210     220     230     240
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSIRSPHL
gi|594  TLTVLDIVSLFNSYDSRRYPIRTVSQLTREIYTNPVLENFDGSRFGMAQRIEQNIRQPHL
250     260     270     280     290     300
Cry1Ac  MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVALGQ
gi|594  MDILNSITITYTDVHRGFNYWSGHQITASPVGFSGPEFAPFLFGNAGNAAPPV-LVSLTGL
310     320     330     340     350
Cry1Ac  GVYRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPASAVYRKSQVDSLDLDEIP
gi|594  GIFRTLSSPLYRRIILGSGPNQQLFVLDGTEFSFASLTNLPSTIYRQRTVDSLVDLDEIP
370     380     390     400     410
Cry1Ac  PQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRA--PMFSWIHRSAEFNIIASDSIT
gi|594  PQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRA--PMFSWIHRSAEFNIIASDSIT

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gi|594 PQDNSVPPRAGFSHRLSHVTMSLQ--AAGAVYTLRAQRPMFSWIHRSAEFNNIIASDSIT
      420      430      440      450      460      470
      480      490      500      510      520      530
Cry1Ac QIPAVKGNFLFNQSGVSGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      .....
gi|594 QIPAVKGNFLFNQSGVSGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac YASVTPIHNLVNWGNSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNF
      .....
gi|594 YASVTPIHNLVNWGNSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNF
      540      550      560      570      580      590
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|594 SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650
      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      .....
gi|594 VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710
      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
      .....
gi|594 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYLIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      .....
gi|594 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830
      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      .....
gi|594 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
      .....
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVPP
      .....
gi|594 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVPP
      960      970      980      990      1000      1010
      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVRRVCPGRGYILLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN

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      .....
gi|594 EWEAEVSQEVRRVCPGRGYILLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020      1030      1040      1050      1060      1070
      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPECFNRGYR
      .....
gi|594 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPECFNRGYR
      1080      1090      1100      1110      1120      1130
      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|594 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|112061966|gb|ABH98784.1| Sequence 34 from patent US (1177 aa)
      initn: 7231 init1: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
      Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
      (5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      .....
gi|112 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      .....
gi|112 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVRYNQFREL
      .....
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVRYNQFREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      .....
gi|112 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|112 MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLSLDEIIPPQ

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gi|112 360 370 380 390 400 410
Cry1Ac 430 440 450 460 470 480
gi|112 420 430 440 450 460 470
Cry1Ac 490 500 510 520 530
gi|112 480 490 500 510 520 530
Cry1Ac 540 550 560 570 580 590
gi|112 540 550 560 570 580 590
Cry1Ac 600 610 620 630 640 650
gi|112 600 610 620 630 640 650
Cry1Ac 660 670 680 690 700 710
gi|112 660 670 680 690 700 710
Cry1Ac 720 730 740 750 760 770
gi|112 720 730 740 750 760 770
Cry1Ac 780 790 800 810 820 830
gi|112 780 790 800 810 820 830
Cry1Ac 840 850 860 870 880 890
gi|112 840 850 860 870 880 890
Cry1Ac 900 910 920 930 940 950
gi|112 900 910 920 930 940 950
Cry1Ac 960 970 980 990 1000 1010

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Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHVDVEEQNNQRSVLVVP
gi|112 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHVDVEEQNNQRSVLVVP
Cry1Ac 1020 1030 1040 1050 1060 1070
gi|112 1020 1030 1040 1050 1060 1070
Cry1Ac 1080 1090 1100 1110 1120 1130
gi|112 1080 1090 1100 1110 1120 1130
Cry1Ac 1140 1150 1160 1170 1180
gi|112 1140 1150 1160 1170
Cry1Ac 1200 1210 1220 1230 1240 1250
gi|112 1200 1210 1220 1230 1240 1250
Cry1Ac 1260 1270 1280 1290 1300 1310
gi|112 1260 1270 1280 1290 1300 1310
Cry1Ac 1320 1330 1340 1350 1360 1370
gi|112 1320 1330 1340 1350 1360 1370
Cry1Ac 1380 1390 1400 1410 1420 1430
gi|112 1380 1390 1400 1410 1420 1430
Cry1Ac 1440 1450 1460 1470 1480 1490
gi|112 1440 1450 1460 1470 1480 1490
Cry1Ac 1500 1510 1520 1530 1540 1550
gi|112 1500 1510 1520 1530 1540 1550
Cry1Ac 1560 1570 1580 1590 1600 1610
gi|112 1560 1570 1580 1590 1600 1610
Cry1Ac 1620 1630 1640 1650 1660 1670
gi|112 1620 1630 1640 1650 1660 1670
Cry1Ac 1680 1690 1700 1710 1720 1730
gi|112 1680 1690 1700 1710 1720 1730
Cry1Ac 1740 1750 1760 1770 1780 1790
gi|112 1740 1750 1760 1770 1780 1790
Cry1Ac 1800 1810 1820 1830 1840 1850
gi|112 1800 1810 1820 1830 1840 1850
Cry1Ac 1860 1870 1880 1890 1900 1910
gi|112 1860 1870 1880 1890 1900 1910
Cry1Ac 1920 1930 1940 1950 1960 1970
gi|112 1920 1930 1940 1950 1960 1970
Cry1Ac 1980 1990 2000 2010 2020 2030
gi|112 1980 1990 2000 2010 2020 2030
Cry1Ac 2040 2050 2060 2070 2080 2090
gi|112 2040 2050 2060 2070 2080 2090
Cry1Ac 2100 2110 2120 2130 2140 2150
gi|112 2100 2110 2120 2130 2140 2150
Cry1Ac 2160 2170 2180 2190 2200 2210
gi|112 2160 2170 2180 2190 2200 2210
Cry1Ac 2220 2230 2240 2250 2260 2270
gi|112 2220 2230 2240 2250 2260 2270
Cry1Ac 2280 2290 2300 2310 2320 2330
gi|112 2280 2290 2300 2310 2320 2330
Cry1Ac 2340 2350 2360 2370 2380 2390
gi|112 2340 2350 2360 2370 2380 2390
Cry1Ac 2400 2410 2420 2430 2440 2450
gi|112 2400 2410 2420 2430 2440 2450
Cry1Ac 2460 2470 2480 2490 2500 2510
gi|112 2460 2470 2480 2490 2500 2510
Cry1Ac 2520 2530 2540 2550 2560 2570
gi|112 2520 2530 2540 2550 2560 2570
Cry1Ac 2580 2590 2600 2610 2620 2630
gi|112 2580 2590 2600 2610 2620 2630
Cry1Ac 2640 2650 2660 2670 2680 2690
gi|112 2640 2650 2660 2670 2680 2690
Cry1Ac 2700 2710 2720 2730 2740 2750
gi|112 2700 2710 2720 2730 2740 2750
Cry1Ac 2760 2770 2780 2790 2800 2810
gi|112 2760 2770 2780 2790 2800 2810
Cry1Ac 2820 2830 2840 2850 2860 2870
gi|112 2820 2830 2840 2850 2860 2870
Cry1Ac 2880 2890 2900 2910 2920 2930
gi|112 2880 2890 2900 2910 2920 2930
Cry1Ac 2940 2950 2960 2970 2980 2990
gi|112 2940 2950 2960 2970 2980 2990
Cry1Ac 3000 3010 3020 3030 3040 3050
gi|112 3000 3010 3020 3030 3040 3050
Cry1Ac 3060 3070 3080 3090 3100 3110
gi|112 3060 3070 3080 3090 3100 3110
Cry1Ac 3120 3130 3140 3150 3160 3170
gi|112 3120 3130 3140 3150 3160 3170
Cry1Ac 3180 3190 3200 3210 3220 3230
gi|112 3180 3190 3200 3210 3220 3230
Cry1Ac 3240 3250 3260 3270 3280 3290
gi|112 3240 3250 3260 3270 3280 3290
Cry1Ac 3300 3310 3320 3330 3340 3350
gi|112 3300 3310 3320 3330 3340 3350
Cry1Ac 3360 3370 3380 3390 3400 3410
gi|112 3360 3370 3380 3390 3400 3410
Cry1Ac 3420 3430 3440 3450 3460 3470
gi|112 3420 3430 3440 3450 3460 3470
Cry1Ac 3480 3490 3500 3510 3520 3530
gi|112 3480 3490 3500 3510 3520 3530
Cry1Ac 3540 3550 3560 3570 3580 3590
gi|112 3540 3550 3560 3570 3580 3590
Cry1Ac 3600 3610 3620 3630 3640 3650
gi|112 3600 3610 3620 3630 3640 3650
Cry1Ac 3660 3670 3680 3690 3700 3710
gi|112 3660 3670 3680 3690 3700 3710
Cry1Ac 3720 3730 3740 3750 3760 3770
gi|112 3720 3730 3740 3750 3760 3770
Cry1Ac 3780 3790 3800 3810 3820 3830
gi|112 3780 3790 3800 3810 3820 3830
Cry1Ac 3840 3850 3860 3870 3880 3890
gi|112 3840 3850 3860 3870 3880 3890
Cry1Ac 3900 3910 3920 3930 3940 3950
gi|112 3900 3910 3920 3930 3940 3950
Cry1Ac 3960 3970 3980 3990 4000 4010
gi|112 3960 3970 3980 3990 4000 4010

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>>gi|77376722|gb|ABA70269.1| Sequence 34 from patent US (1177 aa)
initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)

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Cry1Ac MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|773 MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQ
gi|773 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|773 NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS
gi|773 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|773 TTNLRITYVTVAGERIFAGQFNKMTDGTGDLTFQSFYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|773 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|773 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYSIRYNAK
gi|773 DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYLRIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|773 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|773 IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|773 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQSRVSLVVP
gi|773 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQSRVSLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIIYPNN
gi|773 EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIIYPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGYR
gi|773 TVTCNDYTVNQEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGYR
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|773 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170

>>gi|29718515|gb|AAP01239.1| Sequence 34 from patent US (1177 aa)
      initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(:) 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|297 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
gi|297 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|297 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|297 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

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      250      260      270      280      290      300
Cry1Ac TLTVLDIIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKRSRPHL
gi|297 TLTVLDIIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|297 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
gi|297 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFsHRLSHVSMFRSGFSNSsVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|297 NNNVPPRQGFsHRLSHVSMFRSGFSNSsVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNgs-VISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAHTLQSGTtTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VPIHLNvNwGNSsIFsNTVPATATSLDNLQSSDFgyFESANAFTSSLGN---IVGVRNF
gi|297 TTNLRiYVtVAGERIFaGQFNKtMDTGDPLTFQsFSYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYnLERAQKAVNALFTSTnQLGLKtNVTDYHIDQVSNL
gi|297 SSGNEVYIDRFELIPVTATLEAEYnLERAQKAVNALFTSTnQLGLKtNVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTyLsDEfCLDEKRELSEKvKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|297 VTyLsDEfCLDEKRELSEKvKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeySIRyNAK
gi|297 DDVFKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRyNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVnVPGTgSLWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHfSLD
gi|297 HETVnVPGTgSLWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHfSLD
      780      790      800      810      820      830

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      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWDRKRE
gi|297 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWDRKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMiHAADKRVHSiREAYLPELSVIP
gi|297 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMiHAADKRVHSiREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
gi|297 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEEIYPNN
gi|297 EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEEIYPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDyTVNQEeyGgAYTSRNRgyNEAPsVPADYASVYEEKsSYTDGRENpCEfNRgyR
gi|297 TVTCNDyTVNQEeyGgAYTSRNRgyNEAPsVPADYASVYEEKsSYTDGRENpCEfNRgyR
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac DYtPLPVgyVtKELEyFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|297 DYtPLPVgyVtKELEyFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170

>>gi|47257347|gb|AAT23510.1| Sequence 34 from patent US (1177 aa)
      initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|472 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPsQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWIGIFGPsQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

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60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|316 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
gi|316 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|316 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180      190      200      210      220      230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
gi|316 TLTVLDIVALFPNYDSRRYPRTVSQTLREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
240      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
gi|316 TLTVLDIVALFPNYDSRRYPRTVSQTLREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
240      250      260      270      280      290
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|316 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|316 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350
Cry1Ac GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVYRKSQGTVDLDEIIPPQ
gi|316 GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVYRKSQGTVDLDEIIPPQ
360      370      380      390      400      410
Cry1Ac GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVYRKSQGTVDLDEIIPPQ
gi|316 GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVYRKSQGTVDLDEIIPPQ
360      370      380      390      400      410
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|316 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
420      430      440      450      460      470
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|316 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
420      430      440      450      460      470
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|316 VKAHTLQSGTTFVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|316 VKAHTLQSGTTFVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530
Cry1Ac VTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|316 TTNLRIVYTVAGERIFAGQFNKTMDTGDPLTFQSF SYATINTAFTPMSQSSFTVGADTF
540      550      560      570      580      590
Cry1Ac VTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|316 TTNLRIVYTVAGERIFAGQFNKTMDTGDPLTFQSF SYATINTAFTPMSQSSFTVGADTF
540      550      560      570      580      590
Cry1Ac SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|316 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|316 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

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gi|316 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
660      670      680      690      700      710
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|316 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
gi|316 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720      730      740      750      760      770
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|316 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|316 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|316 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|316 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|316 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|316 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNQSRVSLVVP
gi|316 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNQSRVSLVVP
960      970      980      990      1000     1010
Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNQSRVSLVVP
gi|316 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNQSRVSLVVP
960      970      980      990      1000     1010
Cry1Ac EWAEVVSQEVVRCVGRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCFVEEIIYPNN
gi|316 EWAEVVSQEVVRCVGRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCFVEEIIYPNN
1020     1030     1040     1050     1060     1070
Cry1Ac EWAEVVSQEVVRCVGRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCFVEEIIYPNN
gi|316 EWAEVVSQEVVRCVGRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCFVEEIIYPNN
1020     1030     1040     1050     1060     1070
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
gi|316 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
gi|316 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
1080     1090     1100     1110     1120     1130
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|316 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140     1150     1160     1170
>>gi|16242914|gb|AAE80144.1| Sequence 34 from patent US (1177 aa)
initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)
10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLEFVPGAGF

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gi|162      MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
              10      20      30      40      50
              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|162 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
              60      70      80      90      100     110
              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170
              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
              180     190     200     210     220     230
              250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
gi|162 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
              240     250     260     270     280     290
              310     320     330     340     350     360
Cry1Ac MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162 MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
              300     310     320     330     340     350
              370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
gi|162 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
              360     370     380     390     400     410
              430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|162 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
              420     430     440     450     460     470
              490     500     510     520     530
Cry1Ac VKGNFLFNGS--VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|162 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINQQLPQ--RYRARIRYAS
              480     490     500     510     520     530
              540     550     560     570     580     590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|162 TTNLRITYVTVAGERIFAGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFVVGADTF
              540     550     560     570     580     590
              600     610     620     630     640     650
Cry1Ac SGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL

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              . . . . .
gi|162 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL
              600     610     620     630     640     650
              660     670     680     690     700     710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGG
              . . . . .
gi|162 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGG
              660     670     680     690     700     710
              720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAK
              . . . . .
gi|162 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAK
              720     730     740     750     760     770
              780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHFSLD
              . . . . .
gi|162 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHFSLD
              780     790     800     810     820     830
              840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
              . . . . .
gi|162 IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
              840     850     860     870     880     890
              900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
              . . . . .
gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
              900     910     920     930     940     950
              960     970     980     990     1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNQRSVLVVP
              . . . . .
gi|162 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNQRSVLVVP
              960     970     980     990     1000    1010
              1020    1030    1040    1050    1060    1070
Cry1Ac EWEAEVSQEVVRCVCPGRGYILRVTAAYKEGYGEGCVTIEIENNTDELKFSNCVEEIEYPNN
              . . . . .
gi|162 EWEAEVSQEVVRCVCPGRGYILRVTAAYKEGYGEGCVTIEIENNTDELKFSNCVEEIEYPNN
              1020    1030    1040    1050    1060    1070
              1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYR
              . . . . .
gi|162 TVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYR
              1080    1090    1100    1110    1120    1130
              1140    1150    1160    1170    1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
              . . . . .
gi|162 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
              1140    1150    1160    1170
>>gi|15126309|gb|AAE73545.1| Sequence 34 from patent US (1177 aa)

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Regulatory Product Characterization Team

initn: 7231 init1: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|151 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|151 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYNQFRREL
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYNQFRREL
Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
gi|151 TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
Cry1Ac MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQORIVAQLGQ
gi|151 MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQORIVAQLGQ
Cry1Ac GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ
gi|151 GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ
Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
gi|151 NNNVPPRQGF SHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
Cry1Ac VKGNFLFN GS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYRVRVRYAS
gi|151 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS

Cry1Ac VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|151 TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMQSSFTVGDATF
Cry1Ac SGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151 SSGNEVYIDRFELIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
Cry1Ac VTYLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|151 VTYLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|151 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|151 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
Cry1Ac IDVGCITDLNEDLGVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|151 IDVGCITDLNEDLGVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|151 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
Cry1Ac GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHVDVEEQNNQRSVLVVP
gi|151 GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHVDVEEQNNQRSVLVVP
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTA YKEGEGCVT IHEIENNTDELKFSNCV EEEIYPNN
gi|151 EWEAEVSEQEVRVCPGRGYILRVTA YKEGEGCVT IHEIENNTDELKFSNCV EEEIYPNN

Regulatory Product Characterization Team

1140 1150 1160 1170 1180  
 Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 :::  
 gi|151 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|162500744|gb|ABY14168.1| Sequence 34 from patent US (1177 aa)  
 initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0  
 Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap  
 (5-1182:1-1177)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 :::  
 gi|162 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 :::  
 gi|162 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 :::  
 gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 :::  
 gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSRGSAQGIERSIRSPHL  
 :::  
 gi|162 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ  
 :::  
 gi|162 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKS GTVDSLDEIPPQ  
 :::  
 gi|162 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKS GTVDSLDEIPPQ  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL  
 :::  
 gi|162 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL  
 420 430 440 450 460 470

490 500 510 520 530  
 Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS  
 :::  
 gi|162 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS  
 480 490 500 510 520 530

540 550 560 570 580 590  
 Cry1Ac VTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
 :::  
 gi|162 TTNLRIYVTVAGERIFAGQFNKTMGTGDLPTFFQSFYATINTAFTFPMSSQSSFTVGADTF  
 540 550 560 570 580 590

600 610 620 630 640 650  
 Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 :::  
 gi|162 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 600 610 620 630 640 650

660 670 680 690 700 710  
 Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITIQGG  
 :::  
 gi|162 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITIQGG  
 660 670 680 690 700 710

720 730 740 750 760 770  
 Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
 :::  
 gi|162 DDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYLIRYNAK  
 720 730 740 750 760 770

780 790 800 810 820 830  
 Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 :::  
 gi|162 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 780 790 800 810 820 830

840 850 860 870 880 890  
 Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 :::  
 gi|162 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 840 850 860 870 880 890

900 910 920 930 940 950  
 Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP  
 :::  
 gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP  
 900 910 920 930 940 950

960 970 980 990 1000 1010  
 Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLPVVP  
 :::  
 gi|162 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLPVVP  
 960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
 Cry1Ac EWEAEVVSQEVVRCVPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEIIYPNN  
 :::  
 gi|162 EWEAEVVSQEVVRCVPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCEVEEIIYPNN  
 1020 1030 1040 1050 1060 1070

Regulatory Product Characterization Team

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1080      1090      1100      1110      1120      1130
Cry1Ac TVTCDNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
gi|162 TVTCDNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
      1080      1090      1100      1110      1120      1130

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1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|162 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170

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>>gi|12824343|gb|AAE49249.1| Sequence 34 from patent US (1177 aa)  
 initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0  
 Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap  
 (5-1182:1-1177)

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      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

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      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

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      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

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      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIERSIRSPHL
gi|128 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNVLENFDGSRFGSAQGIERSIRSPHL
      240     250     260     270     280     290

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      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITIIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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      370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEIIPPQ
gi|128 GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEIIPPQ
      360     370     380     390     400     410

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      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
      420     430     440     450     460     470

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      490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480     490     500     510     520     530

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      540     550     560     570     580     590
Cry1Ac VTPIHNLVNWGSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|128 TTNLRIYVTVAGERIFAGQFNKTMDTGDP LTFQSFYATINTAFTFPMSQSSFTVGADTF
      540     550     560     570     580     590

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      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600     610     620     630     640     650

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      660     670     680     690     700     710
Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQQG
gi|128 VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQQG
      660     670     680     690     700     710

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      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
gi|128 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
      720     730     740     750     760     770

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      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFLSLD
gi|128 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFLSLD
      780     790     800     810     820     830

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      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|128 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840     850     860     870     880     890

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      900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|128 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900     910     920     930     940     950

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      960     970     980     990    1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|128 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP

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          960      970      980      990      1000      1010
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIEHEIENNTDELKFSNCVEEEIYPNN
gi|128 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIEHEIENNTDELKFSNCVEEEIYPNN
          1020      1030      1040      1050      1060      1070

          1080      1090      1100      1110      1120      1130
Cry1Ac TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYR
gi|128 TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYR
          1080      1090      1100      1110      1120      1130

          1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|128 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
          1140      1150      1160      1170

>>gi|53937594|gb|AAV01845.1| Sequence 34 from patent US (1177 aa)
  initn: 7231 initl: 3919 opt: 7222 Z-score: 8507.7 bits: 1586.2 E(): 0
Smith-Waterman score: 7222; 92.047% identity (95.601% similar) in 1182 aa overlap
(5-1182:1-1177)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|539 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|539 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFRREL
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVRYNQFRREL
          180     190     200     210     220     230

          250     260     270     280     290     300
Cry1Ac TLTVLDIIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|539 TLTVLDIIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
          240     250     260     270     280     290

          310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|539 MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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          300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|539 GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|539 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|539 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac VTFIHLNVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|539 TTNLRIYVTVAGERIFAGQFNKTMDDTGLTTFQSFYATINTAFTFPMSQSSFTVGADTF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac SGTAGVILDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|539 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|539 VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|539 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|539 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
          780      790      800      810      820      830

          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|539 IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
          840      850      860      870      880      890

          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELSVIP

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gi|539 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP

gi|539 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN

gi|539 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCDNDYTVNQEEYGGAYTSRNRGYNEAPSV PADYASVYEEKSYTDGRRENPC EFNRGYR

gi|539 TVTCDNDYTVNQEEYGGAYTSRNRGYNEAPSV PADYASVYEEKSYTDGRRENPC EFNRGYR
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE

gi|539 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
1140 1150 1160 1170

>>gi|37728786|gb|AA039719.1| insecticidal crystal protei (1181 aa)
initn: 6481 initl: 4163 opt: 7186 Z-score: 8465.3 bits: 1578.3 E(): 0
Smith-Waterman score: 7186; 90.625% identity (96.030% similar) in 1184 aa overlap
(5-1182:1-1181)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

gi|377 MDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi|377 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIP LFAVQNYQVPLLSVYVQAANHLHSVLRDVS

gi|377 WEADPTNPALREEMRIQFNDMNSALTTAIP LFAVQNYQVPLLSVYVQAANHLHSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDH AVRWYNTGLERVWGPDSRDWIRYNQFRREL

gi|377 VFGQRWGFDAATINSRYNDLTRLIGNYTDH AVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTR EITYTNPVLENFDGSRGSAQGI EGSIRSPHL

gi|377 TLTVLDIVSLFPNYSRTPYPIRTVSQLTR EITYTNPVLENFDGSRGSAQGI EGSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTD AHRGEYYSWGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIV AQLGQ

gi|377 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAP LFLGNAGNAAPPV-LVSLTGL
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410
GVYRTLSSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKS GTVDSLDEIP

gi|377 GIFRTLSSPLYRRIILGSGPNQELFVLDGTEFASFALTTNLPSTIYRQRGTVDSL DVIP
360 370 380 390 400 410

Cry1Ac 420 430 440 450 460 470
PQNNVPPRQGFSHR LSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFN NIIASDSITQI

gi|377 PQDNSVPPRAGFSHR LSHVMTLSQ--AAGAVYTLRAPTF SWQHRSAEFN NIIASDSITQI
420 430 440 450 460 470

Cry1Ac 480 490 500 510 520 530
PAVKGNFLPNGSVISGPGFTGGDLVRLN SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA

gi|377 PAVKGNFLPNGSVISGPGFTGGDLVRLN SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
SVTPIHLNWNWGNSSIFSNTPV PATATSLDNLQSSDFGYFESANAFTSS LGNIVGVRNFGS

gi|377 SVTPIHLNWNWGNSSIFSNTPV PATATSLDNLQSSDFGYFESANAFTSS LGNIVGVRNFGS
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
TAGVIIDRFEFIPVTATLEAEYNLER AQAQNALFTSTNQLGLKTNVTDYHIDQVSNLVT

gi|377 TAGVIIDRFEFIPVTATLEAEYNLER AQAQNALFTSTNQLGLKTNVTDYHIDQVSNLVT
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD

gi|377 YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
VFKENYVTLSGTFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE

gi|377 VFKENYVTLSGTFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830
TVNVPGTGLSLWPLSAQSPIGKCEPNRCAP HLEWNPDLDCSCRDEKCAHSHHFFSLDID

gi|377 TLNVPGTGLSLWPLAVKSPIGRCCEPNRCAP IEWKPDVDCSCRDEKCAHSHHFFSLDID
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890
VGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEF LEEKPLVGEALARVKRAEKKWRDKREKL

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gi|377 VGCTDLNEDLGVVWIFKIKTQDGHAKIGNLEFLEKLLLGEALARVKAEEKWRDKREKL
      840      850      860      870      880      890
Cry1Ac 900      910      920      930      940      950
EWETNIVYKEAKESVDALFVNSQYDQLQADTNMIAMIHAADKRVHSIREAYLPELSVIPGV
gi|377 EWETNIVYKEAKESVDALFVDSQYNRLQTDTNMIAMIHAADKRVHRIREAYLPELSVIPGV
      900      910      920      930      940      950
Cry1Ac 960      970      980      990      1000     1010
NAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLVVPVW
gi|377 NAAIFEELEGLIFTAFSLYDARNVIKNGDFNYGLSCWVNVKGVHVDVEEQNNHRSVLVPIVW
      960      970      980      990      1000     1010
Cry1Ac 1020     1030     1040     1050     1060     1070
EAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNIV
gi|377 EAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCVEEIVPNNIV
      1020     1030     1040     1050     1060     1070
Cry1Ac 1080     1090     1100     1110     1120     1130
TCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFNRG
gi|377 TCNDYTATQEEYEGTYTSRNRGYDGYESNNSVPADYASAYEEKAYTDGRDNPCESNRG
      1080     1090     1100     1110     1120     1130
Cry1Ac 1140     1150     1160     1170     1180
YRDYTPPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|377 YRDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170     1180
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL

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>>gi|15126304|gb|AAE73540.1| Sequence 12 from patent US (1177 aa)
  initn: 7168  initl: 3919  opt: 7159  Z-score: 8433.4  bits: 1572.4  E(): 0
Smith-Waterman score: 7159; 91.286% identity (95.008% similar) in 1182 aa overlap
(5-1182:1-1177)

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gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL
gi|151 TLTVLIDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSRGSAQIERSIRSPHL
      240      250      260      270      280      290
Cry1Ac 310      320      330      340      350      360
MDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
gi|151 MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO
gi|151 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|151 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLFNLS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|151 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHNLVNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|151 TTNLRIVYVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMSQSSFTVGDATF
      540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQQG
gi|151 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQQG
      660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|151 DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830

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Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 gi|151 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 780 790 800 810 820 830

840 850 860 870 880 890  
 Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 gi|151 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 840 850 860 870 880 890

900 910 920 930 940 950  
 Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP  
 gi|151 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP  
 900 910 920 930 940 950

960 970 980 990 1000 1010  
 Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP  
 gi|151 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP  
 960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
 Cry1Ac EWEAEVSQEVVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN  
 gi|151 EWEAEVSQEVVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN  
 1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130  
 Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPECFNRGYR  
 gi|151 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPECFNRGYR  
 1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180  
 Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|151 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|19577427|emb|CAD28601.1| unnamed protein product [s (1177 aa)  
 initn: 7168 initl: 3919 opt: 7159 Z-score: 8433.4 bits: 1572.4 E(): 0  
 Smith-Waterman score: 7159; 91.286% identity (95.008% similar) in 1182 aa overlap  
 (5-1182:1-1177)

10 20 30 40 50 60  
 Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|195 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 gi|195 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|195 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 gi|195 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLNFDGSGFRGSAQGIERSIRSPHL  
 gi|195 TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLNFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 gi|195 MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO  
 gi|195 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 gi|195 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 420 430 440 450 460 470

490 500 510 520 530  
 Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
 gi|195 VKAHTLQSGTTPVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS  
 480 490 500 510 520 530

540 550 560 570 580 590  
 Cry1Ac VTPIHNLVNWGNSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
 gi|195 TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMSQSSFTVQADTF  
 540 550 560 570 580 590

600 610 620 630 640 650  
 Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 gi|195 SSGNEVYIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 600 610 620 630 640 650

660 670 680 690 700 710  
 Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
 gi|195 VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
 660 670 680 690 700 710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFCDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|195 DDVFKENYVTLTSGTFCDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|195 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

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840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|195 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|195 KLEWETNIVYKAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|195 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
      960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|195 EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020     1030     1040     1050     1060     1070

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRYR
gi|195 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRYR
      1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|195 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170

```

>>gi|16242909|gb|AAE80139.1| Sequence 12 from patent US (1177 aa)  
 initn: 7168 initl: 3919 opt: 7159 Z-score: 8433.4 bits: 1572.4 E(): 0  
 Smith-Waterman score: 7159; 91.286% identity (95.008% similar) in 1182 aa overlap  
 (5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|162 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|162 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|162 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162 MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|162 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|162 NNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|162 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHNLVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|162 TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFTFPMQSSFTVGADTF
      540     550     560     570     580     590

```

```

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162 SSGNEVYIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600     610     620     630     640     650

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660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTIQGG
gi|162 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTIQGG
      660      670      680      690      700      710

```

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSTGTFDECYPTLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYSIRYNAK
gi|162 DDVFKENYVTLSTGTFDECYPTLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYLRIRYNAK
      720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|162 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|162 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVLVVP
gi|162 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVLVVP
      960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWAEVSVQEVVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|162 EWAEVSVQEVVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
      1020     1030     1040     1050     1060     1070

```

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1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
gi|162 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
      1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|162 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170

```

```

>>gi|12824338|gb|AAE49244.1| Sequence 12 from patent US (1177 aa)
  initn: 7168 initl: 3919 opt: 7159 Z-score: 8433.4 bits: 1572.4 E(): 0
Smith-Waterman score: 7159; 91.286% identity (95.008% similar) in 1182 aa overlap
(5-1182:1-1177)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|128 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNFREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYQNFREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|128 TLTVLDIVSLFPNYSRRYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITIIYTDHARGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQ
gi|128 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQ
      360     370     380     390     400     410

```

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430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|128 VKAHTLQSGTTVVRGPGFTGGDILLRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|128 TTNLRIVYTVAGERIFAGQFNKTMDTGDLPTQSFYSYATINTAFTFPMQSSFTVGDATF

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Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVSDLSDEIPPQ  
gi|297 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVSDLSDEIPPQ  
360 370 380 390 400 410

430 440 450 460 470 480  
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|297 NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL  
420 430 440 450 460 470

490 500 510 520 530  
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
gi|297 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS  
480 490 500 510 520 530

540 550 560 570 580 590  
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF  
gi|297 TTNLRITYVTIVAGERIFAGQFNKTMGTGDLPTFQSFYATINTAFTFPMSSFTVGDATF  
540 550 560 570 580 590

600 610 620 630 640 650  
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNL  
gi|297 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGKTDVTDYHIDQVSNL  
600 610 620 630 640 650

660 670 680 690 700 710  
Cry1Ac VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
gi|297 VDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKINRQLDRGWRGSTDITIQRG  
660 670 680 690 700 710

720 730 740 750 760 770  
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYLSIRYNAK  
gi|297 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYLIRYNAK  
720 730 740 750 760 770

780 790 800 810 820 830  
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD  
gi|297 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD  
780 790 800 810 820 830

840 850 860 870 880 890  
Cry1Ac IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|297 IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
840 850 860 870 880 890

900 910 920 930 940 950  
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPPELSVIP  
gi|297 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPPELSVIP  
900 910 920 930 940 950

960 970 980 990 1000 1010  
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSLVLPV  
gi|297 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSLVLPV  
960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
Cry1Ac EWEAEVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN  
gi|297 EWEAEVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN  
1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130  
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRGRY  
gi|297 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRGRY  
1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180  
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|297 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1140 1150 1160 1170

>>gi|20221575|gb|AAE87148.1| Sequence 28 from patent US (1177 aa)  
initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0  
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap  
(5-1182:1-1177)

10 20 30 40 50 60  
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF  
gi|202 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF  
10 20 30 40 50

70 80 90 100 110 120  
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE  
gi|202 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

130 140 150 160 170 180  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|202 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYQFRREL  
gi|202 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYQFRREL  
180 190 200 210 220 230

250 260 270 280 290 300  
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFVDFGSRGSAQGIERSIRSPHL  
gi|202 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFVDFGSRGSAQGIERSIRSPHL  
240 250 260 270 280 290

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          310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|202 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPPQ
gi|202 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|202 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|202 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|202 TTNLRITYVTVAGERIFAGQFNKMTDGTGDLTQFSFSYATINTAFTFPMSQSSFTVGADTF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|202 SSGNEVYIDRFELIPVPTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
gi|202 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTITIQRG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK
gi|202 DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLIRYNAK
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHHSFLD
gi|202 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHHSFLD
          780      790      800      810      820      830

          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|202 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
          840      850      860      870      880      890

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          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
gi|202 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
          900      910      920      930      940      950

          960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
gi|202 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
          960      970      980      990      1000      1010

          1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVRCVPCGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|202 EWEAEVSQEVVRCVPCGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
          1020      1030      1040      1050      1060      1070

          1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYR
gi|202 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYR
          1080      1090      1100      1110      1120      1130

          1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|202 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140      1150      1160      1170

>>gi|12824341|gb|AAE49247.1| Sequence 28 from patent US (1177 aa)
initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
          180      190      200      210      220      230

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                250      260      270      280      290      300
Cry1Ac  TLTVLDIIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSIIRSPHL
gi|128  TLTVLDIIVALFPNYSRRYPPIRTVSQLTREIYTNVLENFDGSRFGSAQGIERSIRSPHL
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac  GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIIPPQ
gi|128  GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIIPPQ
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128  NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
                420      430      440      450      460      470

                490      500      510      520      530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNssGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
gi|128  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
                480      490      500      510      520      530

                540      550      560      570      580      590
Cry1Ac  VTIPIHLNVNwGNSsIFSNtVpATATSLDNLQSSDFGyFESANAFTSSLGN---IVGVRNF
gi|128  TTNLRiYVtVAGERIFAGQFNKtMDtGDPLTFQSFsYATINTAFTFPMSQSSFTVgADTF
                540      550      560      570      580      590

                600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVtATLEAEYnLERAQKAVNALFTStNQLGLKtNVTDYHIDQVSNL
gi|128  SSGNEVYIDRFELIPVtATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
                600      610      620      630      640      650

                660      670      680      690      700      710
Cry1Ac  VTyLsDEfCLDEKRElSEKvKHAKRLSDERNLLQDSNFKDINRQPERGWGSgtGITIQGG
gi|128  VDCLsDEfCLDEKRElSEKvKHAKRLSDERNLLQDPNFKGINRQLDRGWRGStDITIQRG
                660      670      680      690      700      710

                720      730      740      750      760      770
Cry1Ac  DDVfKEnYVTLsGTFDEcYPTyLYQKIDESKLKAFTRyQLRGYIEDsQDLeySIRYNAK
gi|128  DDVfKEnYVTLpGTFDEcYPTyLYQKIDESKLKAFTRyQLRGYIEDsQDLeyLIRYNAK
                720      730      740      750      760      770

                780      790      800      810      820      830
Cry1Ac  HETVnVpGTGSLwPLsAQSPiGKCGEPnRCAPHLewNPDLDCsCRDGEKCAHSHHfSLD
gi|128  HETVnVpGTGSLwPLsAQSPiGKCGEPnRCAPHLewNPDLDCsCRDGEKCAHSHHfSLD

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                780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|128  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
                840      850      860      870      880      890

                900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|128  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
                900      910      920      930      940      950

                960      970      980      990      1000      1010
Cry1Ac  GVNAaIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
gi|128  GVNAaIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
                960      970      980      990      1000      1010

                1020      1030      1040      1050      1060      1070
Cry1Ac  EWEAEVsqEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKfSNCVVEEIEYPNN
gi|128  EWEAEVsqEVRVCPGRGYILRVTAYKEGYGEGCVTIHEIENNTDELKfSNCVVEEIEYPNN
                1020      1030      1040      1050      1060      1070

                1080      1090      1100      1110      1120      1130
Cry1Ac  TVTCNDYtVNQEEYGGAYTSRNRGYNEAPsVPADYASVVEEKsYTDGRRENpCEFNrgYR
gi|128  TVTCNDYtVNQEEYGGAYTSRNRGYNEAPsVPADYASVVEEKsYTDGRRENpCEFNrgYR
                1080      1090      1100      1110      1120      1130

                1140      1150      1160      1170      1180
Cry1Ac  DYtPLPVGyVtKELEyFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|128  DYtPLPVGyVtKELEyFPETDKVWIEIGETEGTFIVDSVELLMEE
                1140      1150      1160      1170

>>gi|162500742|gb|ABY14166.1| Sequence 28 from patent US (1177 aa)
  initn: 7118 init1: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

                10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|162  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|162  VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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120      130      140      150      160      170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|162  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180      190      200      210      220      230
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|162  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290      300
Cry1Ac  MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162  MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310      320      330      340      350      360
Cry1Ac  GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
gi|162  GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
370      380      390      400      410      420
Cry1Ac  NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNIIASDSITQIPa
gi|162  NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNIIASDSITQIPa
430      440      450      460      470      480
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNssGNNIQNRgyIEVPIHFPSTSTRYVRVRYAS
gi|162  VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
490      500      510      520      530
Cry1Ac  VTIPIHLNVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|162  TTNLRIYVTVAGERIFAGQFNKTMdTGDPLTFQSFsYATINTAFTFPMSQSSFTVgADTF
540      550      560      570      580      590
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINIGIKTDPVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac  VTyLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|162  VDCLsDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGStDITIQRG
660      670      680      690      700      710
Cry1Ac  DDVFKENYVTLsGTFDECYPTyLYQKIDESKLKAFTRyQLRGYIEDSQDLEIYSIRYNAK
gi|162  DDVFKENYVTLsGTFDECYPTyLYQKIDESKLKAFTRyQLRGYIEDSQDLEIYSIRYNAK

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gi|162  DDVFKENYVTLPGTFDECYPTyLYQKIDESKLKAFTRyQLRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770
Cry1Ac  HETVNVPGTGSWLPsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLD
gi|162  HETVNVPGTGSWLPsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLD
780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEFLEEKPLVGEALARVKRAEKkWRDKRE
gi|162  IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEFLEEKPLVGEALARVKRAEKkWRDKRE
840      850      860      870      880      890
Cry1Ac  KLEWETNIvYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRvHSIREAYLPELSVIP
gi|162  KLEWETNIvYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRvHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac  GVNAAIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
gi|162  GVNAAIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
960      970      980      990      1000      1010
Cry1Ac  EWEAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKfSNCVVEEIEYPNN
gi|162  EWEAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKfSNCVVEEIEYPNN
1020     1030     1040     1050     1060     1070
Cry1Ac  TVTCNDYTVNqEEYGGAYTSRNrgYNEAPsVPADYASVYEEKSYTDGRRENpCEFNrgYR
gi|162  TVTCNDYTVNqEEYGGAYTSRNrgYNEAPsVPADYASVYEEKSYTDGRRENpCEFNrgYR
1080     1090     1100     1110     1120     1130
Cry1Ac  DYTPLPVGYVtKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|162  DYTPLPVGYVtKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170
>>gi|40189706|gb|AAR76446.1| Sequence 28 from patent US (1177 aa)
initn: 7118 init1: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEFVPGAGF
gi|401  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEFVPGAGF
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGPsQWDAFLVQIEQLINQRIEEFARNAISRLGLSnlYQIYAESFRE

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gi|401 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|401 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      .....
gi|401 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHL
      .....
gi|401 TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|401 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
      .....
gi|401 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|401 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNGLS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|401 VKAHTLQSGTIVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
      .....
gi|401 TTNLRITYVIVAGERIFAGQFNKTMDDTGDPLTFQSFYATINTAFTFPMSQSSFTVGADTF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNL
      .....
gi|401 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600     610     620     630     640     650
      660     670     680     690     700     710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

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      .....
gi|401 VDCLSEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQRG
      660     670     680     690     700     710
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
      .....
gi|401 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
      720     730     740     750     760     770
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSFLD
      .....
gi|401 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSFLD
      780     790     800     810     820     830
      840     850     860     870     880     890
Cry1Ac IDVGCIDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      .....
gi|401 IDVGCIDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840     850     860     870     880     890
      900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIP
      .....
gi|401 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIP
      900     910     920     930     940     950
      960     970     980     990     1000    1010
Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
      .....
gi|401 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
      960     970     980     990     1000    1010
      1020    1030    1040    1050    1060    1070
Cry1Ac EWEAEVSQEVVRCPRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCVVEEYIPNN
      .....
gi|401 EWEAEVSQEVVRCPRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCVVEEYIPNN
      1020    1030    1040    1050    1060    1070
      1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
      .....
gi|401 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
      1080    1090    1100    1110    1120    1130
      1140    1150    1160    1170    1180
Cry1Ac DYTPLPGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
      .....
gi|401 DYTPLPGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
      1140    1150    1160    1170
>>gi|83329855|gb|ABC06984.1| Sequence 28 from patent US (1177 aa)
      initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF

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gi|833      MNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTLQFLLSSEFVPGAGF
              10      20      30      40      50
Cry1Ac     70      80      90      100     110     120
VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|833     VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
              60      70      80      90      100     110
Cry1Ac     130     140     150     160     170     180
WEADPTN PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|833     WEADPTN PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170
Cry1Ac     190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|833     VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
              180     190     200     210     220     230
Cry1Ac     250     260     270     280     290     300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGLEGSIRSPHL
gi|833     TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGLEGSIRSPHL
              240     250     260     270     280     290
Cry1Ac     310     320     330     340     350     360
MDILNSIT IYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|833     MDILNSIT IYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
              300     310     320     330     340     350
Cry1Ac     370     380     390     400     410     420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEI PPQ
gi|833     GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEI PPQ
              360     370     380     390     400     410
Cry1Ac     430     440     450     460     470     480
NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
gi|833     NNVVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
              420     430     440     450     460     470
Cry1Ac     490     500     510     520     530
VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|833     VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
              480     490     500     510     520     530
Cry1Ac     540     550     560     570     580     590
VTPIHLNWNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|833     TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSF SYATINTAFTFPPMSQSSFTVGADTF
              540     550     560     570     580     590
Cry1Ac     600     610     620     630     640     650

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Cry1Ac     SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
              . . . . .
gi|833     SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
              600     610     620     630     640     650
Cry1Ac     660     670     680     690     700     710
VTYLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|833     VDCLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
              660     670     680     690     700     710
Cry1Ac     720     730     740     750     760     770
DDVFKENYVTLSGTFDECYPTLYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|833     DDVFKENYVTLPGTFDECYPTLYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
              720     730     740     750     760     770
Cry1Ac     780     790     800     810     820     830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFLSD
gi|833     HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFLSD
              780     790     800     810     820     830
Cry1Ac     840     850     860     870     880     890
IDVGCCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|833     IDVGCCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
              840     850     860     870     880     890
Cry1Ac     900     910     920     930     940     950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
gi|833     KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
              900     910     920     930     940     950
Cry1Ac     960     970     980     990     1000    1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNQRSVLPVVP
gi|833     GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNQRSVLPVVP
              960     970     980     990     1000    1010
Cry1Ac     1020    1030    1040    1050    1060    1070
EWEAEVSEQEVRVCPGRGYLLRVTA YKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
gi|833     EWEAEVSEQEVRVCPGRGYLLRVTA YKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
              1020    1030    1040    1050    1060    1070
Cry1Ac     1080    1090    1100    1110    1120    1130
TVCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
gi|833     TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
              1080    1090    1100    1110    1120    1130
Cry1Ac     1140    1150    1160    1170    1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|833     DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
              1140    1150    1160    1170

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Regulatory Product Characterization Team

>>gi|19577443|emb|CAD28604.1| unnamed protein product [s (1177 aa)
initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|195 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50
70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|195 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
60 70 80 90 100 110
130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|195 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170
190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|195 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230
250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSIIRSPHL
gi|195 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSIIRSPHL
240 250 260 270 280 290
310 320 330 340 350 360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|195 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350
370 380 390 400 410 420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
gi|195 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
360 370 380 390 400 410
430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|195 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
420 430 440 450 460 470
490 500 510 520 530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
gi|195 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGN---IVGVRNF
gi|195 TTNLRIVYTVAGERIFAGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSQSSFTVGADTF
540 550 560 570 580 590
600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|195 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDVTDYHIDQVSNL
600 610 620 630 640 650
660 670 680 690 700 710
Cry1Ac VTYSLDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG
gi|195 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660 670 680 690 700 710
720 730 740 750 760 770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|195 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770
780 790 800 810 820 830
Cry1Ac HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|195 HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
780 790 800 810 820 830
840 850 860 870 880 890
Cry1Ac IDVGCTDLNEDLVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|195 IDVGCTDLNEDLVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890
900 910 920 930 940 950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|195 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950
960 970 980 990 1000 1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVVLVVP
gi|195 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVVLVVP
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070
Cry1Ac EWEAEVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNN
gi|195 EWEAEVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNN
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
Cry1Ac TVTCNDYTNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGRY
gi|195 TVTCNDYTNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGRY
1080 1090 1100 1110 1120 1130



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1020      1030      1040      1050      1060      1070
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
gi|316 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
1080      1090      1100      1110      1120      1130

1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|316 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140      1150      1160      1170

>>gi|112061963|gb|ABH98782.1| Sequence 28 from patent US (1177 aa)
initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|112 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|112 VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNVLENFDGFSFRGSAQGIERSIRSPHL
gi|112 TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNVLENFDGFSFRGSAQGIERSIRSPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112 MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
gi|112 GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q

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360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|112 NNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRYAS
gi|112 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|112 TTNLRIYVTVAGERIFAGQFNKTMDTGDLPTFQSFYATINTAFTFPMQSSFTVGADTF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINGIKTDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQQG
gi|112 VDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
gi|112 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|112 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|112 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

960      970      980      990      1000     1010
Cry1Ac GVNAAFELEEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVEEQNNQRSVLVVP

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gi|112 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVP
960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIEHEIENNTDELKFSNCVVEEIIYPNN

gi|112 EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIEHEIENNTDELKFSNCVVEEIIYPNN
1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130
Cry1Ac TVTCDNDYTVNQEYEGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR

gi|112 TVTCDNDYTVNQEYEGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|112 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

>>gi|16242912|gb|AAE80142.1| Sequence 28 from patent US (1177 aa)
initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

10 20 30 40 50 60
Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

gi|162 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESPFE

gi|162 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESPFE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL

gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDDIVSLFPNYSRRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL

gi|162 TLTVLDDIVSLFPNYSRRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ

gi|162 MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

370 380 390 400 410 420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ

gi|162 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
360 370 380 390 400 410

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA

gi|162 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
420 430 440 450 460 470

490 500 510 520 530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHPSTSTRYRVRVRYAS

gi|162 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTPIHLLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF

gi|162 TTNLRIVYVAGERIFAGQFNKTMDTGDPDLPQSFYSYATINTAFTFPMQSSFTVGDATF
540 550 560 570 580 590

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|162 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600 610 620 630 640 650

660 670 680 690 700 710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

gi|162 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660 670 680 690 700 710

720 730 740 750 760 770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK

gi|162 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770

780 790 800 810 820 830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHSHFLSD

gi|162 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHSHFLSD
780 790 800 810 820 830

840 850 860 870 880 890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

gi|162 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

900 910 920 930 940 950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP

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gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

Cry1Ac 960      970      980      990      1000     1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSV L VVP
gi|162 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSV L VVP
      960      970      980      990      1000     1010

Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
gi|162 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
      1020     1030     1040     1050     1060     1070

Cry1Ac 1080     1090     1100     1110     1120     1130
TVTCONDYTVNQEEYGGAYTSRNRGYNEAPSV PADYASVYEEKSYTDGRREN PCEFNRGYR
gi|162 TVTCONDYTVNQEEYGGAYTSRNRGYNEAPSV PADYASVYEEKSYTDGRREN PCEFNRGYR
      1080     1090     1100     1110     1120     1130

Cry1Ac 1140     1150     1160     1170     1180
DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
gi|162 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
      1140     1150     1160     1170

>>gi|53937592|gb|AAV01843.1| Sequence 28 from patent US (1177 aa)
  initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
      10      20      30      40      50

Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|539 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV LRDVDS
gi|539 WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV LRDVDS
      120     130     140     150     160     170

Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

Cry1Ac 250     260     270     280     290     300
TLTVLDIVSLFPNYDSRRTYPIRTVSQLTREIYTNVLENFDG SFRGSAQGI EGSIRSPHL

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gi|539 TLTVLDIVSLFPNYDSRRTYPIRTVSQLTREIYTNVLENFDG SFRGSAQGI ERSIRSPHL
      240     250     260     270     280     290

Cry1Ac 310     320     330     340     350     360
MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIV AQLGQ
gi|539 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIV AQLGQ
      300     310     320     330     340     350

Cry1Ac 370     380     390     400     410     420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNL PSAVYRKSGTVDSLDEIP PQ
gi|539 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNL PSAVYRKSGTVDSLDEIP PQ
      360     370     380     390     400     410

Cry1Ac 430     440     450     460     470     480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSW IHRSAEFNNIIASDSITQI PA
gi|539 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSW IHRSAEFNNIIASDSITQI PL
      420     430     440     450     460     470

Cry1Ac 490     500     510     520     530
VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYI EVP IHPFSTSTRYRVRVRYAS
gi|539 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RRYRIRVRYAS
      480     490     500     510     520     530

Cry1Ac 540     550     560     570     580     590
VTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFES ANAFTSSLGN---IVGVRNF
gi|539 TTNLRIYVTVAGERIFAGQFNKTMDTGDLPTFQSF SYATINTAFTFPMSQSSFTVGADTF
      540     550     560     570     580     590

Cry1Ac 600     610     620     630     640     650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTS TNQLGLKTNVTDYHIDQVSNL
gi|539 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTS INQIGIKTDVTDYHIDQVSNL
      600     610     620     630     640     650

Cry1Ac 660     670     680     690     700     710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNF KDINRQPERGWGGSTGITIQGG
gi|539 VDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDP NFKGINRQLDRGWRGSTDITIQRG
      660     670     680     690     700     710

Cry1Ac 720     730     740     750     760     770
DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTR YQLRGYIEDSQDLEIYLSIRYNAK
gi|539 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTR YQLRGYIEDSQDLEIYLSIRYNAK
      720     730     740     750     760     770

Cry1Ac 780     790     800     810     820     830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDL DDCSCRDGEKCAHSHHFFSLD
gi|539 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDL DDCSCRDGEKCAHSHHFFSLD
      780     790     800     810     820     830

Cry1Ac 840     850     860     870     880     890

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Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

gi|539 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP

gi|539 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP

Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSVLVVP

gi|539 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSVLVVP

Cry1Ac EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN

gi|539 EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN

Cry1Ac TVTCNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNCPFNRYR

gi|539 TVTCNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNCPFNRYR

Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE

gi|539 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE

>>gi|77376720|gb|ABA70267.1| Sequence 28 from patent US (1177 aa)
in1tn: 7118 in1t1: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

gi|773 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

gi|773 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|773 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL

gi|773 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

gi|773 TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi|773 MDILNSITTYTDAHRGEYYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ

gi|773 GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ

Cry1Ac NNNVPPRQGFSHRSLHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPL

gi|773 NNNVPPRQGFSHRSLHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPL

Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|773 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS

Cry1Ac VTPIHNLVNWGNSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF

gi|773 TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLPFQSFYATINTAFTFPMSQSSFTVGADTF

Cry1Ac SGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|773 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL

Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

gi|773 VDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG

Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK

gi|773 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|773 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

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840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|773 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|773 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

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960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
gi|773 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
      960      970      980      990      1000     1010

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1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|773 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020     1030     1040     1050     1060     1070

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1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
gi|773 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
      1080     1090     1100     1110     1120     1130

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1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|773 DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170

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>>gi|47257345|gb|AAT23508.1| Sequence 28 from patent US (1177 aa)
  initn: 7118 initl: 3806 opt: 7109 Z-score: 8374.4 bits: 1561.5 E(): 0
Smith-Waterman score: 7109; 90.694% identity (94.755% similar) in 1182 aa overlap
(5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|472 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      180      190      200      210      220      230

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250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|472 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290

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310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

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370      380      390      400      410      420
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|472 GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      360      370      380      390      400      410

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430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
      420      430      440      450      460      470

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490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|472 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480      490      500      510      520      530

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540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|472 TTNLRLYVTVAGERIFAGQFNKTMDTGDLPTFQSFYATINTAFTFPMQSSFTVGADTF
      540      550      560      570      580      590

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600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

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660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
gi|472 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITIQRG
      660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNK
gi|472 DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNK
      720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|472 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

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840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|472 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVVLVVP
gi|472 GVNAAIFEELEGRIFAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVVLVVP
      960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|472 EWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
      1020     1030     1040     1050     1060     1070

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1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
gi|472 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
      1080     1090     1100     1110     1120     1130

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1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|472 DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170

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>>gi|20221573|gb|AAE87146.1| Sequence 14 from patent US (1177 aa)
  initn: 7093 initl: 3806 opt: 7084 Z-score: 8345.0 bits: 1556.1 E(): 0
Smith-Waterman score: 7084; 90.440% identity (94.416% similar) in 1182 aa overlap
(5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|202 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPGSQWDAFLVQIEQLINQRIE EFARNQAI SRLEGLSNLYQIYAESFRE
gi|202 VLGLVDIIWIGIFGPGSQWDAFLVQIEQLINQRIE EFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|202 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
gi|202 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
      180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
gi|202 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|202 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
gi|202 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360     370     380     390     400     410

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430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|202 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420     430     440     450     460     470

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490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|202 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480     490     500     510     520     530

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540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|202 TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYSATINTAFTFPMSQSSFTVGADTF
      540     550     560     570     580     590

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600     610     620     630     640     650
Cry1Ac SGTAGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|202 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNL

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        600      610      620      630      640      650
Cry1Ac  660      670      680      690      700      710
: VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: .....: .....: .....: .....: .....: .....:
gi|202  VDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
        660      670      680      690      700      710

        720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
: .....: .....: .....: .....: .....: .....:
gi|202  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
        720      730      740      750      760      770

        780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
: .....: .....: .....: .....: .....: .....:
gi|202  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
        780      790      800      810      820      830

        840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
: .....: .....: .....: .....: .....: .....:
gi|202  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
        840      850      860      870      880      890

        900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
: .....: .....: .....: .....: .....: .....:
gi|202  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
        900      910      920      930      940      950

        960      970      980      990      1000     1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVVVP
: .....: .....: .....: .....: .....: .....:
gi|202  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVVVP
        960      970      980      990      1000     1010

        1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
: .....: .....: .....: .....: .....: .....:
gi|202  EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
        1020     1030     1040     1050     1060     1070

        1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRRGYR
: .....: .....: .....: .....: .....: .....:
gi|202  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRRGYR
        1080     1090     1100     1110     1120     1130

        1140     1150     1160     1170     1180
Cry1Ac  DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
: .....: .....: .....: .....: .....: .....:
gi|202  DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
        1140     1150     1160     1170

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>>gi|15126305|gb|AAE73541.1| Sequence 14 from patent US (1177 aa)
  initn: 7093  init1: 3806  opt: 7084  Z-score: 8345.0  bits: 1556.1  E(): 0

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Smith-Waterman score: 7084; 90.440% identity (94.416% similar) in 1182 aa overlap
(5-1182:1-1177)

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        10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: .....: .....: .....: .....: .....: .....:
gi|151  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
        10      20      30      40      50

        70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
: .....: .....: .....: .....: .....: .....:
gi|151  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
        60      70      80      90      100     110

        130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNMDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: .....: .....: .....: .....: .....: .....:
gi|151  WEADPTNPALREEMRIQFNMDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        120     130     140     150     160     170

        190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
: .....: .....: .....: .....: .....: .....:
gi|151  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
        180     190     200     210     220     230

        250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDFGSRGSAQIEGSIRSPHL
: .....: .....: .....: .....: .....: .....:
gi|151  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDFGSRGSAQIEGSIRSPHL
        240     250     260     270     280     290

        310     320     330     340     350     360
Cry1Ac  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
: .....: .....: .....: .....: .....: .....:
gi|151  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
        300     310     320     330     340     350

        370     380     390     400     410     420
Cry1Ac  GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
: .....: .....: .....: .....: .....: .....:
gi|151  GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
        360     370     380     390     400     410

        430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
: .....: .....: .....: .....: .....: .....:
gi|151  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
        420     430     440     450     460     470

        490     500     510     520     530
Cry1Ac  VKGNFLNGS-VISGPGFTGGDLVRLNLSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: . . . . .: . . . . .: . . . . .: . . . . .: . . . . .: . . . . .
gi|151  VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
        480     490     500     510     520     530

        540     550     560     570     580     590
Cry1Ac  VPIHLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF

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Cry1Ac VKGNFLFNNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
gi|195 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS  
480 490 500 510 520 530

540 550 560 570 580 590  
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
gi|195 TTNLRIRYVTVAGERIFAGQFNKMTDGTGDLTFQSFYATINTAFTFPMSQSSFTVGADTF  
540 550 560 570 580 590

600 610 620 630 640 650  
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
gi|195 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL  
600 610 620 630 640 650

660 670 680 690 700 710  
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG  
gi|195 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG  
660 670 680 690 700 710

720 730 740 750 760 770  
Cry1Ac DDVFKENYVTLGSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
gi|195 DDVFKENYVTLGSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYLRIRYNAK  
720 730 740 750 760 770

780 790 800 810 820 830  
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD  
gi|195 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD  
780 790 800 810 820 830

840 850 860 870 880 890  
Cry1Ac IDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|195 IDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
840 850 860 870 880 890

900 910 920 930 940 950  
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP  
gi|195 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP  
900 910 920 930 940 950

960 970 980 990 1000 1010  
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP  
gi|195 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP  
960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTITHEIENNTDELKFSNCVVEEIIYPNN  
gi|195 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTITHEIENNTDELKFSNCVVEEIIYPNN  
1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130  
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFENRGYR  
gi|195 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFENRGYR  
1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180  
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|195 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1140 1150 1160 1170

>>gi|16242910|gb|AAE80140.1| Sequence 14 from patent US (1177 aa)  
initn: 7093 init1: 3806 opt: 7084 Z-score: 8345.0 bits: 1556.1 E(): 0  
Smith-Waterman score: 7084; 90.440% identity (94.416% similar) in 1182 aa overlap  
(5-1182:1-1177)

10 20 30 40 50 60  
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF  
gi|162 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF  
10 20 30 40 50

70 80 90 100 110 120  
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLEGLSNLYQIYAESFRE  
gi|162 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

130 140 150 160 170 180  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

250 260 270 280 290 300  
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH  
gi|162 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH  
240 250 260 270 280 290

310 320 330 340 350 360  
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ  
gi|162 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ  
300 310 320 330 340 350

370 380 390 400 410 420  
Cry1Ac GVYRSLSSLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
gi|162 GVYRSLSSLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
360 370 380 390 400 410

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      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|162 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNGYIEVPIHFPSTSTRYRVRYAS
gi|162 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTPIHNLNVWGNSSIFSNTVPATATSLDNLQSSDFGYPESANAFTSSLGN---IVGVRNF
gi|162 TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMQSSFTVGADTF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFFFIPTVATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162 SSGNEVYIDRFELIPVTATFEAEYDLERAKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|162 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYSIRYNAK
gi|162 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYLIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|162 HETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|162 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVPP
gi|162 GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVPP
      960      970      980      990      1000      1010

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      1020      1030      1040      1050      1060      1070
Cry1Ac EWAEVSVQEVRRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNN
gi|162 EWAEVSVQEVRRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRGYR
gi|162 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRGYR
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|162 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170

>>gi|12824339|gb|AAE49245.1| Sequence 14 from patent US (1177 aa)
  initn: 7093 init1: 3806 opt: 7084 Z-score: 8345.0 bits: 1556.1 E(): 0
Smith-Waterman score: 7084; 90.440% identity (94.416% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|128 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH
gi|128 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

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          370      380      390      400      410      420
Cry1Ac  GYVRTLSSTLYRRPFNIGLNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIIPPQ
gi|128  GYVRTLSSTLYRRPFNIGLNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIIPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac  VTIPIHLNVNNGSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|128  TTNLRIFYVTVAGERIFAGQFNKTMDTGDPLTFQSFYSYATINTAFTFPMSQSSFTVGADTF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac  VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|128  VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYSIRYNAK
gi|128  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYLIRYNAK
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|128  HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
          780      790      800      810      820      830

          840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|128  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
          840      850      860      870      880      890

          900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|128  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP

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          900      910      920      930      940      950
Cry1Ac  960      970      980      990      1000      1010
gi|128  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
          960      970      980      990      1000      1010

          1020      1030      1040      1050      1060      1070
Cry1Ac  EWAEAVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
gi|128  EWAEAVSQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
          1020      1030      1040      1050      1060      1070

          1080      1090      1100      1110      1120      1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
gi|128  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
          1080      1090      1100      1110      1120      1130

          1140      1150      1160      1170      1180
Cry1Ac  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|128  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140      1150      1160      1170

>>gi|112061962|gb|ABH98781.1| Sequence 26 from patent US (1177 aa)
initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|112  MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|112  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|112  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|112  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
          180      190      200      210      220      230

          250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|112  TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

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240      250      260      270      280      290
Cry1Ac MDILNSITIIYTDahrgeyywshgqimaspvgfsgpeftfpplvgtmgnaaPQQRIVAQLGQ
gi|112 MDILNSITIIYTDahrgeyywshgqimaspvgfsgpeftfpplvgtmgnaaPQQRIVAQLGQ
300      310      320      330      340      350
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
gi|112 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
360      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
gi|112 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
360      370      380      390      400      410
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWihRsaefNniIASDSITQIPA
gi|112 NNNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWihRsaefNniIASDSITQIPA
420      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWihRsaefNniIASDSITQIPA
gi|112 NNNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWihRsaefNniIASDSITQIPA
420      430      440      450      460      470
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNssGNniQNRgyIEVPIHFPSTSTRYVRVRYAS
gi|112 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNingQLPQ--RYRARIRYAS
480      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNssGNniQNRgyIEVPIHFPSTSTRYVRVRYAS
gi|112 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNingQLPQ--RYRARIRYAS
480      490      500      510      520      530
Cry1Ac VPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|112 TTNLRiYVTVAGERIFAGQFNKtMDTGDPLTFQSFsYATINTAFtPMSQSSFTVGADTF
540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|112 TTNLRiYVTVAGERIFAGQFNKtMDTGDPLTFQSFsYATINTAFtPMSQSSFTVGADTF
540      550      560      570      580      590
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac VTYLSDfECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|112 VDCLSDfECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGhNRQLDRGWRGSTDITIQRG
660      670      680      690      700      710
Cry1Ac VTYLSDfECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|112 VDCLSDfECLDEKRELSEKVKHAKRLSDERNLLQDPNFKGhNRQLDRGWRGSTDITIQRG
660      670      680      690      700      710
Cry1Ac DDVfKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRyNAK
gi|112 DDVfKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRyNAK
720      730      740      750      760      770
Cry1Ac DDVfKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRyNAK
gi|112 DDVfKENyVTLsGTFDECYPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRyNAK
720      730      740      750      760      770
Cry1Ac HETVNPgTGSWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSrdGekCAHSHHfSLD
gi|112 HETVNPgTGSWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSrdGekCAHSHHfSLD
780      790      800      810      820      830
Cry1Ac HETVNPgTGSWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSrdGekCAHSHHfSLD
gi|112 HETVNPgTGSWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSrdGekCAHSHHfSLD
780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

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gi|112 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKghVDVEEQNNQRsVLVVP
gi|112 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKghVDVEEQNNQRsVLVVP
960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKghVDVEEQNNQRsVLVVP
gi|112 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKghVDVEEQNNQRsVLVVP
960      970      980      990      1000      1010
Cry1Ac EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEIEYpNN
gi|112 EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEIEYpNN
1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEIEYpNN
gi|112 EWEAEVsqEVRVCPGRgyILRVtAYKEgyGEGCVTIHEIENNTDELKfSNcVEEIEYpNN
1020      1030      1040      1050      1060      1070
Cry1Ac TVTCNDYtVnQEEYGGAYtSRNrgyNEAPsVPADYASVYEEKsYTDGRENpCEFNrgYR
gi|112 TVTCNDYtVnQEEYGGAYtSRNrgyNEAPsVPADYASVYEEKsYTDGRENpCEFNrgYR
1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYtVnQEEYGGAYtSRNrgyNEAPsVPADYASVYEEKsYTDGRENpCEFNrgYR
gi|112 TVTCNDYtVnQEEYGGAYtSRNrgyNEAPsVPADYASVYEEKsYTDGRENpCEFNrgYR
1080      1090      1100      1110      1120      1130
Cry1Ac DYTPLPVGyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
gi|112 DYTPLPVGyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
1140      1150      1160      1170
>>gi|29718512|gb|AAP01236.1| Sequence 26 from patent US (1177 aa)
initn: 7074 init1: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)
10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|297 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10      20      30      40      50
Cry1Ac VLGLVDIIWGIgPgsQWDAFLVQIEQLINQRIEEFARNQAIrSLRGLSNLYQIYAESFR
gi|297 VLGLVDIIWGIgPgsQWDAFLVQIEQLINQRIEEFARNQAIrSLRGLSNLYQIYAESFR
60      70      80      90      100      110
Cry1Ac WEADPTNPALREEMRIQFNdmNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|297 WEADPTNPALREEMRIQFNdmNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAvRWYNTGLERVWGPDSRDWIRYNQFRREL

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gi|162 WEADPTN PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVXVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
.....
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
.....
gi|162 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240      250      260      270      280      290
Cry1Ac 310      320      330      340      350      360
MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
.....
gi|162 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDELIPPQ
.....
gi|162 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDELIPPQ
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
.....
gi|162 NNVVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
.....
gi|162 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS
      480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
.....
gi|162 TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYSYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQGLKTNVTDYHIDQVSNL
.....
gi|162 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
.....
gi|162 VDCLSEDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770

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Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
.....
gi|162 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
.....
gi|162 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830
Cry1Ac 840      850      860      870      880      890
IDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
.....
gi|162 IDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
.....
gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac 960      970      980      990      1000      1010
GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLPV
.....
gi|162 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLPV
      960      970      980      990      1000      1010
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIPYNN
.....
gi|162 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIPYNN
      1020      1030      1040      1050      1060      1070
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEPNRGYR
.....
gi|162 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEPNRGYR
      1080      1090      1100      1110      1120      1130
Cry1Ac 1140      1150      1160      1170      1180
DYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
.....
gi|162 DYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|20221574|gb|AAE87147.1| Sequence 26 from patent US (1177 aa)
initn: 7074 init1: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)
Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
.....
gi|202 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10 20 30 40 50
Cry1Ac 70 80 90 100 110 120

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Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|202 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|202 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|202 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
gi|202 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|202 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGLNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLDEIIPPQ
gi|202 GVYRTLSSTLYRRPFNIGLNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLDEIIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNMIASDSITQIPA
gi|202 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATPTNTIDPERITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|202 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|202 TTNLRIYVTVAGERIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMSSQSSFTVGADTF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|202 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600     610     620     630     640     650

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      660     670     680     690     700     710
Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|202 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660     670     680     690     700     710
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|202 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLD
gi|202 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLD
      780     790     800     810     820     830
      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|202 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840     850     860     870     880     890
      900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
gi|202 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
      900     910     920     930     940     950
      960     970     980     990    1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|202 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
      960     970     980     990    1000    1010
      1020    1030    1040    1050    1060    1070
Cry1Ac EWAEVVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
gi|202 EWAEVVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
      1020    1030    1040    1050    1060    1070
      1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEKSYTDGRENPCFENRGYR
gi|202 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEKSYTDGRENPCFENRGYR
      1080    1090    1100    1110    1120    1130
      1140    1150    1160    1170    1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|202 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140    1150    1160    1170

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>>gi|40189705|gb|AAR76445.1| Sequence 26 from patent US (1177 aa)
  initn: 7074 init1: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

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Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
gi|401 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|401 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|401 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|401 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVDLIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL  
gi|401 TLTVDLIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
gi|401 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQ  
gi|401 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQ

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|401 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
gi|401 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS

Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
gi|401 TTNLR IYVTVAGERIFAGQFNKMTDGTGDFLTFQSFYSATINTAFTPMPSQSSFTVGADTF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
gi|401 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL

Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
gi|401 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG

Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
gi|401 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRNAK

Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD  
gi|401 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD

Cry1Ac IDVGCSDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|401 IDVGCSDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP  
gi|401 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP

Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVVP  
gi|401 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVVP

Cry1Ac EWEAEVVSQEVVRCPRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN  
gi|401 EWEAEVVSQEVVRCPRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN

Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFENRGYR  
gi|401 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFENRGYR

Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|401 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

Regulatory Product Characterization Team

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1140      1150      1160      1170
>>gi|19577441|emb|CAD28603.1| unnamed protein product [B (1177 aa)
  initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|195  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|195  VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|195  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|195  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPNVLENFDGSGFRGSAQGIERSIRSPHL
gi|195  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPNVLENFDGSGFRGSAQGIERSIRSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|195  MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEI PPQ
gi|195  GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEI PPQ
      360     370     380     390     400     410
Cry1Ac NNVVPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|195  NNVVPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      420     430     440     450     460     470
Cry1Ac VKNFNLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYRVRVRYAS
gi|195  VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS

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480      490      500      510      520      530
540      550      560      570      580      590
Cry1Ac VTP IHLNVNWGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|195  TTNLR IYVTVAGERIFAGQFNKMTMDTGDPLTFQSF SYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|195  SSGNEVIIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTITIQGG
gi|195  VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAK
gi|195  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|195  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
      780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|195  IDVGCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|195  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
gi|195  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
      960      970      980      990     1000     1010
Cry1Ac EWEAEVSVQEVVRCVPGRGYILRVTA YKEGEGCVTTIHEIENNTDELKFSNCVVEE IYPNN
gi|195  EWEAEVSVQEVVRCVPGRGYILRVTA YKEGEGCVTTIHEIENNTDELKFSNCVVEE IYPNN
      1020     1030     1040     1050     1060     1070
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPECFNRGYR
gi|195

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gi|195 TVTCNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRGYR
1080 1090 1100 1110 1120 1130

Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|195 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170

>>gi|83329854|gb|ABC06983.1| Sequence 26 from patent US (1177 aa)
initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|833 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60
10 20 30 40 50

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLLEGLSNLYQIYAESFRE
gi|833 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLLEGLSNLYQIYAESFRE
70 80 90 100 110 120
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|833 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
gi|833 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
190 200 210 220 230 240
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVENFDGSGFRGSAQGIERSIRSPHL
gi|833 TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVENFDGSGFRGSAQGIERSIRSPHL
250 260 270 280 290 300
240 250 260 270 280 290

Cry1Ac MDILNSITTYDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|833 MDILNSITTYDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360
300 310 320 330 340 350

Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDLDEIPPQ
gi|833 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDLDEIPPQ
370 380 390 400 410 420
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
1020 1030 1040 1050 1060 1070

gi|833 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|833 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
480 490 500 510 520 530

Cry1Ac VTPIHNLVNWGSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|833 TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMSSSFTVGDATF
540 550 560 570 580 590
540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|833 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600 610 620 630 640 650
600 610 620 630 640 650

Cry1Ac VTLYSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG
gi|833 VDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRGSTDITIQRG
660 670 680 690 700 710
660 670 680 690 700 710

Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|833 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770
720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|833 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
780 790 800 810 820 830
780 790 800 810 820 830

Cry1Ac IDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|833 IDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890
840 850 860 870 880 890

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|833 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950
900 910 920 930 940 950

Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHVDVEEQNNQRSVLPV
gi|833 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHVDVEEQNNQRSVLPV
960 970 980 990 1000 1010
960 970 980 990 1000 1010

Cry1Ac EWEAEVSQEVVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNVCVEEIIYPNN

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gi|833 EWEAEVSEQEVRVCPGRGYLLRVTAKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020      1030      1040      1050      1060      1070
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
gi|833 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
      1080      1090      1100      1110      1120      1130
Cry1Ac 1140      1150      1160      1170      1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|833 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170

>>gi|15126306|gb|AAE73542.1| Sequence 26 from patent US (1177 aa)
  initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|151  MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNAQAIISRLLEGLSNLYQIYAESFRE
gi|151  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNAQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|151  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac 250     260     270     280     290     300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHL
gi|151  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHL
      240     250     260     270     280     290
Cry1Ac 310     320     330     340     350     360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|151  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac 370     380     390     400     410     420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPQ

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gi|151 GYVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPQ
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|151 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYLEVPIHFPSTSTRYRVRVRYAS
gi|151 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|151 TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLTFQSFYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWSTGITIQGG
gi|151 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNK
gi|151 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYNK
      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLD
gi|151 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLD
      780      790      800      810      820      830
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|151 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|151 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac 960      970      980      990     1000     1010

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Cry1Ac GVNAAI... gi|151 GVNAAI... 960 970 980 990 1000 1010

Cry1Ac EWEAEV... gi|151 EWEAEV... 1020 1030 1040 1050 1060 1070

Cry1Ac TVTCND... gi|151 TVTCND... 1080 1090 1100 1110 1120 1130

Cry1Ac DYTPLP... gi|151 DYTPLP... 1140 1150 1160 1170 1180

>>gi|31688817|gb|AAP60982.1| Sequence 26 from patent US (1177 aa) Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap

Cry1Ac CMQAMN... gi|316 MDNNPN... 10 20 30 40 50 60

Cry1Ac VLGLVD... gi|316 VLGLVD... 70 80 90 100 110 120

Cry1Ac WEADPT... gi|316 WEADPT... 120 130 140 150 160 170

Cry1Ac VFGQRW... gi|316 VFGQRW... 180 190 200 210 220 230

Cry1Ac TLTVLD... gi|316 TLTVLD... 240 250 260 270 280 290

310 320 330 340 350 360

Cry1Ac MDILNS... gi|316 MDILNS... 300 310 320 330 340 350

Cry1Ac GVYRTL... gi|316 GVYRTL... 360 370 380 390 400 410 420

Cry1Ac NNNVPP... gi|316 NNNVPP... 420 430 440 450 460 470 480

Cry1Ac VKGNFL... gi|316 VKAHTL... 480 490 500 510 520 530

Cry1Ac VTPHIL... gi|316 TTNLRI... 540 550 560 570 580 590

Cry1Ac SGTAGV... gi|316 SSGNEV... 600 610 620 630 640 650

Cry1Ac VTYLSD... gi|316 VDCLSD... 660 670 680 690 700 710

Cry1Ac DDVFKEN... gi|316 DDVFKEN... 720 730 740 750 760 770

Cry1Ac HETVNV... gi|316 HETVNV... 780 790 800 810 820 830

Cry1Ac IDVGCT... gi|316 IDVGCT... 840 850 860 870 880 890

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          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|316 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
          900      910      920      930      940      950

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          960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQORSVLVVP
gi|316 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQORSVLVVP
          960      970      980      990      1000     1010

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        1020     1030     1040     1050     1060     1070
Cry1Ac EWAEAVSQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|316 EWAEAVSQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
        1020     1030     1040     1050     1060     1070

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        1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
gi|316 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
        1080     1090     1100     1110     1120     1130

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        1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|316 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
        1140     1150     1160     1170

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>>gi|53937591|gb|AAV01842.1| Sequence 26 from patent US (1177 aa)  
 initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0  
 Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap  
 (5-1182:1-1177)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

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          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|539 VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

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        130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        120      130      140      150      160      170

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        190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
        180      190      200      210      220      230

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        250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|539 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
        240      250      260      270      280      290

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        310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|539 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
        300      310      320      330      340      350

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        370      380      390      400      410      420
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
gi|539 GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
        360      370      380      390      400      410

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        430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
gi|539 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
        420      430      440      450      460      470

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        490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|539 VKAHTLQSGTTVVRGPGFTGGDLRLRTSGGPFAYT--IVNINGQLPQ--RYSRIRIRYAS
        480      490      500      510      520      530

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        540      550      560      570      580      590
Cry1Ac VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|539 TTNLRIVYVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMQSSFTVGDFTF
        540      550      560      570      580      590

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        600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|539 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
        600      610      620      630      640      650

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        660      670      680      690      700      710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|539 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
        660      670      680      690      700      710

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        720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|539 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
        720      730      740      750      760      770

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        780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|539 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
        780      790      800      810      820      830

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      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|539 IDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|539 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

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      960      970      980      990     1000     1010
Cry1Ac GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVVEEQNNQRSVLVVVP
gi|539 GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVVEEQNNQRSVLVVVP
      960      970      980      990     1000     1010

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     1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
gi|539 EWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
     1020     1030     1040     1050     1060     1070

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     1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
gi|539 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRGYR
     1080     1090     1100     1110     1120     1130

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     1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|539 DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
     1140     1150     1160     1170     1180

```

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>>gi|16242911|gb|AAE80141.1| Sequence 26 from patent US (1177 aa)
  initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

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      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|162 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

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      70      80      90     100     110     120
Cry1Ac VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNAQAI SRLEGLSNLYQIYAESFRE
gi|162 VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNAQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90     100     110

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     130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVSVQAANLHLSVLRDVS
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVSVQAANLHLSVLRDVS
     120     130     140     150     160     170

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     190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQNFRREL
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQNFRREL
     180     190     200     210     220     230

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     250     260     270     280     290     300
Cry1Ac TLTVLVDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|162 TLTVLVDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
     240     250     260     270     280     290

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     310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQQLGQ
gi|162 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQQLGQ
     300     310     320     330     340     350

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     370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPO
gi|162 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPO
     360     370     380     390     400     410

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     430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|162 NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
     420     430     440     450     460     470

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```

     490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|162 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
     480     490     500     510     520     530

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     540     550     560     570     580     590
Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|162 TTNLRIVYVAGERIFAGQFNKTMDTGDLPTFQSFYSATINTAFTFPMSSQSSFTVGDFTF
     540     550     560     570     580     590

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     600     610     620     630     640     650
Cry1Ac SGTAGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
     600     610     620     630     640     650

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     660     670     680     690     700     710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|162 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
     660     670     680     690     700     710

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     720     730     740     750     760     770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|162 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK

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      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|162 HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|162 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|162 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990     1000     1010
Cry1Ac 960      970      980      990     1000     1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVEEQNNQRSVLVVP
gi|162 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVEEQNNQRSVLVVP
      960      970      980      990     1000     1010

     1020     1030     1040     1050     1060     1070
Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|162 EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
     1020     1030     1040     1050     1060     1070

     1080     1090     1100     1110     1120     1130
Cry1Ac 1080     1090     1100     1110     1120     1130
TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNCPCEFNRGYR
gi|162 TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNCPCEFNRGYR
     1080     1090     1100     1110     1120     1130

     1140     1150     1160     1170     1180
Cry1Ac 1140     1150     1160     1170     1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|162 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
     1140     1150     1160     1170

>>gi|47257344|gb|AAT23507.1| Sequence 26 from patent US (1177 aa)
  initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|472 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90     100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

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      60      70      80      90     100     110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac 250      260      270      280      290      300
TLTVLTDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
gi|472 TLTVLTDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac 310      320      330      340      350      360
MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac 370      380      390      400      410      420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDSDLEIPPO
gi|472 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDSDLEIPPO
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|472 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac 490      500      510      520      530
VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|472 VKAHTLQSGTTFVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac 540      550      560      570      580      590
VTPIHLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|472 TTNLRIYVTVAGERIFAGQFNKTMDTGDLTFQSFYATINTAFTFPPMQSSFTYADTF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

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gi|472 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWGSDTITIQRG
      660      670      680      690      700      710
      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
      .....
gi|472 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYLIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      .....
gi|472 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830
      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      .....
gi|472 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIP
      .....
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
      .....
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
      960      970      980      990      1000      1010
      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      .....
gi|472 EWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020      1030      1040      1050      1060      1070
      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
      .....
gi|472 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
      1080      1090      1100      1110      1120      1130
      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|472 DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|77376719|gb|ABA70266.1| Sequence 26 from patent US (1177 aa)
      initn: 7074 initl: 3806 opt: 7065 Z-score: 8322.5 bits: 1551.9 E(): 0
      Smith-Waterman score: 7065; 90.271% identity (94.247% similar) in 1182 aa overlap
      (5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....

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gi|773 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      .....
gi|773 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|773 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
      .....
gi|773 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
      .....
gi|773 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|773 MDILNSITITYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      .....
gi|773 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      360      370      380      390      400      410
      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|773 NNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|773 VKAHTLQSGTTVVRRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTIHNLVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
      .....
gi|773 TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLTFQSFYATINTAFTFPMQSSFTVGADTF
      540      550      560      570      580      590
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

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300      310      320      330      340      350
Cry1Ac  GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDSLDEIPPQ
gi|316  GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410      420
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|316  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      430      440      450      460      470      480
Cry1Ac  VKNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|316  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS
      490      500      510      520      530
Cry1Ac  VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|316  TTNLRIYVTVAGERIFAGQFNKTMDTGDLPTFQSFYSYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
Cry1Ac  SGTAGVIIDRFFFIPTVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|316  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac  VTYLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|316  VDCLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710
Cry1Ac  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYLRIRYNAK
gi|316  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYLRIRYNAK
      720      730      740      750      760      770
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|316  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
      780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|316  IDVGCTDLNEDLGWVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|316  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP

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gi|316  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSLVLPV
gi|316  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSLVLPV
      960      970      980      990      1000      1010
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEIEYPNN
gi|316  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEIEYPNN
      1020      1030      1040      1050      1060      1070
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGYR
gi|316  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGYR
      1080      1090      1100      1110      1120      1130
Cry1Ac  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|316  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|12824337|gb|AAE49243.1| Sequence 10 from patent US (1177 aa)
      initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|128  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      70      80      90      100      110      120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
gi|128  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
      130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
gi|128  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|128  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
      250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSRPHL

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gi|128 TLTVLDIVALFPNYDSRRYPVRTVSQTLTREIYTNPVLENFDGFSFRGSAQGIERSIRSPHL
      240      250      260      270      280      290
          310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          .....
gi|128 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDSLDEIPpQ
          .....
gi|128 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDSLDEIPpQ
      360      370      380      390      400      410
          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPa
          .....
gi|128 NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWThRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
          490      500      510      520      530
Cry1Ac VKGNFLFNgs-VISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYRVrVRYAS
          .....
gi|128 VKAHTLQSGTtTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530
          540      550      560      570      580      590
Cry1Ac VtPIHLNvNwGnSSIFsNTVPATATSLDNLQSSDFgyFESANAFTSSLGN---IVGVRNF
          .....
gi|128 TTNLRiYVtVAGERiFAGQFNKtMDTGDPLTFQSFsYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
          600      610      620      630      640      650
Cry1Ac SGTAGViIDRFEFiPVTATLEAEYnLERAQKAVNALFTStnQLGLKtNVtDYHIDQVSNL
          .....
gi|128 SSGNEVYIDRFELiPVTATFEAEYDLERAQKAVNALFTSiNQiGikTdvTYHIDQVSNL
      600      610      620      630      640      650
          660      670      680      690      700      710
Cry1Ac VtYLSDFeClDEKRElSEKvKHAKRLSDERNLLQDSNFKDiNRQPERGWGStGITiQGG
          .....
gi|128 VDCLSDFeClDEKRElSEKvKHAKRLSDERNLLQDPNFKGiNRQLDRGWRGStDITiQRG
      660      670      680      690      700      710
          720      730      740      750      760      770
Cry1Ac DDVfKEnYVtLPGTFDeCYPTyLYQKiDESKLKAfTRYQLRgyIEDsQDLeySIRyNAK
          .....
gi|128 DDVfKEnYVtLPGTFDeCYPTyLYQKiDESKLKAfTRYQLRgyIEDsQDLeyLIRyNAK
      720      730      740      750      760      770
          780      790      800      810      820      830
Cry1Ac HETVnVPGtGSLWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGekCAHSHHfSLD
          .....
gi|128 HETVnVPGtGSLWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGekCAHSHHfSLD
      780      790      800      810      820      830
          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

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          .....
gi|128 IDVGCTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRvHSIREAYLPELSVIP
          .....
gi|128 KLEWETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRvHSIREAYLPELSVIP
      900      910      920      930      940      950
          960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFtAFSLyDARNvIKNGDFNNGLSCWNVKghVDVEEQNNQRsVLVVP
          .....
gi|128 GVNAAIFEELEGRIFtAFSLyDARNvIKNGDFNNGLSCWNVKghVDVEEQNNQRsVLVVP
      960      970      980      990      1000      1010
          1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVrVCPGRgyILRvTAYKEgyGEGCVtIHEIENntDELKfSNcVVEEeyPNn
          .....
gi|128 EWEAEVSQEVrVCPGRgyILRvTAYKEgyGEGCVtIHEIENntDELKfSNcVVEEeyPNn
      1020      1030      1040      1050      1060      1070
          1080      1090      1100      1110      1120      1130
Cry1Ac TVtCNdyTVNQEeyGGAYtSRNRgyNEAPsVPADYASvYEEKsYtDgRENpCEfNRgyR
          .....
gi|128 TVtCNdyTVNQEeyGGAYtSRNRgyNEAPsVPADYASvYEEKsYtDgRENpCEfNRgyR
      1080      1090      1100      1110      1120      1130
          1140      1150      1160      1170      1180
Cry1Ac DYtPLPVgyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
          .....
gi|128 DYtPLPVgyVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
      1140      1150      1160      1170
>>gi|47257343|gb|AAT23506.1| Sequence 14 from patent US (1177 aa)
      initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
      Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
      (5-1182:1-1177)
          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYtPIDISLSLtQFLlSEfVPGAGF
          .....
gi|472 MDNPNINeCIPYNCLSNPEVEVLGGERIETGYtPIDISLSLtQFLlSEfVPGAGF
          10      20      30      40      50
          70      80      90      100      110      120
Cry1Ac VLGLVDiIWGIFGPsQWDAFLVQIEQLINQRIEEFARNQAIrSREGLSNLYQIYAESfRE
          .....
gi|472 VLGLVDiIWGIFGPsQWDAFLVQIEQLINQRIEEFARNQAIrSREGLSNLYQIYAESfRE
      60      70      80      90      100      110
          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNdMNSALtTAiPLFAVQNYQVPLlSVYVQAANLHLSVLRdVS
          .....
gi|472 WEADPTNPALREEMRIQFNdMNSALtTAiPLFAVQNYQVPLlSVYVQAANLHLSVLRdVS
      120      130      140      150      160      170
          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLiGNYtDHAVRWYntGLERVWGPDSRDWIRYnQFRREL

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gi|472 VFGQRWGFDAAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGDSDRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL
gi|472 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDADRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITIIYTDADRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ
gi|472 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|472 NNVVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFNFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|472 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYSRIRIYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|472 TTNLRIYVTVAGERIFAGQFNKTMDTGDLPTFQSFYSYATINTAFTFPMSQSSFTVGADTF
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
gi|472 VDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|472 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830

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Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|472 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFFSLD
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890
IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|472 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEIEYPNN
gi|472 EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEIEYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRGRY
gi|472 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRGRY
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE
gi|472 DYTPLPVGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170

>>gi|83329851|gb|ABC06980.1| Sequence 10 from patent US (1177 aa)
initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|833 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE
gi|833 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180

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Regulatory Product Characterization Team

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|833 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL  
gi|833 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL  
180 190 200 210 220 230

250 260 270 280 290 300  
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL  
gi|833 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL  
240 250 260 270 280 290

310 320 330 340 350 360  
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
gi|833 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
300 310 320 330 340 350

370 380 390 400 410 420  
Cry1Ac GYVRTLSSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSSTVDSLDEIIPPQ  
gi|833 GYVRTLSSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSSTVDSLDEIIPPQ  
360 370 380 390 400 410

430 440 450 460 470 480  
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNLIASDSITQIPA  
gi|833 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNLIASDSITQIPA  
420 430 440 450 460 470

490 500 510 520 530  
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
gi|833 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS  
480 490 500 510 520 530

540 550 560 570 580 590  
Cry1Ac VTIPIHLNVNWNSSIFSNTVDPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF  
gi|833 TTNLRIVYTVAGERIFAGQFNKMTMDTGFQSFYATINTAFTFPMSQSSFTVGADTF  
540 550 560 570 580 590

600 610 620 630 640 650  
Cry1Ac SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
gi|833 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGKTDVTDYHIDQVSNL  
600 610 620 630 640 650

660 670 680 690 700 710  
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG  
gi|833 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWGSGTDITIQRG  
660 670 680 690 700 710

720 730 740 750 760 770  
Cry1Ac DDVFKENYVTLPGTDFDECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK  
gi|833 DDVFKENYVTLPGTDFDECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK  
720 730 740 750 760 770

780 790 800 810 820 830  
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
gi|833 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
780 790 800 810 820 830

840 850 860 870 880 890  
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|833 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
840 850 860 870 880 890

900 910 920 930 940 950  
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP  
gi|833 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP  
900 910 920 930 940 950

960 970 980 990 1000 1010  
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQSRVSLVVP  
gi|833 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQSRVSLVVP  
960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
Cry1Ac EWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNVCVEEIIYPNN  
gi|833 EWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNVCVEEIIYPNN  
1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130  
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYR  
gi|833 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYR  
1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180  
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|833 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1140 1150 1160 1170

>>gi|53937588|gb|AAV01839.1| Sequence 10 from patent US (1177 aa)  
initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
(5-1182:1-1177)

10 20 30 40 50 60  
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
10 20 30 40 50

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Cry1Ac 70 80 90 100 110 120
VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|539 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
gi|539 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHRGEYYSWGSHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ
gi|539 MDILNSITIIYTDHRGEYYSWGSHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSTLYRRPFIINNNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
gi|539 GVYRTLSTLYRRPFIINNNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|539 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|539 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|539 TTNLRIRYVTVAGERIFAGQFNKTMDTGDP LTFQSF SYATINTAF TFPMSQSSFTVGADTF
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVVIDRFFFI PVTTATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNL
gi|539 SSGNEVYIDRFELIPVTTATFEAEYDLERAQKAVNALFTSINQIGIKTVDVTDYHIDQVSNL
600 610 620 630 640 650

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Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKIDINRQPERGWGGSTGITIQGG
gi|539 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
DDVFKENYVTLSGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|539 DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|539 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890
IDVGC TDLNEDLG VVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|539 IDVGC TDLNEDLG VVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|539 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
gi|539 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
gi|539 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
gi|539 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
gi|539 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
1140 1150 1160 1170

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>>gi|47257342|gb|AAT23505.1| Sequence 12 from patent US (1177 aa)
initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

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Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVPGAGF  
gi|472 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVPGAGF

Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|472 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFRREL  
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNVLENFDGSGFRGSAQGLEGSIRSPHL  
gi|472 TLTVLDIVALFPNYSRRYPPIRTVSQTLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL

Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ  
gi|472 MDILNSITTYTDAHRGYYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ  
gi|472 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ

Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIP A  
gi|472 NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL

Cry1Ac VKGNFLFN GS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYRVRVRYAS  
gi|472 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
gi|472 TTNLR IYVTVAGERIFAGQFNK TMDTGDPLTFQSF SYATINTAFTFPMSQSSTTVGADTF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
gi|472 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNL

Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
gi|472 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG

Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
gi|472 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK

Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLD  
gi|472 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLD

Cry1Ac IDVGCITDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|472 IDVGCITDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP

Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHVDVEEQNNQRSVLVVP  
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHVDVEEQNNQRSVLVVP

Cry1Ac EWEAEVSVQEVVRCVCPGRGYLLRV TAYKEGYGEGCVTTHEIENNTDELKFSNCV EEEIYPNN  
gi|472 EWEAEVSVQEVVRCVCPGRGYLLRV TAYKEGYGEGCVTTHEIENNTDELKFSNCV EEEIYPNN

Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRGYR  
gi|472 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRGYR

Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|472

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gi|472 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|112061957|gb|ABH98778.1| Sequence 10 from patent US (1177 aa)  
 inith: 7055 inilt: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
 Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
 (5-1182:1-1177)

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 gi|112 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 gi|112 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGSDSRDWIRYNQFRREL  
 gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGSDSRDWIRYNQFRREL

250 260 270 280 290 300  
 Cry1Ac TLTVDLIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGI EGSIRSPHL  
 gi|112 TLTVDLIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGI ERSIRSPHL

310 320 330 340 350 360  
 Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ  
 gi|112 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ

370 380 390 400 410 420  
 Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKSGTVDSLDEIIPPQ  
 gi|112 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKSGTVDSLDEIIPPQ

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA  
 gi|112 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL

490 500 510 520 530  
 Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS

gi|112 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS  
 480 490 500 510 520 530

540 550 560 570 580 590  
 Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
 gi|112 TTNLRIVYVAGERIFAGQFNKTMIDTGDPLTFQSFYSATINTAFTFPMSSSFTVGDFTF

600 610 620 630 640 650  
 Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQVSNL

660 670 680 690 700 710  
 Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG  
 gi|112 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG

720 730 740 750 760 770  
 Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
 gi|112 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK

780 790 800 810 820 830  
 Cry1Ac HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 gi|112 HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD

840 850 860 870 880 890  
 Cry1Ac IDVGCTDLNEDLGVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 gi|112 IDVGCTDLNEDLGVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

900 910 920 930 940 950  
 Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP  
 gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP

960 970 980 990 1000 1010  
 Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLPVVP  
 gi|112 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLPVVP

1020 1030 1040 1050 1060 1070  
 Cry1Ac EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFNCSNVEEIEYPNN  
 gi|112 EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFNCSNVEEIEYPNN

1080 1090 1100 1110 1120 1130  
 Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRYGR

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gi|112 TVTCDNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNPCEFNRYR
1080 1090 1100 1110 1120 1130

Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180

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1140 1150 1160 1170

>>gi|77376716|gb|ABA70263.1| Sequence 10 from patent US (1177 aa)
inith: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

gi|773 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|773 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|773 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL
190 200 210 220 230 240

gi|773 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVDLIVSLFNPYDSRTPYIRTVSQTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
250 260 270 280 290 300

gi|773 TLTVDLIVSLFNPYDSRTPYIRTVSQTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360

gi|773 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GTVDSLDEIPPQ
370 380 390 400 410 420

gi|773 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GTVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|773 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATPNTIDPERITQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480 490 500 510 520 530

Cry1Ac VTFIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRIYVTVAGERIFAGQFNKTMDTGDP LTFQSFYATINTAFTFPMQSSFTVGADTF
540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
660 670 680 690 700 710

gi|773 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660 670 680 690 700 710

Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720 730 740 750 760 770

gi|773 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFFSLD
780 790 800 810 820 830

gi|773 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFFSLD
780 790 800 810 820 830

Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

gi|773 IDVGCTDLNEDLGVVWVIFKIKTDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPESLVIP
900 910 920 930 940 950

gi|773 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPESLVIP
900 910 920 930 940 950

Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
960 970 980 990 1000 1010

gi|773 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070

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Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
gi | 773 EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
gi | 773 TVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYR
1080 1090 1100 1110 1120 1130

Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi | 773 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170

>>gi|47257341|gb|AAT23504.1| Sequence 10 from patent US (1177 aa)
initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi | 472 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi | 472 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi | 472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi | 472 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRYPPIRTVSQTLREIYTNPVLENFDGSPFRGSAQGIERSIRSPHL
gi | 472 TLTVLDIVSLFPNYDSRYPPIRTVSQTLREIYTNPVLENFDGSPFRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi | 472 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

370 380 390 400 410 420

Cry1Ac GVYRTLSSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPO
gi | 472 GVYRTLSSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPO
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi | 472 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi | 472 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RVRARIRYAS
480 490 500 510 520 530

Cry1Ac VTPIHNLVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi | 472 TTNLRIYVTVAGERIFAGQFNKIMDTGDLPTFQSFYSYATINTAFTFPMQSSFTVGDATF
540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNL
gi | 472 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi | 472 VDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGTDITIQRG
660 670 680 690 700 710

Cry1Ac DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi | 472 DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi | 472 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
780 790 800 810 820 830

Cry1Ac IDVGCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi | 472 IDVGCTDLNEDLGVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi | 472 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

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960      970      980      990      1000     1010
Cry1Ac  GVNAAI FEELEGRIFAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|472  GVNAAI FEELEGRIFAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVP
          960      970      980      990      1000     1010

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```

1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEV SQEVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
gi|472  EWEAEV SQEVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
          1020     1030     1040     1050     1060     1070

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1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
gi|472  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
          1080     1090     1100     1110     1120     1130

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1140     1150     1160     1170     1180
Cry1Ac  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|472  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140     1150     1160     1170

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>>gi|19577425|emb|CAD28600.1| unnamed protein product [s (1177 aa)
  in1tn: 7055 in1t1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

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```

10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|195  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

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```

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEEFARNQAI SRL EGLSNLYQIYAESFRE
gi|195  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEEFARNQAI SRL EGLSNLYQIYAESFRE
          60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|195  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFRREL
gi|195  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFRREL
          180     190     200     210     220     230

```

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250     260     270     280     290     300
Cry1Ac  TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGI EGSIRSPHL
gi|195  TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGI ERSIRSPHL
          240     250     260     270     280     290

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```

310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGP EFTFPLYGTMGNAAPQQRIVAQLGQ
gi|195  MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGP EFTFPLYGTMGNAAPQQRIVAQLGQ
          300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
gi|195  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
          360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|195  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|195  VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
          480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac  VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|195  TTNLRIYVTVAGERIFAGQFNKTMDTGDP LTFQSFYSATINTAFTFPMSQSSFTVGADTF
          540     550     560     570     580     590

```

```

600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|195  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
          600     610     620     630     640     650

```

```

660     670     680     690     700     710
Cry1Ac  VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|195  VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
          660     670     680     690     700     710

```

```

720     730     740     750     760     770
Cry1Ac  DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|195  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
          720     730     740     750     760     770

```

```

780     790     800     810     820     830
Cry1Ac  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD
gi|195  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD
          780     790     800     810     820     830

```

```

840     850     860     870     880     890
Cry1Ac  IDVGCTDLNEDLG VVWVIFKIKTDGHARLGNLEFLEEKPLVGEALARVRAEKKWRDKRE
gi|195  IDVGCTDLNEDLG VVWVIFKIKTDGHARLGNLEFLEEKPLVGEALARVRAEKKWRDKRE
          840     850     860     870     880     890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSTREAYLPELSVIP
gi|195 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSTREAYLPELSVIP
          900      910      920      930      940      950

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVVLVVP
gi|195 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVVLVVP
          960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|195 EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
          1020     1030     1040     1050     1060     1070

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1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNGYNEAPSVADYASVYEEKSYTDGRRNCPCEFNRGYR
gi|195 TVTCNDYTVNQEEYGGAYTSRNGYNEAPSVADYASVYEEKSYTDGRRNCPCEFNRGYR
          1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|195 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140     1150     1160     1170

```

```

>>gi|15126303|gb|AAE73539.1| Sequence 10 from patent US (1177 aa)
  initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|151 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

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```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|151 VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

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```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGSDSRDWIRYNQFRREL
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGSDSRDWIRYNQFRREL
          180     190     200     210     220     230

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```

250      260      270      280      290      300
Cry1Ac TLTVLDIVLFFPNYDSRRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGESIRSPHL
gi|151 TLTVLDIVLFFPNYDSRRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGESIRSPHL
          240      250      260      270      280      290

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```

310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ
gi|151 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVVAQLGQ
          300      310      320      330      340      350

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370      380      390      400      410      420
Cry1Ac GVYRRLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
gi|151 GVYRRLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
          360      370      380      390      400      410

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|151 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          420      430      440      450      460      470

```

```

490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFSTSTRYRVRVRYAS
gi|151 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
          480      490      500      510      520      530

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```

540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|151 TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSSFTVGADTF
          540      550      560      570      580      590

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
          600      610      620      630      640      650

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```

660      670      680      690      700      710
Cry1Ac VTYSLDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWWGGSTGITIQGG
gi|151 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
          660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
gi|151 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
          720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGEKCAHSHHFFSLD
gi|151 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGEKCAHSHHFFSLD

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      780      790      800      810      820      830
Cry1Ac  840      850      860      870      880      890
IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|151  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
gi|151  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990     1000     1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|151  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
      960      970      980      990     1000     1010

     1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|151  EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
     1020     1030     1040     1050     1060     1070

     1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
gi|151  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYR
     1080     1090     1100     1110     1120     1130

     1140     1150     1160     1170     1180
Cry1Ac  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|151  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
     1140     1150     1160     1170

>>gi|40189703|gb|AAR76443.1| Sequence 12 from patent US (1177 aa)
  in1n: 7055 in1l: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac  CMQAMNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|401  MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|401  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

     130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|401  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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     120     130     140     150     160     170
Cry1Ac  190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|401  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
     180     190     200     210     220     230

     250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKRSRPHL
gi|401  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKRSRPHL
     240     250     260     270     280     290

     310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHARGYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|401  MDILNSITIIYTDHARGYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQ
     300     310     320     330     340     350

     370     380     390     400     410     420
Cry1Ac  GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|401  GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
     360     370     380     390     400     410

     430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|401  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
     420     430     440     450     460     470

     490     500     510     520     530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
     480     490     500     510     520     530

     540     550     560     570     580     590
Cry1Ac  VTIHILNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|401  TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLTFQSFYATINTAFTFPMSQSSFTVIGADTF
     540     550     560     570     580     590

     600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
     600     610     620     630     640     650

     660     670     680     690     700     710
Cry1Ac  VTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|401  VDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
     660     670     680     690     700     710

     720     730     740     750     760     770
Cry1Ac  DDVFKENYVTLSGTFDECYPTLYLQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK

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gi|401 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      .....
gi|401 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830
      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      .....
gi|401 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
      .....
gi|401 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
      960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
      .....
gi|401 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
      960      970      980      990      1000     1010
      1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      .....
gi|401 EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020     1030     1040     1050     1060     1070
      1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRYR
      .....
gi|401 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNPCEFNRYR
      1080     1090     1100     1110     1120     1130
      1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|401 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170
>>gi|53937590|gb|AAV01841.1| Sequence 14 from patent US (1177 aa)
  initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E( ): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      .....

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gi|539 VLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      .....
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      .....
gi|539 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|539 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      .....
gi|539 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      360      370      380      390      400      410
      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|539 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      420      430      440      450      460      470
      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|539 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
      .....
gi|539 TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFSYATINTAFTFPMQSSFTVGADTF
      540      550      560      570      580      590
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|539 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650
      660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG

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Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCFVEEEIYPNN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCFVEEEIYPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEEKSYTDGRENPECFNRGYR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 TVTCNDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEEKSYTDGRENPECFNRGYR
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 202 DYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170

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>>gi|162500740|gb|ABY14164.1| Sequence 14 from patent US (1177 aa)
      initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFSAQIGESIRSPHL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 TLTVLDIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSRFSAQIGESIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPYGTMGNAAPQQRIVAQLGQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 MDILNSITITYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRFLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 GVYRFLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 162 NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . : . . :
gi | 162 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530

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490 500 510 520 530  
 Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRVYRVRVRYAS  
 gi|112 VKAHTLQSGTIVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYSRIRYRYAS  
 480 490 500 510 520 530

540 550 560 570 580 590  
 Cry1Ac VTPIHNLNWNWNGSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF  
 gi|112 TTNLRIRYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMSQSSFTVGADTF  
 540 550 560 570 580 590

600 610 620 630 640 650  
 Cry1Ac SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL  
 600 610 620 630 640 650

660 670 680 690 700 710  
 Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTIGTIQGG  
 gi|112 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG  
 660 670 680 690 700 710

720 730 740 750 760 770  
 Cry1Ac DDVFKENYVTLPGTDFECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNK  
 gi|112 DDVFKENYVTLPGTDFECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNK  
 720 730 740 750 760 770

780 790 800 810 820 830  
 Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD  
 gi|112 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD  
 780 790 800 810 820 830

840 850 860 870 880 890  
 Cry1Ac IDVGCTDLNEDLGWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 gi|112 IDVGCTDLNEDLGWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 840 850 860 870 880 890

900 910 920 930 940 950  
 Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP  
 gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP  
 900 910 920 930 940 950

960 970 980 990 1000 1010  
 Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQNNQSVLVVP  
 gi|112 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQNNQSVLVVP  
 960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
 Cry1Ac EWAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN  
 gi|112 EWAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN

1020 1030 1040 1050 1060 1070  
 Cry1Ac 1080 1090 1100 1110 1120 1130  
 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGYR  
 gi|112 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGYR  
 1080 1090 1100 1110 1120 1130  
 Cry1Ac 1140 1150 1160 1170 1180  
 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|112 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|40189702|gb|AAR76442.1| Sequence 10 from patent US (1177 aa)  
 initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
 Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
 (5-1182:1-1177)

10 20 30 40 50 60  
 Cry1Ac CMQAMNPNINCEPIYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 gi|401 MDNPNINCEPIYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE  
 gi|401 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|401 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWVRYNQFRREL  
 gi|401 VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWVRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL  
 gi|401 TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNPVLENFDFGSRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 gi|401 MDILNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
 gi|401 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ

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360      370      380      390      400      410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401  NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420      430      440      450      460      470      480
Cry1Ac  VKNFLFNNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVRYAS
gi|401  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530
Cry1Ac  VTPIHLNWNVGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|401  TTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMSSQSFYVADTF
540      550      560      570      580      590
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGKTDVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac  VTYLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPSNFKDINRQPERGWGGSTGTITQGG
gi|401  VDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660      670      680      690      700      710
Cry1Ac  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLRINAK
gi|401  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLRINAK
720      730      740      750      760      770
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|401  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|401  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|401  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac  GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQQNQRSVLVVP

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gi|401  GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQQNQRSVLVVP
960      970      980      990      1000     1010
Cry1Ac  EWEAEVSQEVRRVCPGRGYILRVTAKEGYEGECVTTIHEIENNTDELKFSNCVVEEIIYPNN
gi|401  EWEAEVSQEVRRVCPGRGYILRVTAKEGYEGECVTTIHEIENNTDELKFSNCVVEEIIYPNN
1020     1030     1040     1050     1060     1070
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
gi|401  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGRY
1080     1090     1100     1110     1120     1130
Cry1Ac  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|401  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170
>>gi|29718510|gb|AAP01234.1| Sequence 12 from patent US (1177 aa)
initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)
10      20      30      40      50      60
Cry1Ac  CMQAMNPNINECIPYNCLSNFEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|297  MDNPNINECIPYNCLSNFEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|297  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|297  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|297  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180     190     200     210     220     230
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|297  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240     250     260     270     280     290
Cry1Ac  MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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gi|297 MDILNSITYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDLSDEIPPQ
gi|297 GYVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDLSDEIPPQ
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|297 NNVVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|297 TTNLRIYVTVAGERIFAGQFNKMTDGTGDLTFQSFYSYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEPFVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|297 SSGNEVYIDRFELIPVATFEAEYDLERAKAVNALFTSINQIGIKTVDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|297 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYSIRYNAK
gi|297 DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRDGEKCAHSHHFSLD
gi|297 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRDGEKCAHSHHFSLD
      780      790      800      810      820      830
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
gi|297 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP

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gi|297 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac 960      970      980      990      1000      1010
GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQSRVSVLP
gi|297 GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQSRVSVLP
      960      970      980      990      1000      1010
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSQEVVRCVPGRYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
gi|297 EWEAEVSQEVVRCVPGRYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
      1020      1030      1040      1050      1060      1070
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGRYR
gi|297 TVTCDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRGRYR
      1080      1090      1100      1110      1120      1130
Cry1Ac 1140      1150      1160      1170      1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|297 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170
>>gi|83329853|gb|ABC06982.1| Sequence 14 from patent US (1177 aa)
      initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
      Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
      (5-1182:1-1177)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|833 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100      110      120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|833 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|833 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|833 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHL

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gi|833 240 250 260 270 280 290
Cry1Ac 310 320 330 340 350 360
gi|833 300 310 320 330 340 350
Cry1Ac 370 380 390 400 410 420
gi|833 360 370 380 390 400 410
Cry1Ac 430 440 450 460 470 480
gi|833 420 430 440 450 460 470
Cry1Ac 490 500 510 520 530
gi|833 480 490 500 510 520 530
Cry1Ac 540 550 560 570 580 590
gi|833 540 550 560 570 580 590
Cry1Ac 600 610 620 630 640 650
gi|833 600 610 620 630 640 650
Cry1Ac 660 670 680 690 700 710
gi|833 660 670 680 690 700 710
Cry1Ac 720 730 740 750 760 770
gi|833 720 730 740 750 760 770
Cry1Ac 780 790 800 810 820 830
gi|833 780 790 800 810 820 830
Cry1Ac 840 850 860 870 880 890

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Cry1Ac 900 910 920 930 940 950
Cry1Ac 960 970 980 990 1000 1010
gi|833 960 970 980 990 1000 1010
Cry1Ac 1020 1030 1040 1050 1060 1070
gi|833 1020 1030 1040 1050 1060 1070
Cry1Ac 1080 1090 1100 1110 1120 1130
gi|833 1080 1090 1100 1110 1120 1130
Cry1Ac 1140 1150 1160 1170 1180
gi|833 1140 1150 1160 1170
>>gi|31688816|gb|AAP60981.1| Sequence 14 from patent US (1177 aa)
initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)
Cry1Ac 10 20 30 40 50 60
gi|316 10 20 30 40 50
Cry1Ac 70 80 90 100 110 120
gi|316 70 80 90 100 110
Cry1Ac 130 140 150 160 170 180
gi|316 120 130 140 150 160 170
Cry1Ac 190 200 210 220 230 240
gi|316 190 200 210 220 230 240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|316 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL  
gi|316 TLTVLDIVALFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL  
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlyGTMGNAAPQQRIVAQLGQ  
gi|316 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlyGTMGNAAPQQRIVAQLGQ  
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIPPQ  
gi|316 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIPPQ  
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
NNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|316 NNVPPRQGFShRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEPTNTIDPERITQIPL  
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530  
VKNFLFNgs-VISGPGFTGGDLVRLNssGNNIQNRgyIEVPIHFPSTSTRYVRVRYAS  
gi|316 VKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS  
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590  
VTPIHLNVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
gi|316 TTNLRIYVTVAGERIFAGQFNKTMdTGDPLTFQSFsYATINTAFTPMSQSSFTVGADTF  
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650  
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
gi|316 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINIGIKTDVTDYHIDQVSNL  
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710  
VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG  
gi|316 VDCLsDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSGTDITIQRG  
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770  
DDVFKENYVTLsGTfDECyPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeySIRYNak  
gi|316 DDVFKENYVTLPGTfDECyPTyLYQKIDESKlKAFTRyQLRgyIEDsQDLeyLIRYNak  
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830  
HETVNVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGECaHSHHfSLD  
gi|316 HETVNVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGECaHSHHfSLD  
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890  
IDVGCTDLNEDLGVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
gi|316 IDVGCTDLNEDLGVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950  
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
gi|316 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010  
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP  
gi|316 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP  
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070  
EWEAEVSQEVrVCPGRgyILRVtAYKEgyEGCVtIHEIENNTDELKfSNcVVEEIPNN  
gi|316 EWEAEVSQEVrVCPGRgyILRVtAYKEgyEGCVtIHEIENNTDELKfSNcVVEEIPNN  
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130  
TVTCNDYTVNQEeyGgAYTSRNrgYNEAPsVPADYASVYEEKsYTDGRENPCeFNrgYR  
gi|316 TVTCNDYTVNQEeyGgAYTSRNrgYNEAPsVPADYASVYEEKsYTDGRENPCeFNrgYR  
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180  
DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE  
gi|316 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE  
1140 1150 1160 1170

>>gi|40189704|gb|AAR76444.1| Sequence 14 from patent US (1177 aa)  
initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
(5-1182:1-1177)

Cry1Ac 10 20 30 40 50 60  
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF  
gi|401 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF  
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120  
VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIrSLRGLSnlYQIYAESFRE  
gi|401 VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIrSLRGLSnlYQIYAESFRE  
60 70 80 90 100 110

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130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|401 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|401 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVLSLFPNYSRTPYPIRTVSQTLREIYTNPVENFDGSRGSAQGIIEGSIIRSPHL
gi|401 TLTVLDIVALFPNYSRRYPPIRTVSQTLREIYTNPVENFDGSRGSAQGIERSIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|401 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
gi|401 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VPIHLNVWNGSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|401 TTNLRIYVIVAGERIFAQGFNKMTMDTGDPLTFQSFSYATINTAFTFPMSQSSFTVGADTF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|401 VDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGIYEDSQLEIYLSIRYNAK
gi|401 DDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGIYEDSQLEIYLSIRYNAK
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHSHFSLD
gi|401 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHSHFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|401 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIP
gi|401 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQSRVSLVVP
gi|401 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQSRVSLVVP
960      970      980      990      1000      1010

1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
gi|401 EWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
1020      1030      1040      1050      1060      1070

1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRGYR
gi|401 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFNRGYR
1080      1090      1100      1110      1120      1130

1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|401 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170

>>gi|77376717|gb|ABA70264.1| Sequence 12 from patent US (1177 aa)
initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|773 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
10      20      30      40      50

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              70      80      90      100     110     120
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|773 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
              60      70      80      90      100     110

              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|773 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170

              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|773 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              180     190     200     210     220     230

              250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
gi|773 TLTVLDIVALFPNYDSRRYPPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
              240     250     260     270     280     290

              310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|773 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
              300     310     320     330     340     350

              370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
gi|773 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
              360     370     380     390     400     410

              430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|773 NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
              420     430     440     450     460     470

              490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
gi|773 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
              480     490     500     510     520     530

              540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|773 TTNLRIVYTVAGERIFAGQFNKMTDGTGDLTFQSFYSYATINTAFTFPMSSQSSFTVGADTF
              540     550     560     570     580     590

              600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|773 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL

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              600     610     620     630     640     650
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRSLDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|773 VDCLSEDFCLDEKRELSEKVKHAKRSLDERNLLQDPNFKGINRQLDRGWRGSDTITIQRG
              660     670     680     690     700     710

              720     730     740     750     760     770
Cry1Ac DDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|773 DDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
              720     730     740     750     760     770

              780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|773 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
              780     790     800     810     820     830

              840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|773 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
              840     850     860     870     880     890

              900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|773 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
              900     910     920     930     940     950

              960     970     980     990     1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLPVP
gi|773 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLPVP
              960     970     980     990     1000    1010

              1020    1030    1040    1050    1060    1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPNN
gi|773 EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPNN
              1020    1030    1040    1050    1060    1070

              1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVVEEKSYPDGRRENPCFNRGRY
gi|773 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVVEEKSYPDGRRENPCFNRGRY
              1080    1090    1100    1110    1120    1130

              1140    1150    1160    1170    1180
Cry1Ac DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|773 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
              1140    1150    1160    1170

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>>gi|162500738|gb|ABY14162.1| Sequence 10 from patent US (1177 aa)  
 initn: 7055 init1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0

Regulatory Product Characterization Team

Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap (5-1182:1-1177)

Sequence alignment for Cry1Ac and gi|162. Includes residue numbers 10-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, 430-480, 490-530, 540-590.

Sequence alignment for Cry1Ac and gi|162. Includes residue numbers 540-590, 600-650, 660-710, 720-770, 780-830, 840-890, 900-950, 960-1010, 1020-1070, 1080-1130, 1140-1180.

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Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|162 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170

>>gi|53937589|gb|AAV01840.1| Sequence 12 from patent US (1177 aa)  
 initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
 Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
 (5-1182:1-1177)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|539 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50

Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 gi|539 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYNQFRREL  
 gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVYNQFRREL  
 180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL  
 gi|539 TLTVLDIVSLFPNYDSRRYPPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 gi|539 MDILNSITIIYTDHRGYYYSWGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
 gi|539 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
 360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIIPA  
 gi|539 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL  
 420 430 440 450 460 470

490 500 510 520 530

Cry1Ac VKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
 gi|539 VKAHTLQSGTTVVRRPGFTGGDLLRRTSGGPFAYT--IVNINGQLPQ--RYPARIRYAS  
 480 490 500 510 520 530

Cry1Ac VTPIHLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF  
 gi|539 TTNLRIYVTVAGERIFAGQFNKTMDTGDP LTFQSFYATINTAFTFPMSQSSFTVGADTF  
 540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 gi|539 SSGNEVYIDRFELIPVTATFEAYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL  
 600 610 620 630 640 650

Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG  
 gi|539 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG  
 660 670 680 690 700 710

Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAK  
 gi|539 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYLIRYNAK  
 720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD  
 gi|539 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD  
 780 790 800 810 820 830

Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 gi|539 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 840 850 860 870 880 890

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP  
 gi|539 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP  
 900 910 920 930 940 950

Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP  
 gi|539 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP  
 960 970 980 990 1000 1010

Cry1Ac EWEAEVSVQEVRRVCPGRGYILRVTA YKEGEGCVTTIHEIENNTDELKFSNCVVEEYIPNN  
 gi|539 EWEAEVSVQEVRRVCPGRGYILRVTA YKEGEGCVTTIHEIENNTDELKFSNCVVEEYIPNN  
 1020 1030 1040 1050 1060 1070

1020 1030 1040 1050 1060 1070

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1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPECFNRGYR
gi|539 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPECFNRGYR
1080      1090      1100      1110      1120      1130

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1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|539 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170

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>>gi|112061959|gb|ABH98779.1| Sequence 12 from patent US (1177 aa)
  in1n: 7055 in1l: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|112 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEERFARNAQISRLLEGLSNLYQIYAESFRE
gi|112 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEERFARNAQISRLLEGLSNLYQIYAESFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDFGSRGSAQGLEGSIRSPHL
gi|112 TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDFGSRGSAQGLEGSIRSPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQ
gi|112 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQ
360     370     380     390     400     410

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430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|112 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
420      430      440      450      460      470

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490      500      510      520      530
Cry1Ac VKGNFLFNGLS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYVRVRYAS
gi|112 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
480      490      500      510      520      530

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540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|112 TTNLRIVYTVAGERIFAGQFNKTMGTGDLPTFQSFYSATINTAFTFPMSQSSFTVGADTF
540      550      560      570      580      590

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600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|112 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600      610      620      630      640      650

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660      670      680      690      700      710
Cry1Ac VTYSLDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITIQGG
gi|112 VDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|112 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|112 HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830

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840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|112 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|112 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

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960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDFVEEQNNQSRVSLVVP
gi|112 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDFVEEQNNQSRVSLVVP
960      970      980      990      1000     1010

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1020      1030      1040      1050      1060      1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHELENNTDELKFSNCVVEEIIYPNN
gi|112  EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHELENNTDELKFSNCVVEEIIYPNN
      1020      1030      1040      1050      1060      1070

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1080      1090      1100      1110      1120      1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
gi|112  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
      1080      1090      1100      1110      1120      1130

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1140      1150      1160      1170      1180
Cry1Ac  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|112  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170

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>>gi|16242908|gb|AAE80138.1| Sequence 10 from patent US (1177 aa)  
 initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0  
 Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
 (5-1182:1-1177)

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      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|162  MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

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      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFRE
gi|162  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

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      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYQFRREL
gi|162  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRIRYQFRREL
      180     190     200     210     220     230

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      250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
gi|162  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290

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      310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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      370      380      390      400      410      420
Cry1Ac  GVYRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO
gi|162  GVYRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPO
      360      370      380      390      400      410

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      430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|162  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470

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      490      500      510      520      530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|162  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480      490      500      510      520      530

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      540      550      560      570      580      590
Cry1Ac  VTPIHNLVNWGSSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
gi|162  TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLPQSPFSYATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590

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      600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

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      660      670      680      690      700      710
Cry1Ac  VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQQG
gi|162  VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710

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      720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
gi|162  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
      720      730      740      750      760      770

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      780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFFSLD
gi|162  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFFSLD
      780      790      800      810      820      830

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      840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|162  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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      900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIAADKRVHSIREAYLPELSVIP
gi|162  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIAADKRVHSIREAYLPELSVIP

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          900      910      920      930      940      950
Cry1Ac  960      970      980      990      1000     1010
        GVNAAI FEELEGRIF TAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
        .....
gi|162  960      970      980      990      1000     1010
        GVNAAI FEELEGRIF TAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
        .....

```

```

          1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEV SQEVRVCPGRGY ILLRV TAYKEGYGEGCVT IHEIENNTDELKFSNCVEEEIYPNN
        .....
gi|162  EWEAEV SQEVRVCPGRGY ILLRV TAYKEGYGEGCVT IHEIENNTDELKFSNCVEEEIYPNN
        .....

```

```

          1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
        .....
gi|162  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRGYR
        .....

```

```

          1140     1150     1160     1170     1180
Cry1Ac  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
        .....
gi|162  DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
        .....

```

>>gi|77376718|gb|ABA70265.1| Sequence 14 from patent US (1177 aa)  
 initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(: 0  
 Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap  
 (5-1182:1-1177)

```

          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
        .....
gi|773  MDNNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
        .....

```

```

          70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
        .....
gi|773  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
        .....

```

```

          130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        .....
gi|773  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        .....

```

```

          190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYRFRREL
        .....
gi|773  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVYRFRREL
        .....

```

```

          250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRFGSAQGI EGSIRSPHL
        .....
gi|773  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRFGSAQGI ERSIRSPHL
        .....

```

```

          240     250     260     270     280     290
Cry1Ac  310     320     330     340     350     360
        MDILNSIT IYTD AHRGEYYWSGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIVAQLGQ
        .....
gi|773  310     320     330     340     350     360
        MDILNSIT IYTD AHRGEYYWSGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIVAQLGQ
        .....

```

```

          370     380     390     400     410     420
Cry1Ac  GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
        .....
gi|773  GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
        .....

```

```

          430     440     450     460     470     480
Cry1Ac  NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
        .....
gi|773  NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
        .....

```

```

          490     500     510     520     530
Cry1Ac  VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
        .....
gi|773  VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
        .....

```

```

          540     550     560     570     580     590
Cry1Ac  VTFIHLNVNWGNSSIFSNITVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
        .....
gi|773  TTNLR IYVIVAGERIFAGQFNKTM DTDGDLTFQSFYATINTAFTFPMSQSSFTV GADTF
        .....

```

```

          600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
        .....
gi|773  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
        .....

```

```

          660     670     680     690     700     710
Cry1Ac  VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTITIQGG
        .....
gi|773  VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
        .....

```

```

          720     730     740     750     760     770
Cry1Ac  DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
        .....
gi|773  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
        .....

```

```

          780     790     800     810     820     830
Cry1Ac  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLD
        .....
gi|773  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLD
        .....

```

```

          840     850     860     870     880     890
Cry1Ac  IDVGCTDLNEDLVVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
        .....

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gi|773 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP

gi|773 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVEEQNNQRSVLVVP

gi|773 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVEEQNNQRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN

gi|773 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCNDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEEKSYTDGRENPCFNRGYR

gi|773 TVTCNDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEEKSYTDGRENPCFNRGYR
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE

gi|773 DYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170

>>gi|31688815|gb|AAP60980.1| Sequence 12 from patent US (1177 aa)
initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

gi|316 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRL EGLSNLYQIYAESFRE

gi|316 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRL EGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|316 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL

gi|316 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

gi|316 TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi|316 MDILNSITIIYTDHAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ

gi|316 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi|316 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS

gi|316 VKAHTLQSGTTVVRGPGFTGGDLRLRTSGGPFAYT--IVNINGQLPQ--RYRARIYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF

gi|316 TTNLRIYVTVAGERIFAGQFNKTMDTGDPDLPQSFYSYATINTAFTFPMQSSFTVGADTF
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|316 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTITIQGG

gi|316 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSDTITIQRG
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK

gi|316 DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSFLSD

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gi | 316 HETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
gi | 316 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
gi | 316 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDFVEEQNNQRSVLLVVP
      960      970      980      990      1000      1010
gi | 316 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDFVEEQNNQRSVLLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAIYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
      1020      1030      1040      1050      1060      1070
gi | 316 EWEAEVSEQEVRVCPGRGYILRVTAIYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRYGR
      1080      1090      1100      1110      1120      1130
gi | 316 TVTCNDYTVNQEEYGGAYTSRNGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRYGR
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
gi | 316 DYTPLPVGYYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170

>>gi|29718509|gb|AAP01233.1| Sequence 10 from patent US (1177 aa)
  in1n: 7055 in1t1: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)

      10      20      30      40      50      60
Cry1Ac CMQAMNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
gi | 297 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNAQAI SRLEGLSNLYQIYAESFRE
      70      80      90      100      110
gi | 297 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNAQAI SRLEGLSNLYQIYAESFRE
      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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gi | 297 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQFREL
      190      200      210      220      230
gi | 297 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRWIRYQFREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFRGSAQIEGSI RSPHL
      250      260      270      280      290
gi | 297 TLTVLDIVSLFPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSFRGSAQIEGSI RSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQ
      310      320      330      340      350
gi | 297 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      370      380      390      400      410
gi | 297 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
      430      440      450      460      470
gi | 297 NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490      500      510      520      530
gi | 297 VKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
      540      550      560      570      580      590
gi | 297 TTNLRIVTVAGERIFAGQFNKTMDDTGDPLTFQSFYSATINTAFTFPMSQSSFTVGADTF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVVIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650
gi | 297 SSGNEVVIDRFEFIPVTTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710
gi | 297 VDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
      660      670      680      690      700      710

      720      730      740      750      760      770

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Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|297 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|297 HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
      780      790      800      810      820      830
      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|297 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP
gi|297 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
      960      970      980      990     1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|297 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
      960      970      980      990     1000     1010
      1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCFVEEIIYPNN
gi|297 EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCFVEEIIYPNN
      1020     1030     1040     1050     1060     1070
      1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPFCFNRGYR
gi|297 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPFCFNRGYR
      1080     1090     1100     1110     1120     1130
      1140     1150     1160     1170     1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|297 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170
>>gi|162500739|gb|ABY14163.1| Sequence 12 from patent US (1177 aa)
  initn: 7055 initl: 3806 opt: 7046 Z-score: 8300.1 bits: 1547.8 E(): 0
Smith-Waterman score: 7046; 89.932% identity (94.162% similar) in 1182 aa overlap
(5-1182:1-1177)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|162 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
      70      80      90     100     110     120

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Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|162 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90     100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRRTYPIRTVSQTLREIYTNPVLENFDGSRFGSAQGIERSIRSPHL
gi|162 TLTVLDIVSLFPNYDSRRTYPIRTVSQTLREIYTNPVLENFDGSRFGSAQGIERSIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTPSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|162 GVYRTPSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|162 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWTHRSATPTNTIDPERITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|162 VKAHTLQSGTTPVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGVRNF
gi|162 TTNLRIYVTVAGERIFAGQFNKTMDTGDPPLTFQSPSYATINTAFTFPMQSSFTVQADTF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|162 SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
      600     610     620     630     640     650

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480      490      500      510      520      530
540      550      560      570      580      590
Cry1Ac  VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGVRNF
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  TTNLR IYVTVAGERIFAQQFNKTMDTGDPLTFQFSFYATINTAFTFPMSSQSSFTVGADTF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  SSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac  VTYLSDPEFLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  VDCLSDPEFLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITIQRG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGIYEDSQDLEIYSIRYNK
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  DDVFKENYVTLPGTFDECYPTYLYQKIDESKCLKAFTRYQLRGIYEDSQDLEIYLIRYNK
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  HETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAADKRVHSIREAYLPELSVIP
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

960      970      980      990      1000     1010
Cry1Ac  GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
960      970      980      990      1000     1010

1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
1020     1030     1040     1050     1060     1070

1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRYGR
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|833  TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPECFNRYGR
1080     1090     1100     1110     1120     1130

1140     1150     1160     1170     1180
Cry1Ac  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|833  DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140     1150     1160     1170

>>gi|594597|gb|AAA56204.1| Sequence 4 from Patent EP 022 (1177 aa)
initn: 7011 init1: 3762 opt: 7007 Z-score: 8254.1 bits: 1539.3 E(): 0
Smith-Waterman score: 7007; 89.679% identity (94.416% similar) in 1182 aa overlap
(5-1182:1-1177)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  MDILNSITIIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|594  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
360     370     380     390     400     410

430     440     450     460     470     480
Cry1Ac  NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|594 NNNVPPRQGFHSHRLSHVSMFRSGFSSNSVSIIRAPTFWQHRSAEFNNIIPSSQITQIPL
      420      430      440      450      460      470
Cry1Ac VKNFNLFG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
      490      500      510      520      530
gi|594 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL-----SQRYRVIRYAS
      480      490      500      510      520      530
Cry1Ac VTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
      540      550      560      570      580      590
gi|594 TTNLQFHSTIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTFFNFSSNGSVVFTLSAHVF
      540      550      560      570      580      590
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650
gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac VTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710
gi|594 VECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYSIRYNAK
      720      730      740      750      760      770
gi|594 DDVFKENYVTLTGTDFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSODLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
      780      790      800      810      820      830
gi|594 HETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
      780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
gi|594 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVLVLP
      960      970      980      990      1000      1010
gi|594 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVLVLP
      960      970      980      990      1000      1010
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020      1030      1040      1050      1060      1070

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gi|594 EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020      1030      1040      1050      1060      1070
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVVEEKSQYTDGRRNPCEFNRYR
      1080      1090      1100      1110      1120      1130
gi|594 TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVVEEKSQYTDGRRNPCEFNRYR
      1080      1090      1100      1110      1120      1130
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170      1180
gi|594 DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170
>>gi|2095433|gb|AAB57615.1|I42028 Sequence 17 from paten (1181 aa)
      initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
      Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
      (5-1182:1-1181)
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50      60
gi|209 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLDVLIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      70      80      90      100      110      120
gi|209 VLGLDVLIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130      140      150      160      170      180
gi|209 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      190      200      210      220      230      240
gi|209 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLNFDGSRGSAQIEGSIKRSPLH
      250      260      270      280      290      300
gi|209 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLNFDGSRGSAQIEGSIKRSPLH
      240      250      260      270      280      290
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      310      320      330      340      350      360
gi|209 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
Cry1Ac GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQGTVDLSLDEIPPQ
      370      380      390      400      410      420

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gi|209 GYRFLSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVA RYKSGTVDSLDEIIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480
gi|209 NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530
gi|209 TKSTNLGSGT SVVKGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
480 490 500 510 520 530

Cry1Ac VPIHLNWNWNSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
540 550 560 570 580 590
gi|209 TTNLQFHTSIDGRPINQGNFSA TMSSGSNLQSGSFRTVGF TTPFNFSGSSVFTLSAHVF
540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650
gi|209 NSGNEVYIDRIEFVPAEVTFFAEYDLERAQKAVNELFTSSNIQLKTDVTDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac VTYLSDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
660 670 680 690 700 710
gi|209 VECLSDDEFCLDEKRELSKVHAKRLSDERNLLQDPNFRGINRQLDRGWGGSTGITIQGG
660 670 680 690 700 710

Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
720 730 740 750 760 770
gi|209 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
780 790 800 810 820 830
gi|209 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
780 790 800 810 820 830

Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890
gi|209 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950
gi|209 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac
960 970 980 990 1000 1010

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Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|209 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVLVVP
960 970 980 990 1000 1010

Cry1Ac EWEAEVSQEVVRVCPGRGYILRVTA YKEGYEGECVTTIHEIENNTDELKFSNCVVEE IYPNN
1020 1030 1040 1050 1060 1070
gi|209 EWEAEVSQEVVRVCPGRGYILRVTA YKEGYEGECVTTIHEIENNTDELKFSNCVVEE IYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEN
1080 1090 1100 1110 1120 1130
gi|209 TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCESN
1080 1090 1100 1110 1120 1130

Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180
gi|209 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180

>>gi|47270466|gb|AAT27228.1| Sequence 13 from patent US (1181 aa)
initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50 60
gi|472 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120
gi|472 VLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRREL
190 200 210 220 230 240
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
250 260 270 280 290 300
gi|472 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
240 250 260 270 280 290

Cry1Ac
310 320 330 340 350 360

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Cry1Ac MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
gi|472 MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
gi|472 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ  
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530  
gi|472 VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS  
TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS  
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590  
gi|472 VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF  
TTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRITVGFNPFNFSSNGSSVFTLSAHVF  
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650  
gi|472 SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
NSGENEYVIDRIEFVPAEVTFAEAYDLERAQKAVNELFTSSNIGLKTVDYHIDQVSNL  
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710  
gi|472 VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG  
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770  
gi|472 DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
DDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYFLIRYNAK  
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830  
gi|472 HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
HETVNVPGTGLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890  
gi|472 IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE  
IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE  
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950  
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010  
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP  
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVLVVP  
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070  
gi|472 EWEAEVSQEVVRCVGRGYILRVTA YKEGYGEGCVTTHEIENNTDELKFSNCV EEEIYPNN  
EWEAEVSQEVVRCVGRGYILRVTA YKEGYGEGCVTTHEIENNTDELKFSNCV EEEVYPNN  
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130  
gi|472 TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN  
TVTCNDYATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN  
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180  
gi|472 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1140 1150 1160 1170 1180

>>gi|21690367|emb|CAD37456.1| unnamed protein product [s (1181 aa)  
initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0  
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap  
(5-1182:1-1181)

Cry1Ac 10 20 30 40 50 60  
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|216 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120  
gi|216 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180  
gi|216 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
gi|216 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL  
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL  
180 190 200 210 220 230

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                250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH
gi|216 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|216 MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPP
gi|216 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPP
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|216 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASSQITQIPL
                420      430      440      450      460      470

                490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|216 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQLSTLRVNITAPL-----SQRYRVRIRYAS
                480      490      500      510      520      530

                540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|216 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRFTVGFPTTFNFSNGSSVFTLSAHVF
                540      550      560      570      580      590

                600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|216 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
                600      610      620      630      640      650

                660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|216 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
                660      670      680      690      700      710

                720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK
gi|216 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLIRYNAK
                720      730      740      750      760      770

                780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFFSLD
gi|216 HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFFSLD
                780      790      800      810      820      830

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                840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|216 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
                840      850      860      870      880      890

                900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
gi|216 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
                900      910      920      930      940      950

                960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSRVLPV
gi|216 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHRSVLPV
                960      970      980      990      1000      1010

                1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVRCVPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
gi|216 EWEAEVSQEVVRCVPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
                1020      1030      1040      1050      1060      1070

                1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTNVQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFEN
gi|216 TVTCNDYATQEEYEGTYTSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPCESN
                1080      1090      1100      1110      1120      1130

                1140      1150      1160      1170      1180
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|216 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
                1140      1150      1160      1170      1180

>>gi|47270464|gb|AAT27227.1| Sequence 11 from patent US (1181 aa)
  initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

                10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|472 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac VLGLVDIIGWIFGPGSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIGWIFGPGSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
                120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGDSRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGDSRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|472 TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIIPPQ
gi|472 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|472 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|472 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
gi|472 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSGTDITIQGG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK
gi|472 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLIRYNAK

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720      730      740      750      760      770
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|472 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830

780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|472 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

900      910      920      930      940      950
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQSRVSVLVVP
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVSVLVVP
960      970      980      990      1000      1010

960      970      980      990      1000      1010
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
gi|472 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
1020      1030      1040      1050      1060      1070

1020      1030      1040      1050      1060      1070
Cry1Ac TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
gi|472 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080      1090      1100      1110      1120      1130

1080      1090      1100      1110      1120      1130
Cry1Ac RGYDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|472 RGYDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170      1180

1140      1150      1160      1170      1180
>>gi|21694629|emb|CAD37807.1| unnamed protein product [s (1181 aa)
initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|216 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|216 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE

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60      70      80      90      100     110
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|216  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|216  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|216  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
240      250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|216  TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|216  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350
Cry1Ac  GVYRTLSTLYRRPFIINQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIIPPQ
gi|216  GVYRTLSTLYRRPFIINQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIIPPQ
360      370      380      390      400      410      420
Cry1Ac  GVYRTLSTLYRRPFIINQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIIPPQ
gi|216  GVYRTLSTLYRRPFIINQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIIPPQ
360      370      380      390      400      410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|216  NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIIPSQITQIPL
420      430      440      450      460      470
Cry1Ac  VKGNFLEFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|216  TKSTNLGSGTSSVVKPGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
480      490      500      510      520      530
Cry1Ac  VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV--GVRNF
gi|216  TTNLQFHTSIDGRPINQGNFSAATMSSGSNLSQSGSFRVTFGFTTTPNFNSVFTLSAHVF
540      550      560      570      580      590
Cry1Ac  SGTAGVVIDRFFIIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|216  NSGNEVYIDRIEFVPAEVTFFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac  VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|216  VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

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gi|216  VECLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710
Cry1Ac  DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|216  DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
720      730      740      750      760      770
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|216  HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|216  IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|216  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac  GVNAAFIEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQSRVSVLP
gi|216  GVNAAFIEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVSVLP
960      970      980      990      1000     1010
Cry1Ac  EWEAEVSQEVVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
gi|216  EWEAEVSQEVVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYVPPNN
1020     1030     1040     1050     1060     1070
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEFN
gi|216  TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080     1090     1100     1110     1120     1130
Cry1Ac  RGYRDTPLPVGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|216  RGYRDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170     1180
>>gi|47270470|gb|AAT27230.1| Sequence 17 from patent US (1181 aa)
initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)
10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLEFVPGAGF

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gi|472 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIIEGSIIRSPHL
gi|472 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIIEGSIIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQ
gi|472 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|472 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|472 TTNLQFHTSIDGRPLNQGNFSATMSSGSLQSGSFRTVGFPTPFNFSGNGSVFTLSAHVF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL

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.. : ..... : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQILGKTDVTDYHIDQVSNL
      600     610     620     630     640     650
      660     670     680     690     700     710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQQG
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 VECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAK
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYIRYNAK
      720     730     740     750     760     770
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHFSLD
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHFSLD
      780     790     800     810     820     830
      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 IDVGCTDLNEDLGWVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840     850     860     870     880     890
      900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRHSIREAYLPELSVIP
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMHAADKRHSIREAYLPELSVIP
      900     910     920     930     940     950
      960     970     980     990     1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSV L VVP
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSV L VVP
      960     970     980     990     1000    1010
      1020    1030    1040    1050    1060    1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVT IHEIENNTDELKFSNCV EEEIYPNN
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 EWEAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVT IHEIENNTDELKFSNCV EEEIYPNN
      1020    1030    1040    1050    1060    1070
      1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFN
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 TVTCNDYTVNQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1080    1090    1100    1110    1120    1130
      1140    1150    1160    1170    1180
Cry1Ac RGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      : ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|472 RGYGDYTPLVGAVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140    1150    1160    1170    1180

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>>gi|5942795|gb|AAE02327.1| Sequence 11 from patent US 5 (1181 aa)

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initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|594 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHL
gi|594 TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHL
Cry1Ac MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|594 MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
Cry1Ac GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ
gi|594 GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ
Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFN NI IASDSITQIPA
gi|594 NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFN NI IPSSQITQIPL
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS

Cry1Ac VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594 TTNLQFHSTSIDGRPINQGNFSATMSSGSLNQLQSGSFRFTVGF TTFNPNFNSGSSVFTLSAHVF
Cry1Ac SGTAGVIIDRFEFIPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|594 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
Cry1Ac DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|594 DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRVYNAK
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLD
gi|594 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFSLD
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|594 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
Cry1Ac GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNR SVLVVP
gi|594 GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNR SVLVVP
Cry1Ac EWEAEVSVQEVRRVCPGRGYILRV TAYKEGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
gi|594 EWEAEVSVQEVRRVCPGRGYILRV TAYKEGEGCVTIHEIENNTDELKFSNCV EEEVYPPNN
Cry1Ac TVTCNDYTNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN
gi|594 TVTCNDYATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN



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1080      1090      1100      1110      1120      1130
Cry1Ac  TVTCDNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEKSYTDGRRNPCEF
gi|217  TVTCDNDYTATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRNDPCE
1080      1090      1100      1110      1120      1130

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1140      1150      1160      1170      1180
Cry1Ac  RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|217  RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170      1180

```

>>gi|12808293|gb|AAE43513.1| Sequence 28 from patent US (1181 aa)  
 initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0  
 Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap  
 (5-1182:1-1181)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128  MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|128  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|128  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIIEGSI RSPHL
gi|128  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIIEGSI RSPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac  GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
gi|128  GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
360     370     380     390     400     410

```

```

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL
420      430      440      450      460      470

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490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVLSGPGFTGGDLVRLNNSGNNIQNRYIEVPIHFPSTSTRYRVRVRYAS
gi|128  TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRVVRVIRYAS
480      490      500      510      520      530

```

```

540      550      560      570      580      590
Cry1Ac  VTPIHNLVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|128  TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

```

```

600      610      620      630      640      650
Cry1Ac  SGTAGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650

```

```

660      670      680      690      700      710
Cry1Ac  VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|128  VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
gi|128  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLSIRYNAK
720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|128  HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830

```

```

840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|128  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

```

```

900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
gi|128  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

```

```

960      970      980      990     1000     1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|128  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVLVVP
960      970      980      990     1000     1010

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          960      970      980      990      1000      1010
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIEHEIENNTDELKFSNCVEEEIYPNN
gi|128 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIEHEIENNTDELKFSNCVEEEIYPNN
          1020      1030      1040      1050      1060      1070

          1080      1090      1100      1110      1120      1130
Cry1Ac TVTTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPECFN
gi|128 TVTTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPESN
          1080      1090      1100      1110      1120      1130

          1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|128 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140      1150      1160      1170      1180

```

>>gi|21713538|emb|CAD38222.1| unnamed protein product [s (1181 aa)  
 initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0  
 Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap  
 (5-1182:1-1181)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|217 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|217 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|217 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|217 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          180     190     200     210     220     230

          250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHL
gi|217 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHL
          240     250     260     270     280     290

          310     320     330     340     350     360
Cry1Ac MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|217 MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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          300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|217 GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|217 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IPSSQITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVIGSPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|217 TKSTNLGSGTSVVKPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac VTFIHLNVNWGSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|217 TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRTVGFPTTFNFSNGSSVFTLSAHVF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL
gi|217 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|217 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|217 DDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRINA
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|217 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
          780      790      800      810      820      830

          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|217 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
          840      850      860      870      880      890

          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELSVIP

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gi | 217 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVP

gi | 217 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNHRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN

gi | 217 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCDNDYTVNQEEYGGAYTSRNRGYNEA----PSPADYASVYEEKSYTDGRRNPCEFN

gi | 217 TVTCDNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi | 217 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170 1180

>>gi|21713540|emb|CAD38223.1| unnamed protein product [s (1181 aa)
initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

gi | 217 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi | 217 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi | 217 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL

gi | 217 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL

gi | 217 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi | 217 MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ

gi | 217 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi | 217 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHPSTSTRYRVRVRYAS

gi | 217 TKSTNLGSGTSSVVKGPGFTGGDLRLRSTSPGQISTLRVNITAPL----SQRYRVRIRYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF

gi | 217 TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSGSRFTVGTTPFNFNSGSSVFTLSAHVF
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi | 217 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

gi | 217 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK

gi | 217 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD

gi | 217 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890
IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGBALARVKRAEKKWRDKRE

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gi|217 IDVCGTDLNEDLGVVVIKIKTKDGHARLGNLEFLLEEKPLVGEALARKVRAEKKWRDKRE
      840      850      860      870      880      890

Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHVSIREAYLPELSVIP
gi|217 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHVSIREAYLPELSVIP
      900      910      920      930      940      950

Cry1Ac 960      970      980      990      1000     1010
GVNAAFEELLEGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVVLVVP
gi|217 GVNAAFEELLEGRIPTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVVLVVP
      960      970      980      990      1000     1010

Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|217 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      1020     1030     1040     1050     1060     1070

Cry1Ac 1080     1090     1100     1110     1120     1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
gi|217 TVTCNDYTVNQEEYEGTYTSRNRGYD GAYESSNSVPADYASAYEEKAYTDGRRNDPCESN
      1080     1090     1100     1110     1120     1130

Cry1Ac 1140     1150     1160     1170     1180
RGYRDYTPPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|217 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170     1180

>>gi|5942805|gb|AAE02337.1| Sequence 28 from patent US 5 (1181 aa)
  initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|594  MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|594  VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL

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gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      180      190      200      210      220      230

Cry1Ac 250     260     270     280     290     300
TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSI RSPHL
gi|594  TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSI RSPHL
      240     250     260     270     280     290

Cry1Ac 310     320     330     340     350     360
MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQ
gi|594  MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQ
      300     310     320     330     340     350

Cry1Ac 370     380     390     400     410     420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPO
gi|594  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPO
      360     370     380     390     400     410

Cry1Ac 430     440     450     460     470     480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
gi|594  NNVVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
      420     430     440     450     460     470

Cry1Ac 490     500     510     520     530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|594  TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

Cry1Ac 540     550     560     570     580     590
VTPIHNLVNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594  TTNLQFHTSIDGRPINQGNFSATMSSGNSLNQSGSFRFTVGF TTPNFNSNGSSVFTLSAHVF
      540     550     560     570     580     590

Cry1Ac 600     610     620     630     640     650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYDHYHIDQVSNL
      600     610     620     630     640     650

Cry1Ac 660     670     680     690     700     710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|594  VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710

Cry1Ac 720     730     740     750     760     770
DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|594  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770

Cry1Ac 780     790     800     810     820     830

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Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|594 HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|594 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
gi|594 GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNHRSVLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
gi|594 EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIVPNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPCFEFN
gi|594 TVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|594 RGYGDTPLPVAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170      1180

>>gi|12808286|gb|AAE43506.1| Sequence 17 from patent US (1181 aa)
  initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

      10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDDGSRGSAQIEGSIKRSRPHL
gi|128 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDDGSRGSAQIEGSIKRSRPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDIIPPQ
gi|128 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDIIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|128 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVLSGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNITVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|128 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTFFNFNAGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 NSGNEVYIDRIEFVFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRSLDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|128 VECLSDEFCLDEKRELSEKVKHAKRSLDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
gi|128 DDVFKENYVTLTSGTDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSDLEIYLIRYNAK
720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|128 HETVNVPGTGLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|128 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|128 KLEWETNIVYKAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVVP
gi|128 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNHRSVLVVP
960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAKEGYGEGCVTIEHEIENNTDELKFSNCEVEEYIPNN
gi|128 EWEAEVSEQEVRVCPGRGYLLRVTAKEGYGEGCVTIEHEIENNTDELKFSNCEVEEYIPNN
1020     1030     1040     1050     1060     1070

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEFN
gi|128 TVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCEFSN
1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|128 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170     1180

```

```

>>gi|2095430|gb|AAB57612.1|I42025 Sequence 11 from paten (1181 aa)
initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|209 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|209 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|209 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|209 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL
gi|209 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL
240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|209 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
gi|209 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|209 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
gi|209 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRVRYAS
480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHNLVNWGSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|209 TTNLQPHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTFPNFSNGSSVFTLSAHVF
540     550     560     570     580     590

```

```

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|209 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600     610     620     630     640     650

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```

660      670      680      690      700      710
Cry1Ac VTYLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: .....: .....: .....: .....: .....: .....:
gi|209 VECLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
: .....: .....: .....: .....: .....: .....:
gi|209 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
: .....: .....: .....: .....: .....: .....:
gi|209 HETVNVPGTGLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
: .....: .....: .....: .....: .....: .....:
gi|209 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
: .....: .....: .....: .....: .....: .....:
gi|209 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

```

```

960      970      980      990     1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVLVVP
: .....: .....: .....: .....: .....: .....:
gi|209 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNHRSVLVVP
      960      970      980      990     1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWAEVSVQEVVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
: .....: .....: .....: .....: .....: .....:
gi|209 EWAEVSVQEVVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
      1020     1030     1040     1050     1060     1070

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPECFN
: .....: .....: .....: .....: .....: .....:
gi|209 TVTCNDYTATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
: .....: .....: .....: .....: .....: .....:
gi|209 RGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170     1180

```

```

>>gi|21690373|emb|CAD37459.1| unnamed protein product [s (1181 aa)
  initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
: .....: .....: .....: .....: .....: .....:
gi|216 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90     100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
: .....: .....: .....: .....: .....: .....:
gi|216 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90     100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
: .....: .....: .....: .....: .....: .....:
gi|216 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPPDSRDWIRYNQFREL
: .....: .....: .....: .....: .....: .....:
gi|216 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPPDSRDWIRYNQFREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
: .....: .....: .....: .....: .....: .....:
gi|216 TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
: .....: .....: .....: .....: .....: .....:
gi|216 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
: .....: .....: .....: .....: .....: .....:
gi|216 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
      360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
: .....: .....: .....: .....: .....: .....:
gi|216 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVIGSGPFTGGDLVRLNSSGNINQRGYIEVPIHPSTSTRYRVRVRYAS
: .....: .....: .....: .....: .....: .....:
gi|216 TKSTNLGSGTSVVKGPFTGGDILLRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
: .....: .....: .....: .....: .....: .....:
gi|216 TTNLQFHTSIDGRPINQGNFSATMSSGNSLNQSGSFRTVGFTTFFNFSNGSSVFTLSAHVF

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540      550      560      570      580      590
Cry1Ac  600      610      620      630      640      650
SGTAGVIIDRFEFIPVTTALEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . : : : : . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac  VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYSIRYNAK
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLIRYNAK
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  IDVGCTDLNEDLGVVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

960      970      980      990      1000     1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVVLVVP
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVVLVVP
960      970      980      990      1000     1010

1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIVPNN
1020     1030     1040     1050     1060     1070

1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEKSYTDGRRENPCFEN
: : : : . . : : : : : : : : : : : : : : : : : : : : : :
gi|216  TVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080     1090     1100     1110     1120     1130

1140     1150     1160     1170     1180
Cry1Ac  RGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi|216  RGYDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140     1150     1160     1170     1180

>>gi|12808284|gb|AAE43504.1| Sequence 13 from patent US (1181 aa)
initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSRISPHL
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSRISPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac  GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
360     370     380     390     400     410

430     440     450     460     470     480
Cry1Ac  NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
: : : : . . : : : : : : : : : : : : : : : : : : : : : :
gi|128  NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420     430     440     450     460     470

490     500     510     520     530
Cry1Ac  VKGNFLFNS-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
. . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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gi|128 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSSSLGNIV---GVRNF
.: ..... : ... :.: :.: ..... : .: : .: : .: .:
gi|128 TTNLQFHSTIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTFFNFNSNGSSVFTLSAHVF
      540      550      560      570      580      590
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
      600      610      620      630      640      650
      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 VECLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710
      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYSIRYNAK
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSODLEIYLIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 HETVNPVGTGSLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830
      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950
      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQSRVSVLVVP
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNHRSVSVLVVP
      960      970      980      990      1000      1010
      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYIPNN
      1020      1030      1040      1050      1060      1070
      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQBEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFEN

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.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEKAAYDGRDRDNPCESN
      1080      1090      1100      1110      1120      1130
      1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|128 RGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140      1150      1160      1170      1180
>>gi|21713544|emb|CAD38225.1| unnamed protein product [s (1181 aa)
  initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISREGLSNLYQIYAESFRE
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAIISREGLSNLYQIYAESFRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
.: ..... : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|217 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360      370      380      390      400      410
      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA

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Cry1Ac  GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPO
gi|209  GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPO
          360          370          380          390          400          410

          430          440          450          460          470          480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|209  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
          420          430          440          450          460          470

          490          500          510          520          530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|209  TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
          480          490          500          510          520          530

          540          550          560          570          580          590
Cry1Ac  VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|209  TTNLQFHTSIDGRPLNQGNFSATMSSGNSLQSGSFRTVGFTHPFNFSSGSSVFTLSAHVF
          540          550          560          570          580          590

          600          610          620          630          640          650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|209  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
          600          610          620          630          640          650

          660          670          680          690          700          710
Cry1Ac  VTLYLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|209  VECLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
          660          670          680          690          700          710

          720          730          740          750          760          770
Cry1Ac  DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYIRYNK
gi|209  DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYLIRYNK
          720          730          740          750          760          770

          780          790          800          810          820          830
Cry1Ac  HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD
gi|209  HETVNVPGTGLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFSLD
          780          790          800          810          820          830

          840          850          860          870          880          890
Cry1Ac  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRDKRE
gi|209  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRDKRE
          840          850          860          870          880          890

          900          910          920          930          940          950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
gi|209  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPELSVIP
          900          910          920          930          940          950

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          960          970          980          990          1000          1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
gi|209  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVP
          960          970          980          990          1000          1010

          1020          1030          1040          1050          1060          1070
Cry1Ac  EWEAEVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
gi|209  EWEAEVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVYVNN
          1020          1030          1040          1050          1060          1070

          1080          1090          1100          1110          1120          1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEN
gi|209  TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPESN
          1080          1090          1100          1110          1120          1130

          1140          1150          1160          1170          1180
Cry1Ac  RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|209  RGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140          1150          1160          1170          1180

>>gi|21690369|emb|CAD37457.1| unnamed protein product [s (1181 aa)
initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

          10          20          30          40          50          60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|216  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10          20          30          40          50

          70          80          90          100          110          120
Cry1Ac  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|216  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
          60          70          80          90          100          110

          130          140          150          160          170          180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|216  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120          130          140          150          160          170

          190          200          210          220          230          240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|216  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
          180          190          200          210          220          230

          250          260          270          280          290          300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
gi|216  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
          240          250          260          270          280          290

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          310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|216 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPQ
gi|216 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|216 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASSQITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|216 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
gi|216 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNFSNGSSVFTLSAHVF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|216 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|216 VECLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
gi|216 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSDLEIYLIRYNAK
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|216 HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
          780      790      800      810      820      830

          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|216 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
          840      850      860      870      880      890

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          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
gi|216 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVHSIREAYLPELSVIP
          900      910      920      930      940      950

          960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVVP
gi|216 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVP
          960      970      980      990      1000      1010

          1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYYPNN
gi|216 EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYYPNN
          1020      1030      1040      1050      1060      1070

          1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSPADYASVYEEKSYTDGRRENPCFN
gi|216 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
          1080      1090      1100      1110      1120      1130

          1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|216 RGYDGYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1140      1150      1160      1170      1180

>>gi|47270484|gb|AAT27237.1| Sequence 28 from patent US (1181 aa)
  initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|472 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFREL
          180      190      200      210      220      230

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250 260 270 280 290 300  
 Cry1Ac TLTVLVDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSIIRSPHL  
 gi|472 TLTVLVDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSIIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITITDYDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 gi|472 MDILNSITITDYDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIIPPQ  
 gi|472 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIIPPQ  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 gi|472 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL  
 420 430 440 450 460 470

490 500 510 520 530  
 Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
 gi|472 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS  
 480 490 500 510 520 530

540 550 560 570 580 590  
 Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF  
 gi|472 TTNLQFHSTIDGRPINQGNFSAATMSSGSLQSGSFRVTGFTTFFNFNSNGSSVFTLSAHVF  
 540 550 560 570 580 590

600 610 620 630 640 650  
 Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 gi|472 NSGNEVYIDRIEFVPAEVTFAEAYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL  
 600 610 620 630 640 650

660 670 680 690 700 710  
 Cry1Ac VTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG  
 gi|472 VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG  
 660 670 680 690 700 710

720 730 740 750 760 770  
 Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAK  
 gi|472 DDVFKENYVTLGTFDECYPTYLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAK  
 720 730 740 750 760 770

780 790 800 810 820 830  
 Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD  
 gi|472 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD

780 790 800 810 820 830  
 Cry1Ac 840 850 860 870 880 890  
 gi|472 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE  
 840 850 860 870 880 890

900 910 920 930 940 950  
 Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
 gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP  
 900 910 920 930 940 950

960 970 980 990 1000 1010  
 Cry1Ac GVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP  
 gi|472 GVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVLVVP  
 960 970 980 990 1000 1010

1020 1030 1040 1050 1060 1070  
 Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN  
 gi|472 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN  
 1020 1030 1040 1050 1060 1070

1080 1090 1100 1110 1120 1130  
 Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPCEFNP  
 gi|472 TVTCNDYTVNQEEYEGTYTSRNRGYDYGAYESNSSVVPADYASAYEEKAYTDGRRNDPESNP  
 1080 1090 1100 1110 1120 1130

1140 1150 1160 1170 1180  
 Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETGTFIVDSVELLLMEE  
 gi|472 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETGTFIVDSVELLLMEE  
 1140 1150 1160 1170 1180

>>gi|12808283|gb|AAE43503.1| Sequence 11 from patent US (1181 aa)  
 initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0  
 Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap  
 (5-1182:1-1181)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF  
 gi|128 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE  
 gi|128 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190      200      210      220      230      240
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL
      240      250      260      270      280      290
gi|128 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
gi|128 MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
      360      370      380      390      400      410
gi|128 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      420      430      440      450      460      470
gi|128 NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIqNRgyIEVPIHFPSTSTRYRVrVRYAS
      480      490      500      510      520      530
gi|128 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVrIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTPiHLNVNwGSSIFsNTVPATATSLDNLQSSDFGyFESANAFTSSLGNIV---GVRNF
      540      550      560      570      580      590
gi|128 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSPRTVGFTTPFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650
gi|128 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNIQLKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTyLSDEFCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      660      670      680      690      700      710
gi|128 VECLsDEFCLDEKRElSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLsGTFDECYPTyLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAK
      720      730      740      750      760      770

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gi|128 DDVFKENYVTLsGTFDECYPTyLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLD
      780      790      800      810      820      830
gi|128 HETVNVPGTGSWLPLSAPSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCAHSHHfSLD
      780      790      800      810      820      830

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
      840      850      860      870      880      890
gi|128 IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIvYKEAKESVDALFVNSQYDQLADTNIAMIHAADKRvHSIREAYLPELsVIP
      900      910      920      930      940      950
gi|128 KLEWETNIvYKEAKESVDALFVNSQYDRlQADTNIAMIHAADKRvHSIREAYLPELsVIP
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKghVDVVEEQNNQRsVLVVP
      960      970      980      990      1000      1010
gi|128 GVNAAIFEELEGRIFtAFsLYDARNVIKNGDFNNGLSCWNVKghVDVVEEQNNHRSVLVVP
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKfSNcVVEEIEYpNN
      1020      1030      1040      1050      1060      1070
gi|128 EWEAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKfSNcVVEEYVpNN
      1020      1030      1040      1050      1060      1070

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYtVNQEEYGGAYTSRNrgYNEA---PSVPADYASvYEEKsYTDGRRENpCEFN
      1080      1090      1100      1110      1120      1130
gi|128 TVTCNDYtATQEEYEGTYTSRNrgYDgAYESNssVPADYASAYEEKAYtDGRRDnPCESN
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac RGYRDYtPLPVGYVtKELEYFPETDKVWIEIGETEGTFIVDSVellLMEE
      1140      1150      1160      1170      1180
gi|128 RGYGDYtPLPAGYVtKELEYFPETDKVWIEIGETEGTFIVDSVellLMEE
      1140      1150      1160      1170      1180

>>gi|5942796|gb|AAE02328.1| Sequence 13 from patent US 5 (1181 aa)
initn: 6557 init1: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGF
      10      20      30      40      50      60
gi|594 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGF
      10      20      30      40      50      60

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPsQWDAFLVQIEQLINQRIEEFARNAISRLGLSnlYQIYAESfRE
      70      80      90      100      110      120

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gi|209      .....
            MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTLQFLLESEFVPGAGF
            10      20      30      40      50

Cry1Ac      70      80      90      100     110     120
            VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
            .....
gi|209      VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
            60      70      80      90      100     110

Cry1Ac      130     140     150     160     170     180
            WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
            .....
gi|209      WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
            120     130     140     150     160     170

Cry1Ac      190     200     210     220     230     240
            VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
            .....
gi|209      VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
            180     190     200     210     220     230

Cry1Ac      250     260     270     280     290     300
            TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGLEIGSIRSPHL
            .....
gi|209      TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGLEIGSIRSPHL
            240     250     260     270     280     290

Cry1Ac      310     320     330     340     350     360
            MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
            .....
gi|209      MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
            300     310     320     330     340     350

Cry1Ac      370     380     390     400     410     420
            GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEIPPQ
            .....
gi|209      GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEIPPQ
            360     370     380     390     400     410

Cry1Ac      430     440     450     460     470     480
            NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
            .....
gi|209      NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IPSSQITQIPL
            420     430     440     450     460     470

Cry1Ac      490     500     510     520     530
            VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
            .....
gi|209      TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
            480     490     500     510     520     530

Cry1Ac      540     550     560     570     580     590
            VTIPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
            .....
gi|209      TTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTTFPNFNSGSSVFTLSAHVF
            540     550     560     570     580     590

Cry1Ac      600     610     620     630     640     650

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Cry1Ac      SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
            .. : ..... : ..... : ..... : ..... : ..... : .....
gi|209      NSGNEVYIDRIEFVPAEVTFEAYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
            600     610     620     630     640     650

Cry1Ac      660     670     680     690     700     710
            VTYLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
            : ..... : ..... : ..... : ..... : ..... : .....
gi|209      VECLSDEFCLDEKRELSSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
            660     670     680     690     700     710

Cry1Ac      720     730     740     750     760     770
            DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
            720     730     740     750     760     770

Cry1Ac      780     790     800     810     820     830
            HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      HETVNVPGTGSWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD
            780     790     800     810     820     830

Cry1Ac      840     850     860     870     880     890
            IDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVRAEKKWRDKRE
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      IDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVRAEKKWRDKRE
            840     850     860     870     880     890

Cry1Ac      900     910     920     930     940     950
            KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
            900     910     920     930     940     950

Cry1Ac      960     970     980     990     1000    1010
            GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNQRSVLVVP
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDVEEQNNHRSVLVVP
            960     970     980     990     1000    1010

Cry1Ac      1020    1030    1040    1050    1060    1070
            EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      EWEAEVSEQEVRVCPGRGYLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
            1020    1030    1040    1050    1060    1070

Cry1Ac      1080    1090    1100    1110    1120    1130
            TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPECFN
            ..... : ..... : ..... : ..... : ..... : .....
gi|209      TVTCNDYATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
            1080    1090    1100    1110    1120    1130

Cry1Ac      1140    1150    1160    1170    1180
            RGYRDYTPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
            ..... : ..... : ..... : ..... : .....
gi|209      RGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
            1140    1150    1160    1170    1180

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>>gi|5942798|gb|AAE02330.1| Sequence 17 from patent US 5 (1181 aa)
initn: 6557 initl: 3174 opt: 6978 Z-score: 8219.9 bits: 1532.9 E(): 0
Smith-Waterman score: 6978; 88.954% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50
70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|594 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110
130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170
190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230
250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSRSPHL
gi|594 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSRSPHL
240 250 260 270 280 290
310 320 330 340 350 360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|594 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350
370 380 390 400 410 420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
gi|594 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
360 370 380 390 400 410
430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
gi|594 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420 430 440 450 460 470
490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL-----SQRYRVRIRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRFTVGFPTFPNFSNGSSVFTLSAHVF
540 550 560 570 580 590
600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYDHYDQVSNL
600 610 620 630 640 650
660 670 680 690 700 710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG
gi|594 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660 670 680 690 700 710
720 730 740 750 760 770
Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|594 DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770
780 790 800 810 820 830
Cry1Ac HETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|594 HETVNVPGTGSLLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780 790 800 810 820 830
840 850 860 870 880 890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|594 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890
900 910 920 930 940 950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950
960 970 980 990 1000 1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|594 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVLVVP
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070
Cry1Ac EWEAEVSQEVVRCVPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
gi|594 EWEAEVSQEVVRCVPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVPPN
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
Cry1Ac TVTCNDYTVNQBEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNCEFN
gi|594 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080 1090 1100 1110 1120 1130

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      1140      1150      1160      1170      1180
Cry1Ac  RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      ::  ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|594  RGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170      1180

>>gi|21690371|emb|CAD37458.1| unnamed protein product [s (1181 aa)
  initn: 6553 initl: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

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      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

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      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

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      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

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      250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNPVENFDGSGFRGSAQGIIEGSI RSPHL
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  TLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNPVENFDGSGFRGSAQGIIEGSI RSPHL
      240     250     260     270     280     290

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      310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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      370     380     390     400     410     420
Cry1Ac  GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEI P P Q
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEI P P Q
      360     370     380     390     400     410

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      430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470

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      490     500     510     520     530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  TKSTNLGSGTSVVKVGPFTGGDILRRTSPGQISTLRVNI TAPL-----SQRYRVRIRYAS
      480     490     500     510     520     530

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      540     550     560     570     580     590
Cry1Ac  VTPIHNLVNWGNSIFSNIVPATATSLDNLQSSDFGYFESANAF TSSLGNIV---GVRNF
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSGSGFRFTVGF TTPFNFSNGSSVFTLSAHVF
      540     550     560     570     580     590

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      600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQ IGLKTDVTDYHIDQVSNL
      600     610     620     630     640     650

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      660     670     680     690     700     710
Cry1Ac  VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD INRQPERGWGSGTGLTIQGG
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGIN RQLDRGWRGSTDITIQGG
      660     670     680     690     700     710

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      720     730     740     750     760     770
Cry1Ac  DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQL RGYIEDSQDLEIYSIRYNAK
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  DDVFKENYVTLQGTDFDECYPTYLYQPIDESKLFKAYTRYQL RGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770

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      780     790     800     810     820     830
Cry1Ac  HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDC SCR DGEKCAHSHHFLSLD
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDC SCR DGEKCAHSHHFLSLD
      780     790     800     810     820     830

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      840     850     860     870     880     890
Cry1Ac  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPL VGEALARVKRAEKKWRDKRE
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPL VGEALARVKRAEKKWRDKRE
      840     850     860     870     880     890

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      900     910     920     930     940     950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA DKRVHSIREAYLPELSVIP
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAA DKRVHSIREAYLPELSVIP
      900     910     920     930     940     950

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      960     970     980     990     1000    1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVVP
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNHRSVLVVP
      960     970     980     990     1000    1010

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      1020    1030    1040    1050    1060    1070
Cry1Ac  EWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCV EEEIYPNN
      ::::::::::::::::::::::::::::::::::::::::::::::::::::
gi|216  EWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCV EEEVYPNN

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1020      1030      1040      1050      1060      1070
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEYEGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPCEFN
gi|216 TVTCNDYATQEEYEGTYSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1080      1090      1100      1110      1120      1130

1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|216 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170      1180

>>gi|47270468|gb|AAT27229.1| Sequence 15 from patent US (1181 aa)
initn: 6553 initl: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|472 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|472 VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSI RSPHL
gi|472 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSI RSPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
gi|472 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q

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360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|472 NNVVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRYAS
gi|472 TKSTNLGSGTSVVKPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VTIHNLVNWGSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|472 TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSGSGSFRIVGFTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQLGLKTDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG
gi|472 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLQGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|472 DDVFKENYVTLQGTDFDECYPTLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|472 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|472 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNQRSVLPV

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gi|472 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVLVVP
960 970 980 990 1000 1010

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN

gi|472 EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNN
1020 1030 1040 1050 1060 1070

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTCDNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN

gi|472 TVTCDNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
1080 1090 1100 1110 1120 1130

Cry1Ac 1140 1150 1160 1170 1180
RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|472 RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140 1150 1160 1170 1180

>>gi|2095432|gb|AAB57614.1|I42027 Sequence 15 from paten (1181 aa)
initn: 6553 initl: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVPGAGF

gi|209 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi|209 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|209 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL

gi|209 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIIEGSIIRSPHL

gi|209 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIIEGSIIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ

gi|209 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ

gi|209 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi|209 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLENG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|209 VKGNFLENG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF

gi|209 TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRVTGFTTFFNFNSGSSVFTLSAHVF
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|209 NSGNEVYIDRIEFVPAEYVFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

gi|209 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660 670 680 690 700 710

Cry1Ac 720 730 740 750 760 770
DDVFKENYVTLQGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK

gi|209 DDVFKENYVTLQGTDFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
720 730 740 750 760 770

Cry1Ac 780 790 800 810 820 830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD

gi|209 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFSLD
780 790 800 810 820 830

Cry1Ac 840 850 860 870 880 890
IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

gi|209 IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890

Cry1Ac 900 910 920 930 940 950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSVIP

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gi|209 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAKDRVHSIREAYLPELSVIP
      900      910      920      930      940      950
Cry1Ac 960      970      980      990      1000     1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
gi|209 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVLVVP
      960      970      980      990      1000     1010
Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN
gi|209 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEVYPNN
      1020     1030     1040     1050     1060     1070
Cry1Ac 1080     1090     1100     1110     1120     1130
TVTCONDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYE EKS YTDGRRENPC EFN
gi|209 TVTCONDYTATQEEYEGTYTSRNRGYD GAYESSNSVPADYASAYEEKAYTDGR RDNPCESN
      1080     1090     1100     1110     1120     1130
Cry1Ac 1140     1150     1160     1170     1180
RGYRDYTPPLPVGYVTK ELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
gi|209 RGYGDYTPPLPAGYVTK ELEYFPETDKVWIEIGETEGTFIVDSV ELLLMEE
      1140     1150     1160     1170     1180
>>gi|21713542|emb|CAD38224.1| unnamed protein product [s (1181 aa)
      initn: 6553 initl: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
      Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
      (5-1182:1-1181)
Cry1Ac 10      20      30      40      50      60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
gi|217 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL LSEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|217 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|217 WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYQFRREL
gi|217 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYQFRREL
      180     190     200     210     220     230
Cry1Ac 250     260     270     280     290     300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDG SFRGSAQIEGSI RSPHL

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gi|217 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDG SFRGSAQIEGSI RSPHL
      240     250     260     270     280     290
Cry1Ac 310     320     330     340     350     360
MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIV AQLGQ
gi|217 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTF PLYGTMGNAAPQQRIV AQLGQ
      300     310     320     330     340     350
Cry1Ac 370     380     390     400     410     420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
gi|217 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
      360     370     380     390     400     410
Cry1Ac 430     440     450     460     470     480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPA
gi|217 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASSQITQIPL
      420     430     440     450     460     470
Cry1Ac 490     500     510     520     530
VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|217 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac 540     550     560     570     580     590
VTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|217 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRFTVGF TTPFNFSNGSSVFTLSAHVF
      540     550     560     570     580     590
Cry1Ac 600     610     620     630     640     650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|217 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKT DVTDYHIDQVSNL
      600     610     620     630     640     650
Cry1Ac 660     670     680     690     700     710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|217 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
Cry1Ac 720     730     740     750     760     770
DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|217 DDVFKENYVTLQGTDFDECYPTYLYQPIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770
Cry1Ac 780     790     800     810     820     830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCR DGEKCAHSHHFSLD
gi|217 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHEWNPDLDCSCR DGEKCAHSHHFSLD
      780     790     800     810     820     830
Cry1Ac 840     850     860     870     880     890

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Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|217 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPPELSVIP
gi|217 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIMIHAADKRVHSIREAYLPPELSVIP
      900      910      920      930      940      950

      960      970      980      990     1000     1010
Cry1Ac GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSVLVVP
gi|217 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQQNHRSVLVVP
      960      970      980      990     1000     1010

     1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
gi|217 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
     1020     1030     1040     1050     1060     1070

     1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNCPCEFN
gi|217 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEKAYTDGRRDNPCESN
     1080     1090     1100     1110     1120     1130

     1140     1150     1160     1170     1180
Cry1Ac RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|217 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
     1140     1150     1160     1170     1180

>>gi|5942797|gb|AAE02329.1| Sequence 15 from patent US 5 (1181 aa)
  in1n: 6553 in1l: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|594  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|594  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

     130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
     120     130     140     150     160     170

     190     200     210     220     230     240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKRSRPHL
gi|594 TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKRSRPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|594 MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|594 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
gi|594 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594 TTNLQPHSTIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAYDLERAQKAVNELFTSSNQILKTDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTIQQG
gi|594 VECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQQG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
gi|594 DDVFKENYVTLQGTDFDECYPTYLYQPIDESKLFKAYTRYQLRGYIEDSQDLEIYLRIRYNAK
      720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|594 HETVNVPGTGLWPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

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840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|594 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

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900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
gi|594 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

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960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLVVP
gi|594 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVP
      960      970      980      990      1000     1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
gi|594 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIVPNN
      1020     1030     1040     1050     1060     1070

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPECFEN
gi|594 TVTCNDYTATQEBYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1080     1090     1100     1110     1120     1130

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1140     1150     1160     1170     1180
Cry1Ac RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|594 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170     1180

```

```

>>gi|12808285|gb|AAE43505.1| Sequence 15 from patent US (1181 aa)
  initn: 6553 initl: 3174 opt: 6974 Z-score: 8215.2 bits: 1532.1 E(): 0
Smith-Waterman score: 6974; 88.870% identity (94.266% similar) in 1186 aa overlap
(5-1182:1-1181)

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```

10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|128 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

```

```

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      180      190      200      210      220      230

```

```

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
gi|128 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
      240      250      260      270      280      290

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310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

```

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370      380      390      400      410      420
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
gi|128 GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
      360      370      380      390      400      410

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470

```

```

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

```

```

540      550      560      570      580      590
Cry1Ac VTPIHNLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|128 TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFPTFPNFNSGSSVFTLSAHVF
      540      550      560      570      580      590

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 NSGNEVYIDRIEFVPAEVTFAEYDLERAKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650

```

```

660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
gi|128 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGRWGSTDITIQGG
      660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTDFECYPTLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYLRINAK
gi|128 DDVFKENYVTLTQGTDFECYPTLYQPIDESKLFKAYTRYQLRGYIEDSDLEIYLIRINAK
      720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|128 HETVNVPGTGSWLPLSAPSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
      780      790      800      810      820      830

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|128 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      840      850      860      870      880      890

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
gi|128 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPELSVIP
      900      910      920      930      940      950

```

```

960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVEEQNNRQSVLVVP
gi|128 GVNAAIFEELEGRIFAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVEEQNNRHSVLVVP
      960      970      980      990      1000      1010

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
gi|128 EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
      1020     1030     1040     1050     1060     1070

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
gi|128 TVTCNDYTATQEEYEGYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1080     1090     1100     1110     1120     1130

```

```

1140     1150     1160     1170     1180
Cry1Ac RGYRDYTPPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|128 RGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140     1150     1160     1170     1180

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>>gi|142875|gb|AAA22410.1| delta-endotoxin (1181 aa)
  initn: 6795  initl: 3133  opt: 6788  Z-score: 7995.8  bits: 1491.5  E(): 0
Smith-Waterman score: 6788; 86.341% identity (93.423% similar) in 1186 aa overlap
(5-1182:1-1181)

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```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|142 MDNNPKINECEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|142 VLGLIDLIIWIGFVSPQWDAFLVQIEQLISQRIEEFARNQAIISRLEGLSNLYQIYAEAFRE
      60      70      80      90      100      110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAVNLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQFREL
gi|142 VFGQRWGLDVATINSRYNDLTRLIGTYTDYAVRWYNTGLERWVGPDSDRWIRYQFREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSRSPHL
gi|142 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQRIEQSRSPHL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|142 MDILNSITITYTDAHGGYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGSSNLPSAVYRKSQGTVDLSLDEIPPQ
gi|142 GVYRTLSSSTFYRNPFNIGINNQLSVLDGTEFAYGSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360     370     380     390     400     410

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430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
gi|142 DNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|142 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

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540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|142 TTNLQFHTSIDGRPINQGNFSATMSSGGNLQSGSFRVTGFTTFPNFNSGSSVFTLSAHVF
      540     550     560     570     580     590

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600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|142 NSGNEVYIDRIEFVPAEVTFAEYDLERAQEAVALNFTSPNQIGLKTVDYHIDQVSNL

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        600      610      620      630      640      650
Cry1Ac  660      670      680      690      700      710
:  VTLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|142  VECLSEDFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQDRGWRGSTDITIQGG
        660      670      680      690      700      710

        720      730      740      750      760      770
Cry1Ac  720      730      740      750      760      770
:  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|142  DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIRYNAK
        720      730      740      750      760      770

        780      790      800      810      820      830
Cry1Ac  780      790      800      810      820      830
:  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|142  HETVNVPGTGSWPLSFESSIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
        780      790      800      810      820      830

        840      850      860      870      880      890
Cry1Ac  840      850      860      870      880      890
:  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|142  IDVGCIDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
        840      850      860      870      880      890

        900      910      920      930      940      950
Cry1Ac  900      910      920      930      940      950
:  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|142  KLQLETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHTADKRVHRIQEAAYLPELSVIP
        900      910      920      930      940      950

        960      970      980      990      1000     1010
Cry1Ac  960      970      980      990      1000     1010
:  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVP
gi|142  GVNAGIFEELEGRIFTAYSPLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVLVVP
        960      970      980      990      1000     1010

        1020     1030     1040     1050     1060     1070
Cry1Ac  1020     1030     1040     1050     1060     1070
:  EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
gi|142  EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
        1020     1030     1040     1050     1060     1070

        1080     1090     1100     1110     1120     1130
Cry1Ac  1080     1090     1100     1110     1120     1130
:  TVTCNDYTVNQEEYGGAYTSRNGYNEAP---SVPADYASVYEEKSYTDGRRENPCFN
gi|142  TVTCNEYTANQEEYGGAYTSRNGYDETYGNSYSPADYASVYEEKAYTDGRRENPCESN
        1080     1090     1100     1110     1120     1130

        1140     1150     1160     1170     1180
Cry1Ac  1140     1150     1160     1170     1180
:  RGYRDYTPPLVGYVTKLEYPFETDKVWIEIGETEGTFIVDSVELLLMEE
gi|142  RGYGDYTPPLPAGYVTKQLEYPFETDKVWIEIGETEGTFIVDSVELFLMEE
        1140     1150     1160     1170     1180

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>>gi|216284|dbj|BAA00257.1| unnamed protein product [Bac (1176 aa)
initn: 6163 initl: 3766 opt: 6652 Z-score: 7835.4 bits: 1461.8 E(): 0

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Smith-Waterman score: 6652; 85.051% identity (92.314% similar) in 1184 aa overlap
(5-1182:1-1176)

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        10      20      30      40      50      60
Cry1Ac  10      20      30      40      50      60
:  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|216  10      20      30      40      50
        10      20      30      40      50
Cry1Ac  70      80      90      100     110     120
:  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|216  70      80      90      100     110     120
        60      70      80      90      100     110

        130     140     150     160     170     180
Cry1Ac  130     140     150     160     170     180
:  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|216  130     140     150     160     170     180
        120     130     140     150     160     170

        190     200     210     220     230     240
Cry1Ac  190     200     210     220     230     240
:  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVYRQFREL
gi|216  190     200     210     220     230     240
        180     190     200     210     220     230

        250     260     270     280     290     300
Cry1Ac  250     260     270     280     290     300
:  TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDFGSRGSAQGIIEGSIKRSRPHL
gi|216  250     260     270     280     290     300
        240     250     260     270     280     290

        310     320     330     340     350     360
Cry1Ac  310     320     330     340     350     360
:  MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQ
gi|216  310     320     330     340     350
        300     310     320     330     340     350

        370     380     390     400     410
Cry1Ac  370     380     390     400     410
:  GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPASAVYRKSQTVDSLDEIP
gi|216  370     380     390     400     410
        360     370     380     390     400     410

        420     430     440     450     460     470
Cry1Ac  420     430     440     450     460     470
:  PQNNVPPRQGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|216  420     430     440     450     460     470
        420     430     440     450     460     470

        480     490     500     510     520     530
Cry1Ac  480     490     500     510     520     530
:  PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|216  480     490     500     510     520
        480     490     500     510     520

        540     550     560     570     580     590
Cry1Ac  540     550     560     570     580     590
:  ASVTPIHNLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR

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Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRY  
gi|323 PLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRY  
480 490 500 510 520

540 550 560 570 580 590  
Cry1Ac ASVTPPIHLNVNNGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR  
gi|323 ASTTNLQPHSTSIDGRPINQGNFSATMSSGSLQSGSFRITVGFSTPFNFSNGSSVFTLSAH  
530 540 550 560 570 580

600 610 620 630 640 650  
Cry1Ac NFSGTAGVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
gi|323 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYDHYIDQVS  
590 600 610 620 630 640

660 670 680 690 700 710  
Cry1Ac NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ  
gi|323 NLVECLSDDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSDITIQ  
650 660 670 680 690 700

720 730 740 750 760 770  
Cry1Ac GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN  
gi|323 GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN  
710 720 730 740 750 760

780 790 800 810 820 830  
Cry1Ac AKHETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHFS  
gi|323 AKHETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHFS  
770 780 790 800 810 820

840 850 860 870 880 890  
Cry1Ac LDIDVGCITDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDK  
gi|323 LDIDVGCITDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDK  
830 840 850 860 870 880

900 910 920 930 940 950  
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV  
gi|323 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV  
890 900 910 920 930 940

960 970 980 990 1000 1010  
Cry1Ac IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLV  
gi|323 IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLV  
950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070  
Cry1Ac VPEWEAEVSQEVRCVCPGRGYILRVYTAYKEGYGEGCVTIIHEIENNTDELKFSNCFVVEEIIYP  
gi|323 VPEWEAEVSQEVRCVCPGRGYILRVYTAYKEGYGEGCVTIIHEIENNTDELKFSNCFVVEEIIYP  
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120 1130  
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRG  
gi|323 NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNCPCEFNRG  
1070 1080 1090 1100 1110 1120

1140 1150 1160 1170 1180  
Cry1Ac YRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|323 YRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
1130 1140 1150 1160 1170

>>gi|1613206|gb|AAB16186.1| Sequence 10 from patent US 5 (1176 aa)  
initn: 6156 init1: 3766 opt: 6645 Z-score: 7827.1 bits: 1460.3 E(): 0  
Smith-Waterman score: 6645; 84.966% identity (92.314% similar) in 1184 aa overlap  
(5-1182:1-1176)

10 20 30 40 50 60  
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF  
gi|161 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF  
10 20 30 40 50

70 80 90 100 110 120  
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
gi|161 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

130 140 150 160 170 180  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS  
gi|161 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAAANLHLSVLRDVS  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL  
gi|161 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

250 260 270 280 290 300  
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSRISPHL  
gi|161 TLTVLDIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSRGSAQRIEQIRQPHL  
240 250 260 270 280 290

310 320 330 340 350 360  
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ  
gi|161 MDILNSITITYTDVHRGFNYWSGHQITASPVGFSGPEFAPFLPNAGNAAPPV-LVSLTGL  
300 310 320 330 340 350

370 380 390 400 410  
Cry1Ac GVYRSLSSLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPASVYRKSQVDSLDLDEIP  
gi|161 GLFRTLSSPLYRRIILGSGPNQQLFVLDGTEFASLTTNLPSTIYRQRTVDSLDLDEIP  
360 370 380 390 400 410

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420      430      440      450      460      470
Cry1Ac PQNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWHRSAEFNIIASDSITQI
gi|161 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWSQHRSAEFNIIIPSSQITQI
420      430      440      450      460      470

480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|161 PLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRY
480      490      500      510      520

540      550      560      570      580      590
Cry1Ac ASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|161 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVVGFTTFFNFNSNGSSVFTLSAH
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|161 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVS
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac NLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLQDSNFKDINRQPERGGWGSGTITIQ
gi|161 NLVECLSDDEFCLDEKQELSEKVKHAKRLSDERNLQDPNFRGINRQLDRGWRGSDTITIQ
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLSGTFDECYPTLYQKIDESKLKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|161 GGDDVFKENYVTLGTFDECYPTLYQKIDESKLKAYTRYQLRGYIEDSQDLEIYLIRYN
710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFS
gi|161 AKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFS
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|161 LDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSV
gi|161 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSV
890      900      910      920      930      940

960      970      980      990      1000
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLV
gi|161 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVLV
950      960      970      980      990      1000

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1020      1030      1040      1050      1060      1070
Cry1Ac VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
gi|161 VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
1010      1020      1030      1040      1050      1060

1080      1090      1100      1110      1120      1130
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPCEFNRG
gi|161 NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPCEFNRG
1070      1080      1090      1100      1110      1120

1140      1150      1160      1170      1180
Cry1Ac YRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|161 YRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130      1140      1150      1160      1170

>>gi|6687073|emb|CAA70856.1| delta-endotoxin [Bacillus t (1176 aa)
initn: 6156 initl: 3766 opt: 6645 Z-score: 7827.1 bits: 1460.3 E(): 0
Smith-Waterman score: 6645; 84.966% identity (92.314% similar) in 1184 aa overlap
(5-1182:1-1176)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|668 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|668 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100      110

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPPLAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|668 WEADPTNPALREEMRIQFNDMNSALTTAIPPLAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVRYNQFREL
gi|668 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRVRYNQFREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRFGSAQIEGSIKRSRPHL
gi|668 TLTVLVDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRFGMAQRIEQNIRQPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|668 MDILNSITITYTDAHRGEYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
300      310      320      330      340      350

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          370      380      390      400      410
Cry1Ac GVYRFLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPNAVYRKSGVDSLDLEIP
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : :
gi|668 GIFRFLSSPLYRRIILGSGPNNQELFVLDGTEFASFASLTTLNLPSTIYRQRGTVDVSLDVIP
      360      370      380      390      400      410

```

```

          420      430      440      450      460      470
Cry1Ac PQNNNVPRQGFSHRLSHVMSFRSFGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : :
gi|668 PQDNSVPPRAGFSHRLSHVMTLSQ--AAGAVYTLRAPTFWQHRSAEFNNIIPSSQITQI
      420      430      440      450      460      470

```

```

          480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
      : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 PLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPQISTLRVNITAPL-----SQRYRVRIRY
      480      490      500      510      520

```

```

          540      550      560      570      580      590
Cry1Ac ASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
      : : : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTGFTTFNFSNGSSVFTLSAH
      530      540      550      560      570      580

```

```

          600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
      : . . : : : : : . . . . . : : : : : : : : : : : : : : : : : : :
gi|668 VFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYDHYHIDQVS
      590      600      610      620      630      640

```

```

          660      670      680      690      700      710
Cry1Ac NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 NLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
      650      660      670      680      690      700

```

```

          720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 GGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYIRYN
      710      720      730      740      750      760

```

```

          780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFS
      770      780      790      800      810      820

```

```

          840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      830      840      850      860      870      880

```

```

          900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSV

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          890      900      910      920      930      940
          960      970      980      990      1000      1010
Cry1Ac IPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNWKGHVDVEEQNNQRSVLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 IPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNWKGHVDVEEQNNQRSVLV
      950      960      970      980      990      1000

```

```

          1020      1030      1040      1050      1060      1070
Cry1Ac VPEWEAEVSVQEVRCVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 VPEWEAEVSVQEVRCVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
      1010      1020      1030      1040      1050      1060

```

```

          1080      1090      1100      1110      1120      1130
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRG
      1070      1080      1090      1100      1110      1120

```

```

          1140      1150      1160      1170      1180
Cry1Ac YRDYTPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|668 YRDYTPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170

```

>>gi|40267|emb|CAA31886.1| unnamed protein product [Baci (1176 aa)  
 initn: 6147 initl: 3766 opt: 6636 Z-score: 7816.5 bits: 1458.3 E(): 0  
 Smith-Waterman score: 6636; 84.882% identity (92.230% similar) in 1184 aa overlap  
 (5-1182:1-1176)

```

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

```

```

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 VLGLVDIIWGFPGSQWDAFPVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

```

```

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYQAAANLHLSVLRDVS
          120      130      140      150      160      170

```

```

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWVRYNQFRREL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWVRYNQFRREL
          180      190      200      210      220      230

```

```

          250      260      270      280      290      300
Cry1Ac TLTVLDIVLSLFPNYSRYPYPIRTVSQLTREIYTNVPLENFDGSRGSAQIEGSIKIRSPHL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 TLTVLDIVLSLFPNYSRYPYPIRTVSQLTREIYTNVPLENFDGSRGSAQIEGSIKIRSPHL

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240      250      260      270      280      290
Cry1Ac MDILNSITIIYTDahrgeyywshghqimaspvfgspgpeftfplygtmgnaapqqrivaqlgq
      310      320      330      340      350      360
gi|402 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
      300      310      320      330      340      350

370      380      390      400      410
Cry1Ac GVYRTLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDLSLDEIP
      370      380      390      400      410
gi|402 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDSLDVIP
      360      370      380      390      400      410

420      430      440      450      460      470
Cry1Ac PQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
      420      430      440      450      460      470
gi|402 PQDNSVPPRAGFSHRLSHVMTLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
      420      430      440      450      460      470

480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRY
      480      490      500      510      520      530
gi|402 PLTKSTNLGSGTsvkvgpgftggdILRRITSPGQISTLRVNIITAPL----SQRYRVVRY
      480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac ASVTPIHLLNVNNGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
      540      550      560      570      580      590
gi|402 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTTFNFSNGSSVFTLSAH
      530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac NfsgTAGVIIDRFEPiPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
      600      610      620      630      640      650
gi|402 VFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTdVTDYHIDQVS
      590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac NLVtYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
      660      670      680      690      700      710
gi|402 NLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
      650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
      720      730      740      750      760      770
gi|402 GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN
      710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac AKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHFS
      780      790      800      810      820      830
gi|402 AKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHFS
      770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      840      850      860      870      880      890

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gi|402 LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSV
      900      910      920      930      940      950
gi|402 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSV
      890      900      910      920      930      940

960      970      980      990      1000      1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCVNVKGVHDVVEEQNNQRSLV
      960      970      980      990      1000      1010
gi|402 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCVNVKGVHDVVEEQNNQRSLV
      950      960      970      980      990      1000

1020      1030      1040      1050      1060      1070
Cry1Ac VPEWEAEVSEQEVRVCPGRGYILRVTAyKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
      1020      1030      1040      1050      1060      1070
gi|402 VPEWEAEVSEQEVRVCPGRGYILRVTAyKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
      1010      1020      1030      1040      1050      1060

1080      1090      1100      1110      1120      1130
Cry1Ac NNTVTCNDYTVNQEYEGGAYTSRNRYNEAPSVADYASVYEEKSYTDGRRENPCFENRG
      1080      1090      1100      1110      1120      1130
gi|402 NNTVTCNDYTVNQEYEGGAYTSRNRYNEAPSVADYASVYEEKSYTDGRRENPCFENRG
      1070      1080      1090      1100      1110      1120

1140      1150      1160      1170      1180
Cry1Ac YRDYTPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170      1180
gi|402 YRDYTPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170

>>gi|535781|dbj|BAA04468.1| insecticidal crystal protein (1176 aa)
      initn: 6145 init1: 3755 opt: 6634 Z-score: 7814.1 bits: 1457.9 E(): 0
Smith-Waterman score: 6634; 84.882% identity (92.230% similar) in 1184 aa overlap
(5-1182:1-1176)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50      60
gi|535 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50      60

70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      70      80      90      100      110      120
gi|535 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130      140      150      160      170      180
gi|535 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190      200      210      220      230      240

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gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVXVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
.....
gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
.....
gi|142 TLTVLDIVALFNSYDSRRYPPIRTVSQLTREIYTNPVLENFDGSGFRGMAQRIEQNIRQPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITTYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
.....
gi|142 MDILNSITTYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
300 310 320 330 340 350

370 380 390 400 410
Cry1Ac GVRTLSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSQTVDSLDEIP
.....
gi|142 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTTYRQRGTVDVSLDVIP
360 370 380 390 400 410

420 430 440 450 460 470
Cry1Ac PQNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....
gi|142 PQDNSVPPRAGFSHRLSHVMTLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
420 430 440 450 460 470

480 490 500 510 520 530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRVRY
.....
gi|142 PLTKSTNLGSGTSVVKGPFTGGDILRRTSPQISTLRVNITAPL----SQRYRVRIRY
480 490 500 510 520

540 550 560 570 580 590
Cry1Ac ASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
.....
gi|142 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTFPNFNSGSSVFTLSAH
530 540 550 560 570 580

600 610 620 630 640 650
Cry1Ac NFSGTAGVIIIDRFEPVPVATATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
.....
gi|142 VFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTDTVTDYHIDQVS
590 600 610 620 630 640

660 670 680 690 700 710
Cry1Ac NLVITYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
.....
gi|142 NLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSDITIQ
650 660 670 680 690 700

720 730 740 750 760 770

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Cry1Ac GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
.....
gi|142 GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN
710 720 730 740 750 760

780 790 800 810 820 830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFS
.....
gi|142 AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFS
770 780 790 800 810 820

840 850 860 870 880 890
Cry1Ac LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
.....
gi|142 LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830 840 850 860 870 880

900 910 920 930 940 950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV
.....
gi|142 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV
890 900 910 920 930 940

960 970 980 990 1000 1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLV
.....
gi|142 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLV
950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070
Cry1Ac VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
.....
gi|142 LPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120 1130
Cry1Ac NMTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNPCEFNRG
.....
gi|142 NMTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNPCEFNRG
1070 1080 1090 1100 1110 1120

1140 1150 1160 1170 1180
Cry1Ac YRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
.....
gi|142 YRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

>>gi|1612051|gb|AAB15031.1| Sequence 6 from patent US 55 (1176 aa)
initn: 6134 init1: 3753 opt: 6623 Z-score: 7801.2 bits: 1455.5 E(): 0
Smith-Waterman score: 6623; 84.713% identity (92.145% similar) in 1184 aa overlap
(5-1182:1-1176)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
.....
gi|161 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120

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Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
gi|161 VLGLVDIIWGIFGPSQWDAFPVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|161 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|161 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL  
gi|161 TLTVLDIVSLFPNYSRTPRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL  
240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ  
gi|161 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL  
300 310 320 330 340 350

Cry1Ac GVRTLSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDLSLDEIP  
gi|161 GVFRTLSSTLYRRIILGSGPNNQELFVLDGTEFASLTTLNPSIIYRQRGTVDLSLDVIP  
360 370 380 390 400 410

Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI  
gi|161 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWSQHRSAEFNIIIPSSQITQI  
420 430 440 450 460 470

Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRY  
gi|161 PLTKSTNLGSGTSVVKGPGFTGGDLRLRRTSPGQISTLVRNITAPL----SQRYRVRVRY  
480 490 500 510 520 530

Cry1Ac ASVTPIHNLNVNMGNSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIV--GVR  
gi|161 ASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNFSNGSSVFTLSAH  
530 540 550 560 570 580

Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
gi|161 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYDHYHIDQVS  
590 600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710  
NLVITYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ  
gi|161 650 660 670 680 690 700  
NLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ

Cry1Ac 720 730 740 750 760 770  
GGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN  
gi|161 710 720 730 740 750 760  
GGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN

Cry1Ac 780 790 800 810 820 830  
AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS  
gi|161 770 780 790 800 810 820  
AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS

Cry1Ac 840 850 860 870 880 890  
LDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK  
gi|161 830 840 850 860 870 880  
LDIDVGCTHLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK

Cry1Ac 900 910 920 930 940 950  
REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSV  
gi|161 890 900 910 920 930 940  
REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSV

Cry1Ac 960 970 980 990 1000 1010  
IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLV  
gi|161 950 960 970 980 990 1000  
IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLV

Cry1Ac 1020 1030 1040 1050 1060 1070  
VPEWEAEVVSQEVVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYP  
gi|161 1010 1020 1030 1040 1050 1060  
LPEWEAEVVSQEVVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYP

Cry1Ac 1080 1090 1100 1110 1120 1130  
NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFENRG  
gi|161 1070 1080 1090 1100 1110 1120  
NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRENPCFENRG

Cry1Ac 1140 1150 1160 1170 1180  
YRDYTPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|161 1130 1140 1150 1160 1170  
YRDYTPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE

>>gi|5901703|gb|AAD55382.1|AF154676\_1 135 kDa insecticid (1176 aa)  
initn: 6119 initl: 3744 opt: 6604 Z-score: 7778.8 bits: 1451.3 E(): 0  
Smith-Waterman score: 6604; 84.544% identity (92.061% similar) in 1184 aa overlap  
(5-1182:1-1176)

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Cry1Ac CMQAMDNPNINCEIPYNCNLSNPEVEVLGGRIETGYTPIDISLSLTQFLLESEFVPGAGF  
gi|590 MDNNPNINCEIPYNCNLSNPEVEVLGGRIETGYTPIDISLSLTQFLLESEFVPGAGF

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
gi|590 VLGLVDIIWGFGPSQWDTFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|590 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL  
gi|590 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVWGPDSRDWVRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDFGSRFGSAQGIIEGSIIRSPHL  
gi|590 TLTVLDIVALFSNYDSRRYPYPIRTVSQLTREIYTNVLENFDFGSRFGMAQRIEQNIRQPHL

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ  
gi|590 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL

Cry1Ac GVYRTLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSQTVDSLDEIP  
gi|590 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNPTIYRQRTVDSLQVDP

Cry1Ac PQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI  
gi|590 PQDNSVPPRAGFSHRLGHVMTLSQ--AAGAVYTLRAPTFSWQHRSAEFNIIIPSSQITQI

Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRY  
gi|590 PLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVVRY

Cry1Ac ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR  
gi|590 AGTTLNQPHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTFFNFNSNGSSVFTLSAH

Cry1Ac NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
gi|590 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIIGLKTVDVTDYHIDQVS

Cry1Ac NLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ  
gi|590 NLVECLSDDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ

Cry1Ac GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYN  
gi|590 GGDDVFKENYVTLTGTDECYPTYLYQKIDESKLLKAYTRYQLRGYIEDSQDLEIYLIRYN

Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS  
gi|590 AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS

Cry1Ac LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKIAEKKWRDK  
gi|590 LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKIAEKKWRDK

Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSV  
gi|590 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSV

Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLV  
gi|590 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLV

Cry1Ac VPEWEAEVSQEVRCVCPGRGYILRVYAYKEGYEGCVTIHEIENNTDELKFSNCEVEEIIYS  
gi|590 VPEWEAEVSQEVRCVCPGRGYILRVYAYKEGYEGCVTIHEIENNTDELKFSNCEVEEIIYS

Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPCEFNRG  
gi|590 NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNCPCEFNRG

Cry1Ac YRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|590 YRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

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1130      1140      1150      1160      1170
>>gi|67089177|gb|AA66993.1| Cry1Aa [Bacillus thuringien (1163 aa)
  initn: 6062 initl: 3732 opt: 6551 Z-score: 7716.3 bits: 1439.7 E(): 0
Smith-Waterman score: 6551; 84.714% identity (92.143% similar) in 1171 aa overlap
(12-1176:1-1163)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|670      NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|670      VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
50      60      70      80      90      100

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|670      WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
110      120      130      140      150      160

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|670      VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
170      180      190      200      210      220

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVLENFDGFSFRGSAQGIIEGSIIRSPHL
gi|670      TLTVLDIVSLFNPYDSRRYPIRTVSQLTREIYTNVLENFDGFSFRGMAQRIGQINIRQPHL
230      240      250      260      270      280

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|670      MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
290      300      310      320      330      340

      370      380      390      400      410
Cry1Ac GVYRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDLDEIP
gi|670      GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFASFALTTNLPSTIYRQRTVDSLDVIP
350      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQI
gi|670      PQDNSVPPRAGFSHRLSHVMTLSQ--AAGAVYTLRAPTFSWQHRSAEFNIIIPSSQITQI
410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPSTSTRYRVRVRY
gi|670      PLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRVYRIRY

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470      480      490      500      510      520
540      550      560      570      580      590
Cry1Ac ASVTPHILNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR
gi|670      ASTTNLQFHSTSIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTPNFNSNGSSVFTLSAH
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|670      VFNSGNEVIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVS
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac NLVTYLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
gi|670      NLVECLSDDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|670      GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN
710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS
gi|670      AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWRDK
gi|670      LDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWRDK
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV
gi|670      REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV
890      900      910      920      930      940

960      970      980      990      1000      1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQRSVLV
gi|670      IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQRSVLV
950      960      970      980      990      1000

1020      1030      1040      1050      1060      1070
Cry1Ac VPWEAEVSVQEVRCVCPGRGYILRVVTAYKEGYGECVTHEIENNTDELKFSNCVVEEIIYP
gi|670      VPWEAEVSVQEVRCVCPGRGYILRVVTAYKEGYGECVTHEIENNTDELKFSNCVVEEIIYP
1010      1020      1030      1040      1050      1060

1080      1090      1100      1110      1120      1130
Cry1Ac NNTVTNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNPNCFNRRG

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gi | 670 NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFNRG
1070 1080 1090 1100 1110 1120

Cry1Ac YRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
.....

gi | 670 YRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVE
1130 1140 1150 1160

>>gi | 21239436 | gb | AAM44305.1 | AF510713\_1 crystal protein C (1180 aa)
initn: 5609 initl: 3179 opt: 6523 Z-score: 7683.2 bits: 1433.6 E(): 0
Smith-Waterman score: 6523; 83.333% identity (91.498% similar) in 1188 aa overlap
(5-1182:1-1180)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
.....

gi | 212 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
.....

gi | 212 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.....

gi | 212 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
.....

gi | 212 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQTLTREIYTNVLENFDGSRFGSAQGI EGSIRSPHL
.....

gi | 212 TLTVLDIVSLFNPYDSRTYPIRTVSQTLTREIYTNVLENFDGSRFGMAQRIEQNIRQPHL
240 250 260 270 280 290

Cry1Ac MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPYGTMGNAAPQRIVAQLGQ
.....

gi | 212 MDILNRIITTYTDAHRGFNYWSGHQITASPVGFSGPEFAFPFGNAGNAAPPV-LVSLTGL
300 310 320 330 340 350

Cry1Ac GVRTLSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSQVDSLDLEIP
.....

gi | 212 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSLDVIP
360 370 380 390 400 410

Cry1Ac PQQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....

gi | 212 PQQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
420 430 440 450 460 470

Cry1Ac PQQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....

gi | 212 PQQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....

gi | 212 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
420 430 440 450 460 470

Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY
.....

gi | 212 PLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRY
480 490 500 510 520

Cry1Ac ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
.....

gi | 212 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTFGFTTFFNFSNGSSVFTLSAH
530 540 550 560 570 580

Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
.....

gi | 212 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVS
590 600 610 620 630 640

Cry1Ac NLVTVLSDFECLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
.....

gi | 212 NLVTVLSDFECLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
650 660 670 680 690 700

Cry1Ac GGDDVFKENYVTVLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIN
.....

gi | 212 GGDDVFKENYVTVLLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRIN
710 720 730 740 750 760

Cry1Ac AKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFS
.....

gi | 212 AKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFS
770 780 790 800 810 820

Cry1Ac LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
.....

gi | 212 LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830 840 850 860 870 880

Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPPELSV
.....

gi | 212 REKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNAMIHAADKRVHSIREAYLPPELSV
890 900 910 920 930 940

Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVWVKGHVDVEEQNNRQSVLV
.....

gi | 212 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVWVKGHVDVEEQNNRHSVLV
950 960 970 980 990 1000

Cry1Ac VPEWAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
.....

gi | 212 VPEWAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
.....

Cry1Ac VPEWAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
.....

gi | 212 VPEWAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
.....

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gi|212 VPEWEAEVSVQVVRVCPGRGYLLRVTAIKEGYGEGCVTIEIENNTDELKFSNCVEEVEVY
1010 1020 1030 1040 1050 1060

Cry1Ac 1080 1090 1100 1110 1120 1130
NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVVEKSYTDGRRENPE
.....

gi|212 NNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCE
1070 1080 1090 1100 1110 1120

Cry1Ac 1140 1150 1160 1170 1180
FNRGYRDYTPLVGVYTKLEYFPETDKVWIEIGETEGFFIVDSVELLMEE
.....

gi|212 SNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGFFIVDSVELLMEE
1130 1140 1150 1160 1170 1180

>>gi|4666284|dbj|BAA77213.1| BtT84A1 crystal protein [Ba (1180 aa)
initn: 5609 initl: 3179 opt: 6523 Z-score: 7683.2 bits: 1433.6 E(): 0
Smith-Waterman score: 6523; 83.333% identity (91.498% similar) in 1188 aa overlap
(5-1182:1-1180)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
.....
gi|466 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESPFE
.....
gi|466 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESPFE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.....
gi|466 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
.....
gi|466 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSIIRSPHL
.....
gi|466 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGMAQRLEQNIHQPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
.....
gi|466 MDILNRITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410
GVYRTLSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPASAVYRKSQTVDSLDEIP

gi|466 G1FRTLSSPLYRRIILGSGPNQELFVLDGTEFSASLTTNLPSTIYRQGRVDSLDVIP
360 370 380 390 400 410

Cry1Ac 420 430 440 450 460 470
PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....

gi|466 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
420 430 440 450 460 470

Cry1Ac 480 490 500 510 520 530
PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
.....

gi|466 PLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRY
480 490 500 510 520

Cry1Ac 540 550 560 570 580 590
ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR
.....

gi|466 ASTTNLQFHTSIDGRPINQGNFSAATMSSGNSLQSGSFRVTFVGFPTPFNFNGSSVFTLSAH
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650
NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
.....

gi|466 VFNSGNEVYIDRIEFPVAEVTFEAEYDLERAQKAVNELFTSSNQIGLTKTDVTDYHIDQVS
590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710
NLVTYLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
.....

gi|466 NLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770
GGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRYN
.....

gi|466 GGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRYN
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830
AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFS
.....

gi|466 AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFS
770 780 790 800 810 820

Cry1Ac 840 850 860 870 880 890
LDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
.....

gi|466 LDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830 840 850 860 870 880

Cry1Ac 900 910 920 930 940 950
REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPPELSV
.....

gi|466 REKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAKRVHSIREAYLPPELSV
890 900 910 920 930 940

Cry1Ac 960 970 980 990 1000 1010

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Cry1Ac IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSVLV
gi|466 IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNHRSVLV
950 960 970 980 990 1000

Cry1Ac 1020 1030 1040 1050 1060 1070
VPEWEAEVQSEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYP
gi|466 VPEWEAEVQSEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYP
1010 1020 1030 1040 1050 1060

Cry1Ac 1080 1090 1100 1110 1120 1130
NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCE
gi|466 NNTVTCNDYTVNQEEYGGAYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRNPCE
1070 1080 1090 1100 1110 1120

Cry1Ac 1140 1150 1160 1170 1180
FNRGRDYTPPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|466 SNRGYDGYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170 1180

>>gi|37781497|gb|AAP40639.1| Cry1Aa [Bacillus thuringien (1183 aa)
initn: 5582 initl: 3159 opt: 6493 Z-score: 7647.8 bits: 1427.1 E(): 0
Smith-Waterman score: 6493; 82.997% identity (91.246% similar) in 1188 aa overlap
(5-1182:1-1180)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|377 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESPFE
gi|377 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESPFE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|377 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|377 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRFGSAQGIIEGSI RSPHL
gi|377 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRFGMAQRIEQNIRQPHL
240 250 260 270 280 290

310 320 330 340 350 360

Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVALQLG
gi|377 MDILNSITITYTDAHRGFYWSGHQITASPVGFSGPEFAPFLPNAGNAAPPV-LVSLTGL
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410
GVYRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLP SAVYRKSGTVDSLDEIP
gi|377 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRTVDSL DVIP
360 370 380 390 400 410

Cry1Ac 420 430 440 450 460 470
PQNNVPPRQGFHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|377 PQDNSVPPRAGFSLHSHVMTLSQ--AAGAVYTLRAPTFWSQHRSAEFNIIIPSSQVTQI
420 430 440 450 460 470

Cry1Ac 480 490 500 510 520 530
PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|377 PLTKSTNLGSGTSVVKGPFTGGDILRRTPSQQISTLRVNIITAPL----SQRYRVRIRY
480 490 500 510 520

Cry1Ac 540 550 560 570 580 590
ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANAFTSSLGNI VGVRR
gi|377 ASTTNLQPHFHSIDGRPINQGNFSATMCSGSLNLSQSGSFRVTGPTTFNFPNGSSVFTLSAH
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650
NFSGTAGVIIDREFEIPVTATLEAEYNLERAKAVNALFTSTINQLGLKTNVDYHIDQVS
gi|377 VFNSGNEVIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQI GLKTDVTDYHIDQVS
590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710
NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQ
gi|377 NLVECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQ
650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770
GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|377 GGDDVFKENYVTLGTFDECYPTYLYQKIDESKLLKAYTRYQLRGYIEDSQDLEIYLIRYN
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830
AKHETVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFS
gi|377 AKHETVNVPGTGLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHSHHFS
770 780 790 800 810 820

Cry1Ac 840 850 860 870 880 890
LDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|377 LDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830 840 850 860 870 880

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900 910 920 930 940 950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV
gi|377 REKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSV
890 900 910 920 930 940

960 970 980 990 1000 1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLV
gi|377 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVLV
950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070
Cry1Ac VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVEEIIYP
gi|377 VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVEEIIYP
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120 1130
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPCE
gi|377 NNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCE
1070 1080 1090 1100 1110 1120

1140 1150 1160 1170 1180
Cry1Ac FNRGRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLME
gi|377 SNRGRDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEVDA
1130 1140 1150 1160 1170 1180

>>gi|34426443|gb|AAQ70696.1| Sequence 6 from patent US 5 (1184 aa)
initn: 5145 initl: 2232 opt: 6471 Z-score: 7621.8 bits: 1422.3 E(): 0
Smith-Waterman score: 6608; 84.661% identity (91.869% similar) in 1193 aa overlap
(5-1182:1-1184)

10 20 30 40 50 60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|344 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|344 VLGLVDIIWGIIFGPSQWDAFPVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVS
gi|344 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYQAAHLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|344 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
gi|344 TLTVLDIVALFSNYSRRYPVRTVSQLTREIYTNPVLENFDGSRGMAQRIEQNRQPHL
240 250 260 270 280 290

310 320 330 340 350
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ---
gi|344 MDILNSITTYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPQQRIRIAGNAAP
300 310 320 330 340 350

360 370 380 390 400 410
Cry1Ac ---LGQGVYRTLSSSTLYRRP-FNIGINNQLSVLDGTEFAYGTSNLSAVYRKSGTVD
gi|344 VLSLTGLGIFRTLSSPLYRRIILGSGPNNQEFVLDGTEFSFASLTNPNSTIYRQRGTVD
360 370 380 390 400 410

420 430 440 450 460 470
Cry1Ac SLD-EIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIA
gi|344 SLDVEIPPQDQNSVPPRAGFSHRSLSHVTMLSQ--AAGAVYTLRAT-FSWQHRSAEFNIIIP
420 430 440 450 460 470

480 490 500 510 520 530
Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTR
gi|344 SSQITQIPLTKSTNLGSGTSSVVKGPGFTGGHILRRTSPQISTLRVNIITAPL----SQR
480 490 500 510 520

540 550 560 570 580 590
Cry1Ac YRVRVRYASVTPIHNLVNVGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNI
gi|344 YRVRIRYASTTNLQFHTSIDGRFINQGNFSATMSSGSLNQLSGSFRVTVGFTTFFNFSNGSS
530 540 550 560 570 580

600 610 620 630 640
Cry1Ac V---GVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTD
gi|344 VFTLSAHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTDTVTD
590 600 610 620 630 640

650 660 670 680 690 700
Cry1Ac YHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNF-KD-INRQPERGW
gi|344 YHIDQVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSMFRKDGINRQPERGW
650 660 670 680 690 700

710 720 730 740 750 760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQD
gi|344 GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQD
710 720 730 740 750 760

770 780 790 800 810 820
Cry1Ac LEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLWPNPDLDCSCRDGEK
gi|344 LEIYLIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLWPNPDLDCSCRDGEK
770 780 790 800 810 820



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710      720      730      740      750      760
Cry1Ac  780      790      800      810      820      830
AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSHFS
gi|566  770      780      790      800      810      820
AKQQTVNVPGTGLWPLWVSAKPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSHFS

840      850      860      870      880      890
Cry1Ac  LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|566  LDIDVGCTDLNEDLGVVWVIFKIKTEDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK

830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac  REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV
gi|566  REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV

890      900      910      920      930      940

960      970      980      990      1000     1010
Cry1Ac  IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQRSVLV
gi|566  IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQRSVLV

950      960      970      980      990      1000

1020     1030     1040     1050     1060     1070
Cry1Ac  VPEWEAEVSVQEVVRCVPGRYLLRVTAAYKEGYGEGCVTTHEIENNTDELKFSNVCVEEIIYP
gi|566  VPEWEAEVSVQEVVRCVPGRYLLRVTAAYKEGYGEGCVTTHEIENNTDELKFSNVCVEEIIYP

1010     1020     1030     1040     1050     1060

1080     1090     1100     1110     1120     1130
Cry1Ac  NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRG
gi|566  NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRG

1070     1080     1090     1100     1110     1120

1140     1150     1160     1170     1180
Cry1Ac  YRDYTPLPVGVYTKALEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|566  YRDYTPLPVGVYTKALEYFPETDKVWIEIGETEGTFIVDSVELLMEE

1130     1140     1150     1160     1170

>>gi|5669019|gb|AAD46137.1|AF081248_1 lepidoteran-specif (1176 aa)
  initn: 6000 initl: 3617 opt: 6388 Z-score: 7524.0 bits: 1404.2 E(): 0
Smith-Waterman score: 6388; 82.393% identity (90.143% similar) in 1187 aa overlap
(5-1182:1-1176)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLBGLSNLYQIYAESFRE
gi|566  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLBGLSNLYQIYAESFRE

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60      70      80      90      100     110
Cry1Ac  130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566  WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS

120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRVRYNQFRREL
gi|566  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRVRYNQFRREL

180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL
gi|566  TLTVLDIVSLFPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL

240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac  MDILNSITIIYTDHARGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|566  MDILNSISIIYTDVHRGFNYWSGHQITTSVGVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

300      310      320      330      340      350

370      380      390      400      410
Cry1Ac  GVYRTLSSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPASVYRKSQGVVDSLDEIP
gi|566  GVFRTLSSSTLYRRIILGSGPNNQELFVLDGTEFASLTTLNLPSTIYRQRGTVDLSDVIP

360      370      380      390      400      410

420      430      440      450      460      470
Cry1Ac  PQNNVPPRQGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSW----IHRSAEFNIIASDS
gi|566  PQDNSVPPRAGFVSHRSLSHVPMLSQ--AAGAVYTLRASLFLLLVLIHARSIFNIIIPSSQ

420      430      440      450      460      470

480      490      500      510      520      530
Cry1Ac  ITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVR
gi|566  ITQ--SFK-KIISWTSVVKGPFTGGDILRRPSPGLISTLRVINITAPL----SQRYRVR

480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  VRYASVTPIHLLNWNWGNSSIFNSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---
gi|566  IRYAFTTNLQFLTSLIDGRPINQGNFYATMSSGNSLQSGSFRTVGF'TTPFNFSNGSSVFTL

530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac  GVRNFSGTAGVVIDRFEPVPTATLEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
gi|566  SAHVFNQNEVYIDRIEFVPAEVTFEAEYDLERAQNGVNLFTSSNQIGLKTGDYHID

590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  QVSNLVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGSTGI

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gi|566 QVSNLVECLSDDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSHDI
650 660 670 680 690 700

Cry1Ac TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYISI
720 730 740 750 760 770

gi|566 TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDQSKLKAYTSYQLRGYIEDSQDLEIYLI
710 720 730 740 750 760

Cry1Ac RYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHS
780 790 800 810 820 830

gi|566 GYNAKQQTVNVPGTGLSWPVYAPKPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHS
770 780 790 800 810 820

Cry1Ac HFSLDIDVGCTDLNEDLGWVWVIFKIKTDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
840 850 860 870 880 890

gi|566 HFSIDIDVGCTDLNEDLGWVWVIFKIKTEDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
830 840 850 860 870 880

Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
900 910 920 930 940 950

gi|566 RDKRVKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
890 900 910 920 930 940

Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRS
960 970 980 990 1000 1010

gi|566 LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRS
950 960 970 980 990 1000

Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEE
1020 1030 1040 1050 1060 1070

gi|566 VLVVPEWEAEVSEQEVRVCPGRGYFPRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEE
1010 1020 1030 1040 1050 1060

Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFE
1080 1090 1100 1110 1120 1130

gi|566 IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFE
1070 1080 1090 1100 1110 1120

Cry1Ac NRGYRDYTPLPVGYVTKALEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180

gi|566 NRGYRDYTPLPVGYVTKALEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1130 1140 1150 1160 1170

>>gi|34423556|gb|AAQ68985.1| Sequence 2 from patent US 5 (1179 aa)
initn: 5809 initl: 3135 opt: 6321 Z-score: 7444.9 bits: 1389.5 E(): 0
Smith-Waterman score: 6321; 80.101% identity (90.680% similar) in 1191 aa overlap
(2-1182:1-1179)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50 60

gi|344 MEIMNQ---NQCPVYNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|344 VLGLIDLWGFVGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAEAFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|344 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|344 VFGQRWGFVDATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDFGSRGSAQIEGSIRSPHL
250 260 270 280 290 300

gi|344 TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLENFDFGSRGMAQRIEQNIRQPHL
240 250 260 270 280 290

Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLQG
310 320 330 340 350 360

gi|344 MDLLNSITITYTDAHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPV-LISTTGL
300 310 320 330 340 350

Cry1Ac GVYRTLSSLTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSQTVDSLDEIP
370 380 390 400 410

gi|344 GIFRTLSSPLYRRILLGSGPNNQNLFLVDGTEFSFASLTADLPSTIYRQGTVDSLDVIP
360 370 380 390 400 410

Cry1Ac PQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
420 430 440 450 460 470

gi|344 PQDNSVPARAGFSHRLSHVMTLSQ--AAGAVYTLRPTFSWRHRSAEFNSLIPSSQITQI
420 430 440 450 460 470

Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
480 490 500 510 520 530

gi|344 PLTKSINLQSGTSVVKGPFTGGDILRRTSPGQISTLRVTITAPL----SQRYRVRIRY
480 490 500 510 520

Cry1Ac ASVTPIHNLVNVGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR
540 550 560 570 580 590

gi|344 ASTTNLQPHTSIDGRPINQGNFSATMSSGGNLQSGSFRTAGFTTFFNFSNGSSIFITLSAH
530 540 550 560 570 580

Cry1Ac NFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
600 610 620 630 640 650



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Cry1Ac ASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|124 ASSTTNLQFHTSIDGRPIQGNFSATMSSGGNLQSGSFRTAGTTPFNFSNGSSIPTLSAH
530 540 550 560 570 580

600 610 620 630 640 650
Cry1Ac NFSGTAGVIIDRFEPVATATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|124 VFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQEAVALFTSSNQLGLKTNVTDYHIDQVS
590 600 610 620 630 640

660 670 680 690 700 710
Cry1Ac NLVVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
gi|124 NLVECLSGEFLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQ
650 660 670 680 690 700

720 730 740 750 760 770
Cry1Ac GGDDVFKENYVTLPGTFNECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYSIRYN
gi|124 GGDDVFKENYVTLPGTFNECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN
710 720 730 740 750 760

780 790 800 810 820 830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHSHFS
gi|124 TKHETVNVPGTGLWPLSVENPIGKCGEPNRCAPQLEWNPDLDCSCRDEKCAHSHSHFS
770 780 790 800 810 820

840 850 860 870 880 890
Cry1Ac LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDK
gi|124 LDIDIGCTDLNENLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDK
830 840 850 860 870 880

900 910 920 930 940 950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV
gi|124 REKLVQVQTNIVYKEAKESVDALFVNSQYDRLQADTDIAMIHAADKRVHRIREAYLPELSV
890 900 910 920 930 940

960 970 980 990 1000 1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLV
gi|124 IPGVNAGIFEELEGRIFTAYSLYDARNLIKNGDFNNGLSWVNVKGVHVDVEEQNNHRSVLV
950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070
Cry1Ac VPEWEAEVSVQEVVCPGRGYLLRVYAYKEGYGEGCVTTHEIENNTDELKFSNCFVVEEIVP
gi|124 VPEWEAEVSVQEVVCPGRGYLLRVYAYKEGYGEGCVTTHEIEDNTDELKFSNCFVVEEVYP
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120 1130
Cry1Ac NNTVTCNDYTNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPCE
gi|124 NNTVTCNDYTNQEQYGGAYTSRNRGYGESYESNSSIPAEPYAPVYEE-AYIDGRKENPCE
1070 1080 1090 1100 1110 1120

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1140 1150 1160 1170 1180
Cry1Ac FNRGYRDTYPLPVGYVTKLEYFPETDKVWIEIGETEGFFIVDSVLELLMEE
gi|124 SNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGFFIVDSVLELLMEE
1130 1140 1150 1160 1170

>>gi|142744|gb|AAA22340.1| cryIA(d) (1179 aa)
initn: 5773 init1: 3094 opt: 6299 Z-score: 7419.0 bits: 1384.7 E(): 0
Smith-Waterman score: 6299; 79.765% identity (90.596% similar) in 1191 aa overlap
(2-1182:1-1179)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|124 MEIMNNQ---NQCVYNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAEAFRE
gi|124 VLGLIDLIIWGFPGSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAEAFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|124 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|124 VFGQRWGFDAATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSRPHL
gi|124 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGMAQRIEQNIRQPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITIIYTDVHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPV-LISTGL
gi|124 MDLLNSITIIYTDVHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPV-LISTGL
300 310 320 330 340 350

370 380 390 400 410
Cry1Ac GVYRSLSSLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSQVSDSLDEIP
gi|124 GIVRSLSSLYRRIILGSGPNNQNLVFLDGTETFSASLTADLPSTIYRQGTVDLSDVIP
360 370 380 390 400 410

420 430 440 450 460 470
Cry1Ac PQNNVPPRQGFVSHRSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI
gi|124 PQDNSVPARAGFVSHRSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQI
420 430 440 450 460 470

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480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 PLTKSINLGSSTSVVKGPGFTGGDILRITSPGQISTLRVTITAPL----SQRYRVRIRY
480      490      500      510      520

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540      550      560      570      580      590
Cry1Ac ASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 ASTTNLQPFHTSIDGRPIQGNFSATMSSGGNLQSGSFRTAGFTTFFNFNSGSSIFTLTSAH
530      540      550      560      570      580

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600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 VFNSGNEVYIERIEFVPAEVTFAEYDLERAQEAVALFTSSNQLGLKTNVTDYHIDQVS
590      600      610      620      630      640

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660      670      680      690      700      710
Cry1Ac NLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTITIQ
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 NLVECLSGEFCLEKRESEKVKHANRLSDERNLLQDPNFRGINRQPDGRGWRGSDITITIQ
650      660      670      680      690      700

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720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 GGDDVFKENYVTLPGTFNECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQHLEIYLIRYN
710      720      730      740      750      760

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780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHFS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 TKHETVNVPGTGLSLWPLSVENPVGKCGEPNRCAPQLEWNPDLDCSCRDEKCAHSHSHFS
770      780      790      800      810      820

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840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 LDIDIGCTDLNENLVGVVIFKIKMQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830      840      850      860      870      880

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900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 REKLVQETNIVYKEAKESVDALFVNSQYDRLQADTDIAMIHAADKRVHRIREAYLPELSV
890      900      910      920      930      940

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960      970      980      990      1000      1010
Cry1Ac IPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQRSVLV
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 IPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNHRSVLV
950      960      970      980      990      1000

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1020     1030     1040     1050     1060     1070
Cry1Ac VPWEAEVSVQEVVRCPRGYILLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIVP
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 VPWEAEVSVQEVVRCPRGYILLRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCVVEEVYP
1010     1020     1030     1040     1050     1060

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1080     1090     1100     1110     1120     1130
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCPE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 NNTVTCNDYTVNQEEYGGAYTSRNRGYGESYESSNSIPAEYAPVYEE-AYIDGRKENPCPE
1070     1080     1090     1100     1110     1120

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1140     1150     1160     1170     1180
Cry1Ac FNRGRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|142 SNRGYGDYTPPLPAGVYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130     1140     1150     1160     1170

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>>gi|911029|gb|AAA70483.1| Sequence 1 from Patent US 540 (1179 aa)  
 initn: 5773 initl: 3094 opt: 6299 Z-score: 7419.0 bits: 1384.7 E(): 0  
 Smith-Waterman score: 6299; 79.765% identity (90.596% similar) in 1191 aa overlap  
 (2-1182:1-1179)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 MEIMNQ--NQCVPNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

```

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70      80      90      100     110     120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 VLGLIDLWIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 VFGQRWGFDAATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDFGSRGSAQIEGSIKRSRPHL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDFGSRGMAQRIEQNIRQPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITITYDHAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 MDLLNSITITYDVRHGFNYWSGHQITASPVGFAGPEFTFPFRYGTMGNAAPPV-LISETTGL
300     310     320     330     340     350

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370     380     390     400     410
Cry1Ac GYVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFFAYGT-SSNLPASVYRKSGTVDSLDEIP
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|911 GIFRTLSSPLYRRIILGSGPNQNLFLVLDGTEFFASLTADLPSTIYRQGTVDLSDVIP
360     370     380     390     400     410

```

```

420      430      440      450      460      470
Cry1Ac PQNNNVPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|911 PQDNSVPARAGFSHRLSHVTMLSQ--AAGAVTLRAPTFSWRHRSAEFSNLIPSSQITQI
420      430      440      450      460      470

```

```

480      490      500      510      520      530
Cry1Ac PAVKNGFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRY
gi|911 PLTKSINLGSQTSVVKGPGFTGGDILRITSPGQISTLRVTTITAPL----SQRYRVRIRY
480      490      500      510      520

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540      550      560      570      580      590
Cry1Ac ASVTPIHNLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFSTSSLGNIV--GVR
gi|911 ASTTNLQFHTSIDGRPINQGNFSATMSSGGNLQSGSFRTAGFTTTFNFSNGSSIFTLTSAH
530      540      550      560      570      580

```

```

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|911 VFNSGNEVYIERIEFVPAEVTFAEYDLERAQEAVALNFTSSNQLGLKTNVTDYHIDQVS
590      600      610      620      630      640

```

```

660      670      680      690      700      710
Cry1Ac NLVTTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
gi|911 NLVECLSGEFCLDEKRELSKVKHANRLSDERNLLQDPNFRGINRQPDGRGWRGSTDITIQ
650      660      670      680      690      700

```

```

720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLPGTFDECYPTLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYIRYN
gi|911 GGDDVFKENYVTLPGTFNECYPTLYQKIDESKLLKAYTRYQLRGYIEDSQHLEIYLIRYN
710      720      730      740      750      760

```

```

780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHFS
gi|911 TKHETVNVPGTGLWPLSVENPIGKCGEPNRCAPQLEWNPDLDCSCRDGEKCAHSHSHFS
770      780      790      800      810      820

```

```

840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|911 LDIDIGCTDLNENLGVVIFKIKMQDGHARLGNLEFLEEKPLVGESLARVKRAEKKWRDK
830      840      850      860      870      880

```

```

900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSV
gi|911 REKLVQETNIVYKEAKESVDALFVNSQYDRLQADTDIAMIHAADKRVHRIREAYLPELSV
890      900      910      920      930      940

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960      970      980      990      1000      1010
Cry1Ac IPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVVEEQNNQRSVLV
gi|911 IPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGHVDVVEEQNNHRSVLV

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950      960      970      980      990      1000
Cry1Ac VPEWEAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVIYP
gi|911 VPEWEAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVEEVIYP
1010     1020     1030     1040     1050     1060
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPVADYASVYEEKSYTDGRENPCPE
gi|911 NNTVTCNDYTVNQEEYGGAYTSRNRGYGSEYESNSSIPAEYAPVYEE-AYIDGRKENPCE
1070     1080     1090     1100     1110     1120
Cry1Ac FNRGRYDVTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEEM
gi|911 SNRGGDYVTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEEM
1130     1140     1150     1160     1170

```

>>gi|53932143|gb|AAV00425.1| Sequence 2 from patent US 6 (1176 aa)  
initn: 5773 init1: 3094 opt: 6295 Z-score: 7414.3 bits: 1383.9 E(): 0  
Smith-Waterman score: 6295; 80.135% identity (90.786% similar) in 1183 aa overlap  
(10-1182:3-1176)

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|539 MNNQNQCVPYNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFVPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAEAFRE
gi|539 VLGLIDLWGFVPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAEAFRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|539 VFGQRWGFDAATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGPDSRDWIRYNQFREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRSTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQIEGSIKIRPHL
gi|539 TLTVLDIVSLFPNYSRSTYPIRTVSQLTREIYTNVPLENFDGSGFRGMAQRIEQNIRQPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPYLYGTMGNAAPPQQRIVAQLGQ
gi|539 MDLLNSITITYTDAHRGFYWSGHQITASPVGFSGPEFTFPYLYGTMGNAAPPV-LIISTTGL

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Regulatory Product Characterization Team

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.....
gi|128 VFGQRWGFDVATINSRYNDLTRLIGTYTDYAVRWYNTGLERVWGDPSDRDWRVYNGFRREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
      TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQIEGSIKRSRPHL
      .....
gi|128 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGMAQRIEQNIRQPHL
      240      250      260      270      280      290
Cry1Ac 310      320      330      340      350      360
      MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ
      .....
gi|128 MDLLNSITIIYTDVHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPV-LISTTGL
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410
      GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSQTVDSLDEIP
      .....
gi|128 GIFRTLSSPLYRRIILGSGPNNQNLVLDGTEFSPASLTADLPSTIYRQRGTVDVSLDVIP
      360      370      380      390      400      410
Cry1Ac 420      430      440      450      460      470
      PQNNNVPRQGFSHRSLSHVSMFSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
      .....
gi|128 PQDNSVPARAGFSHRSLSHVTMLSQ--AAGAVYTLRAPTFWRHRSAEFNSLIPSSQITQI
      420      430      440      450      460      470
Cry1Ac 480      490      500      510      520      530
      PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRY
      .....
gi|128 PLTKSINLGSQTSVVKGPGFTGGDILRITSPGQISTLRVITITAPL----SQRYRVRIRY
      480      490      500      510      520
Cry1Ac 540      550      560      570      580      590
      ASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
      .....
gi|128 ASTTNLQFHTSIDGRPINQGNFSATMSSGGNLQSGSFRTAGFTTTPFNFSNGSSIFTLTSAH
      530      540      550      560      570      580
Cry1Ac 600      610      620      630      640      650
      NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
      .....
gi|128 VFNSGNEVYIERIEFVPAEVTFAEYDLERAQEAVALFTSSNQLGLKTNVTDYHIDQVS
      590      600      610      620      630      640
Cry1Ac 660      670      680      690      700      710
      NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
      .....
gi|128 NLVECLSGEFCLDEKRELSEKVKHANRLSDERNLLQDPNFRGINRQPDWRGSDITITIQ
      650      660      670      680      690      700
Cry1Ac 720      730      740      750      760      770
      GGDDVFKENYVTLPGTFNFCYPTIYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYN
      .....
gi|128 GGDDVFKENYVTLPGTFNFCYPTIYLYQKIDESKLLKAYTRYQLRGYIEDSQHLEIYLIRYN
      710      720      730      740      750      760
Cry1Ac 780      790      800      810      820      830

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Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSHFS
      .....
gi|128 TKHETVNVPGTGLWPLSVENPIGKCGEPNRCAPQLEWNPDLDCSCRDGKCAHSHHSHFS
      770      780      790      800      810      820
Cry1Ac 840      850      860      870      880      890
      LDIDVGCDDLNEGLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      .....
gi|128 LDIDIGCTDLNENLGVWVIFKIKMQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      830      840      850      860      870      880
Cry1Ac 900      910      920      930      940      950
      REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV
      .....
gi|128 REKLQVETNIVYKEAKESVDALFVNSQYDRLQADTDIAMIHAADKRVHRIREAYLPELSV
      890      900      910      920      930      940
Cry1Ac 960      970      980      990      1000      1010
      IPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLV
      .....
gi|128 IPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLV
      950      960      970      980      990      1000
Cry1Ac 1020      1030      1040      1050      1060      1070
      VPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP
      .....
gi|128 VPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKFSNCVEEIVYP
      1010      1020      1030      1040      1050      1060
Cry1Ac 1080      1090      1100      1110      1120      1130
      NNTVTNCDYTVNQQEYVGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCP
      .....
gi|128 NNTVTNCDYTVNQQEYVGGAYTSRNRGYGESYESNSSIPAEYAPVYEE-AYIDGRKENPCP
      1070      1080      1090      1100      1110      1120
Cry1Ac 1140      1150      1160      1170      1180
      FNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|128 SNRGGDYTPLPAGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1130      1140      1150      1160      1170
>>gi|33734262|gb|AAQ38643.1| Sequence 2 from patent US 6 (1176 aa)
      initn: 5773 init1: 3094 opt: 6295 Z-score: 7414.3 bits: 1383.9 E(): 0
      Smith-Waterman score: 6295; 80.135% identity (90.786% similar) in 1183 aa overlap
      (10-1182:3-1176)
Cry1Ac 10      20      30      40      50      60
      CMQAMDNPNINCEPIYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      .....
gi|337  MNNQNQCVPYCNLDNPTIEILEGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100      110      120
      VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAEAFRE
      .....
gi|337  VLGLLDIWFVGSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAEAFRE
      60      70      80      90      100      110
Cry1Ac 130      140      150      160      170      180

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Regulatory Product Characterization Team

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|337 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 gi|337 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL  
 gi|337 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL  
 240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
 MDILNSITIIYTDahrgeyywshqimaspvgfsgpeftfplygtmgnaapqqrivaqlgq  
 gi|337 MDILNSITIIYTDVHRGFNYWshqitaspvgfagpeftfprygtmgnaappv-listtgl  
 300 310 320 330 340 350

Cry1Ac 370 380 390 400 410  
 GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDEIP  
 gi|337 GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDEIP  
 360 370 380 390 400 410

Cry1Ac 420 430 440 450 460 470  
 PQNNVPRQGFSHRSLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI  
 gi|337 PQNNVPRQGFSHRSLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI  
 420 430 440 450 460 470

Cry1Ac 480 490 500 510 520 530  
 PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRY  
 gi|337 PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRY  
 480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590  
 ASVTPIHNLVNVGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIV--GVR  
 gi|337 ASVTPIHNLVNVGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIV--GVR  
 530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650  
 NFSGTAGVILDRFEPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
 gi|337 NFSGTAGVILDRFEPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
 590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710  
 NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ  
 gi|337 NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPERGWGGSTGITIQ  
 650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770  
 GGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN  
 gi|337 GGDDVFKENYVTLPGTFNECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQHLEIYLIRYN  
 710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830  
 AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFS  
 gi|337 AKHETVNVPGTGLWPLSVENPIGKCGEPNRCAPQLEWNPDLDCSCRDGEKCAHSHHFS  
 770 780 790 800 810 820

Cry1Ac 840 850 860 870 880 890  
 LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK  
 gi|337 LDIDIGCTDLNENLGWVWIFKIKMQDGHARLGNLEFLEEKPLVGESLARVKRAEKKWRDK  
 830 840 850 860 870 880

Cry1Ac 900 910 920 930 940 950  
 REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELSV  
 gi|337 REKLVQETNIVYKEAKESVDALFVNSQYDRLQADTDAMIHAADKRVHRIREAYLPELSV  
 890 900 910 920 930 940

Cry1Ac 960 970 980 990 1000 1010  
 IPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLV  
 gi|337 IPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLV  
 950 960 970 980 990 1000

Cry1Ac 1020 1030 1040 1050 1060 1070  
 VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYP  
 gi|337 VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCVEEIVYP  
 1010 1020 1030 1040 1050 1060

Cry1Ac 1080 1090 1100 1110 1120 1130  
 NNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPCPE  
 gi|337 NNTVTCNDYTVNQEYGGAYTSRNRGYGEGSYESNSSIPAEYAPVYEE-AYIDGRKENPCPE  
 1070 1080 1090 1100 1110 1120

Cry1Ac 1140 1150 1160 1170 1180  
 FNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|337 FNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1130 1140 1150 1160 1170

>>gi|3012929|gb|AAC11772.1|I76775 Sequence 2 from patent (1176 aa)  
 initn: 5773 init1: 3094 opt: 6295 Z-score: 7414.3 bits: 1383.9 E(): 0  
 Smith-Waterman score: 6295; 80.135% identity (90.786% similar) in 1183 aa overlap  
 (10-1182:3-1176)

Cry1Ac 10 20 30 40 50 60  
 CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 gi|301 MNNQNQCVPYNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

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              70      80      90      100     110     120
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|301 VLGLIDL I WGFVGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAEAFRE
              60      70      80      90      100     110

              130     140     150     160     170     180
Cry1Ac WEADPTN PALREEMRIQFNDMNSALTTAIP LFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|301 WEADPTN PALTEEMRIQFNDMNSALTTAIP LFTVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170

              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDH A VRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|301 VFGQRWGFDAATINSRYNDLTRLIGNYTDY A VRWYNTGLERVWGPDSRDWVRYNQFRREL
              180     190     200     210     220     230

              250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTR E IYTNPVLENFDGSGFRGSAQGI EGSIRSPHL
gi|301 TLTVLDIVSLFPNYSRTPYIRTVSQLTR E IYTNPVLENFDGSGFRGMAQRIEQNIRQPHL
              240     250     260     270     280     290

              310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMAS P VGFSGPEFTFP LYGTMGNAAPQQRIVAQLGQ
gi|301 MDLLNSITIIYTDVHRGFNYWSGHQITAS P VGFAGPEFTFP RYGTMGNAAPPV-LISTTGL
              300     310     320     330     340     350

              370     380     390     400     410
Cry1Ac GVYRTLSSTLYRRP-FNIGINNQLSVLDGTE FAYGT-SSNLPSAVYRKS GTVDSLDEIP
gi|301 GIFRTLSSPLYRRIILGSGPNNQNL FVLDGTEF SFASLTADLPSTIYRQR GTVDSL DVIP
              360     370     380     390     400     410

              420     430     440     450     460     470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSN SSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|301 PQDNSVPARAGF SHRLSHVTMLSQ--AAGAVYTLRAPTFSWRHRSAEFSNLI PSSQITQI
              420     430     440     450     460     470

              480     490     500     510     520     530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLN SSGNNIQNRGYIEVPIHFPSTSTRYRVVRY
gi|301 PLTKSINLGS GTSVVKGPGFTGGDILRITSPGQISTLRVTITAPL----SQRYRVRIY
              480     490     500     510     520

              540     550     560     570     580     590
Cry1Ac ASVTP IHLNVNWN GSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|301 ASTTNLQFHTSIDGRPI NQGNFSATMSSGGNLQSGSFRTAGTTPFNFSNGSSIFL TSAH
              530     540     550     560     570     580

              600     610     620     630     640     650
Cry1Ac NFGSGTAGVIIDRFEPVPTATLEAEYNLERA QKAVNALFTSTNQGLKTNVTDYHIDQVS
gi|301 VFNSGNEVYIERIEFVPAEVTFAEYDLERA QEAVNALFTSSNQGLKTNVTDYHIDQVS
              590     600     610     620     630     640

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              660     670     680     690     700     710
Cry1Ac NLVTTYLSDEFCLDEKRELSEKVKHAKRRLSDERNLLQDSNFKDINRQPERGWWGSGSTITIQ
gi|301 NLVTECLSGEFCLDEKRELSEKVKHANRLSDERNLLQDPNFRGINRQPDGRWGRGSDITIQ
              650     660     670     680     690     700

              720     730     740     750     760     770
Cry1Ac GGDDVFKENYVTLSGTFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|301 GGDDVFKENYVTLPGTFNECYPTYLYQKIDESK LKAYTRYQLRGYIEDSQHLEIYLIRYN
              710     720     730     740     750     760

              780     790     800     810     820     830
Cry1Ac AKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAP HLEWNPDLDCSCRDGEKCAHSHHFS
gi|301 TKHETVNVPGTGLWPLSVENPIGKCGEPNRCAP QLEWNPDLDCSCRDGEKCAHSHHFS
              770     780     790     800     810     820

              840     850     860     870     880     890
Cry1Ac LDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNL FLEEKPLVGEALARVKRAEKKWRDK
gi|301 LDIDIGCTDLNENLGWVIFKIKMQDGHARLGNL FLEEKPLVGESLARVKRAEKKWRDK
              830     840     850     860     870     880

              900     910     920     930     940     950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYDQLQAD T NIAMIHAADKRVHSIREAYLP ELSV
gi|301 REKLQVETNIVYKEAKESVDALFVNSQYDRLQAD T DIAMIHAADKRVHRIREAYLP ELSV
              890     900     910     920     930     940

              960     970     980     990     1000    1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDF NNLSCWNVKGVHDVVEEQNNQRSVLV
gi|301 IPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDF NNLSCWNVKGVHDVVEEQNNHRSVLV
              950     960     970     980     990     1000

              1020    1030    1040    1050    1060    1070
Cry1Ac VPEWEAEVSQEV RVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVIYP
gi|301 VPEWEAEVSQEV RVCPGRGYILRV TAYKEGYGEGCVTIHEIEDNTDELKFSNCVEEVIYP
              1010    1020    1030    1040    1050    1060

              1080    1090    1100    1110    1120    1130
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC E
gi|301 NNTVTCNDYTANQEEYGGAYTSRNRGYGESY ESNS SIPAEYAPVYEE-AYIDGRKENPC E
              1070    1080    1090    1100    1110    1120

              1140    1150    1160    1170    1180
Cry1Ac FNRGYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|301 SNRGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
              1130    1140    1150    1160    1170

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>>gi|911500|gb|AAA70954.1| Sequence 4 from patent US 542 (969 aa)  
 initn: 6257 initl: 3338 opt: 6224 Z-score: 7331.8 bits: 1368.3 E(): 0  
 Smith-Waterman score: 6224; 98.729% identity (99.470% similar) in 944 aa overlap  
 (5-948:1-943)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|911  MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
          10      20      30      40      50
          70      80      90     100     110     120
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|911  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
          60      70      80      90     100     110
          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|911  WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|911  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          180     190     200     210     220     230
          250     260     270     280     290     300
Cry1Ac TLTVLDIVLSLFPNYDSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGLEGSIRSPHL
gi|911  TLTVLDIVALSFPNYDSRRYPPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
          240     250     260     270     280     290
          310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|911  MDILNSITIIYTDHRGYYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
          300     310     320     330     340     350
          370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLSLDEIPPQ
gi|911  GVYRTLSTLYRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLSLDEIPPQ
          360     370     380     390     400     410
          430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|911  NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          420     430     440     450     460     470
          490     500     510     520     530     540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|911  VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
          480     490     500     510     520     530
          550     560     570     580     590     600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|911  TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

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          540     550     560     570     580     590
Cry1Ac GVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|911  GVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
          600     610     620     630     640     650     660
          670     680     690     700     710     720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|911  SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
          660     670     680     690     700     710
          730     740     750     760     770     780
Cry1Ac KENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|911  KENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYLIRYNAKHETV
          720     730     740     750     760     770
          790     800     810     820     830     840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
gi|911  NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVG
          780     790     800     810     820     830
          850     860     870     880     890     900
Cry1Ac CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|911  CTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
          840     850     860     870     880     890
          910     920     930     940     950     960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNA
gi|911  ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAWRNHGHSFLCEI
          900     910     920     930     940     950
          970     980     990     1000    1010    1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVPEWEA
gi|911  VIRSQFHTTYEPEA
          960
>>gi|34426444|gb|AAQ70697.1| Sequence 7 from patent US 5 (1188 aa)
  initn: 5768 init1: 2232 opt: 5911 Z-score: 6961.2 bits: 1300.1 E(): 0
Smith-Waterman score: 6508; 83.208% identity (91.395% similar) in 1197 aa overlap
(5-1182:1-1188)
          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|344  MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
          10      20      30      40      50
          70      80      90     100     110     120
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|344  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE

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60      70      80      90      100     110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFVAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|344 WEADPTNPALREEMRIQFNDMNSALTTAIPLFVAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
gi|344 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQTLREIYTNPVLNFDGSGFRGSAQGIIEGSIIRSPHL
gi|344 TLTVLDIVSLFNPYDSRTYPIRTVSQTLREIYTNPVLNFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290

310      320      330      340      350
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ---
gi|344 MDILNSITIIYTDHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPQQRIVAQNAAP
300      310      320      330      340      350

360      370      380      390      400      410
Cry1Ac ---LGQGVYRRLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQGTVD
gi|344 VLSLTGLGIFRFLSSPLYRRIILGSGPNNQEFVSLDGTGTEFASLTTNPSTIYRQGTVD
360      370      380      390      400      410

420      430      440      450      460      470
Cry1Ac SLD-EIPPQNNVPPRQGFSHRSLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNNIIA
gi|344 SLDVEIPPQDNSVPPRAGFSHRSLSHVMTLSQ--AAGAVYTLRAT-FSQHRSAEFNNIIP
420      430      440      450      460      470

480      490      500      510      520      530
Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
gi|344 SSQITQIPLTKSTNLGSGTSSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQR
480      490      500      510      520

540      550      560      570      580      590
Cry1Ac YRVRVRYASVTPIHNLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI
gi|344 YRVRIRYASTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRIVGFTTFFPNFNSGSS
530      540      550      560      570      580

600      610      620      630      640
Cry1Ac V---GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTD
gi|344 VFTLSAHVFNNGEVYIDRIEFVPAEVTFAEAYDLERAQKAVNELFTSSNQIIGLKTVDVTD
590      600      610      620      630      640

650      660      670      680      690      700
Cry1Ac YHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD-INRQPERGW

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gi|344 YHIDQVSNLVECLSEDEFCLDEKQELSEKVKHAKRLSDERNLLQDSMFRKDGINRQPERGW
650      660      670      680      690      700

710      720      730      740      750      760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQD
gi|344 GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQD
710      720      730      740      750      760

770      780      790      800      810      820
Cry1Ac LEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK
gi|344 LEIYLIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK
770      780      790      800      810      820

830      840      850      860      870      880
Cry1Ac CAHSHHFLSLDIDVGCITDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVK
gi|344 C-RHSHHFLSLDIDVGCITDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVK
830      840      850      860      870      880

890      900      910      920      930      940
Cry1Ac RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIR
gi|344 RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHADKRVHSIR
890      900      910      920      930      940

950      960      970      980      990      1000
Cry1Ac EAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEE
gi|344 EAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEE
950      960      970      980      990      1000

1010      1020      1030      1040      1050      1060
Cry1Ac QNNQSVLVVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYEGCVTIHEIENNTDELKFS
gi|344 QNNHRSVLVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYEGCVTIHEIENNTDELKFS
1010      1020      1030      1040      1050      1060

1070      1080      1090      1100      1110      1120
Cry1Ac NCVEEVIYNNVTVCNDYTVNQEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYT
gi|344 NCVEEVIYNNVTVCNDYTVNQEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEEKAYT
1070      1080      1090      1100      1110      1120

1130      1140      1150      1160      1170      1180
Cry1Ac DGRRENPCFNRGYRDTPLPVGYVTKLEYPFETDKVWIEIGETEGTFIVDSVELLME
gi|344 DGRRDNPCESNRGYDTPPLPAGYVTKLEYPFETDKVWIEIGETEGTFIVDSVELLME
1130      1140      1150      1160      1170      1180

Cry1Ac E
:
gi|344 E

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>>gi|911502|gb|AAA70956.1| Sequence 6 from patent US 542 (969 aa)
initn: 5519 init1: 3174 opt: 5519 Z-score: 6500.2 bits: 1214.5 E(): 0

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Smith-Waterman score: 5519; 88.291% identity (93.882% similar) in 948 aa overlap (5-948:1-943)

Sequence alignment for Cry1Ac and gi|911. Includes residue numbers 10-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, 430-480, 490-530, 540-590. Shows high identity between the two sequences.

Sequence alignment for Cry1Ac and gi|597. Includes residue numbers 600-650, 660-710, 720-770, 780-830, 840-890, 900-950, 960-1010, 1020-1070. Shows lower identity compared to the gi|911 alignment.

>>gi|5973542|gb|AAE12822.1| Sequence 29 from patent US 5 (1174 aa)
initn: 4869 initl: 3310 opt: 5443 Z-score: 6409.3 bits: 1197.9 E(): 0
Smith-Waterman score: 5443; 70.732% identity (85.282% similar) in 1189 aa overlap (5-1182:1-1174)

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gi|597 AFGLFDLIWGFITPDSWSLFLQLIEQLIEQRIETLERNAITTLRGLADSYBIYIEALRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180
gi|597 WEANPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNFRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLEN--FDGSRGSAQIEGSIIRSP
250 260 270 280 290
gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPP
240 250 260 270 280 290

Cry1Ac HLMIDLNSITITYTDAHRGEYVWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQL
300 310 320 330 340 350
gi|597 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPSPYGVF--NPGGAIWADED
300 310 320 330 340 350

Cry1Ac GQGVYRTLSSSTLYRRFPNIGINNQQLSV-LDGTAFAYGTSSNLPASAVYKSGTVDLSDEI
360 370 380 390 400 410
gi|597 PRPFYRTLSDPVPVVRG--GFGNPHYVLGLRGVAFQQ--TGTN-HTRTFRNSGTIDLSDEI
360 370 380 390 400

Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
420 430 440 450 460 470
gi|597 PPQDNSGAPWVNDYSHVLNHVTFVRWPEIGSSDSWRAPMFSWTHRSATPTNTIDPERITQ
410 420 430 440 450 460

Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
480 490 500 510 520 530
gi|597 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470 480 490 500 510 520

Cry1Ac YASVTPIHNLNVWNGSSIFSNTVPATATSLDNLQSSDFGFESANAFTSSLGN---IVGV
540 550 560 570 580 590
gi|597 YASTNLRIVYTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMSSQSSFTVGA
530 540 550 560 570 580

Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
600 610 620 630 640 650
gi|597 DTFSSGNEVYIDRFELIPVTATFEABYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590 600 610 620 630 640

660 670 680 690 700 710

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Cry1Ac SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTGITI
650 660 670 680 690 700

Cry1Ac QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
720 730 740 750 760 770
gi|597 QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRY
710 720 730 740 750 760

Cry1Ac NAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
780 790 800 810 820 830
gi|597 NAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
770 780 790 800 810 820

Cry1Ac SLDIDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
840 850 860 870 880 890
gi|597 SLDIDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830 840 850 860 870 880

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
900 910 920 930 940 950
gi|597 KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
890 900 910 920 930 940

Cry1Ac VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
960 970 980 990 1000 1010
gi|597 VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
950 960 970 980 990 1000

Cry1Ac VVPEWEAEVSVQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEIY
1020 1030 1040 1050 1060 1070
gi|597 VVPEWEAEVSVQEVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEVY
1010 1020 1030 1040 1050 1060

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
1080 1090 1100 1110 1120
gi|597 PNNTVTCNDYTVNQEEYEGTYTSRNRGYDGAYESNSVVPADYASAYEEKAYTDGRRDNPC
1070 1080 1090 1100 1110 1120

Cry1Ac EFNRGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170 1180
gi|597 ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

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>>gi|1610953|gb|AAB13932.1| Sequence 29 from patent US 5 (1174 aa)
initn: 4869 init1: 3310 opt: 5443 Z-score: 6409.3 bits: 1197.9 E(): 0
Smith-Waterman score: 5443; 70.732% identity (85.282% similar) in 1189 aa overlap
(5-1182:1-1174)

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10 20 30 40 50 60

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>>gi|5987865|gb|AAE17030.1| Sequence 29 from patent US 5 (1174 aa)
initn: 4869 initl: 3310 opt: 5443 Z-score: 6409.3 bits: 1197.9 E(): 0
Smith-Waterman score: 5443; 70.732% identity (85.282% similar) in 1189 aa overlap
(5-1182:1-1174)

Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|598 MENNIQ-NQCVPNCLNNPEVEILNEER-STGRPLDLSLSTRFLLSEFVPGVGV
10 20 30 40 50 60
10 20 30 40 50

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|598 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIALRE
70 80 90 100 110 120
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|598 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
130 140 150 160 170 180
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|598 SPGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTNRQWARFNQFRDL
190 200 210 220 230 240
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLEN--FDGSFRGSAQIEGSI RSP
gi|598 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPP
250 260 270 280 290
240 250 260 270 280 290

Cry1Ac HLMIDLNSITIIYTDHRGEYYSWGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQL
gi|598 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADSD
300 310 320 330 340 350
300 310 320 330 340 350

Cry1Ac QGGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLP SAVYRKSGTVDSLDEI
gi|598 PRPFYRTLSDPVFVRG--FGFNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360 370 380 390 400
360 370 380 390 400

Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|598 PPQDMSGAPWNDYSVHLNHVTFVRWPGELSGSDSWRAPMFSWTHRSATPTINTIDPERITQ
420 430 440 450 460 470
410 420 430 440 450 460

Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
gi|598 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLFPQ--RVRARIR
480 490 500 510 520 530
470 480 490 500 510 520

Cry1Ac 540 550 560 570 580 590
YASVTP IHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|598 YASTTNLR IYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMSQSSFTVGA
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650
RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQV
gi|598 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710
SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
gi|598 SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770
QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|598 QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRY
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830
NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|598 NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
770 780 790 800 810 820

Cry1Ac 840 850 860 870 880 890
SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|598 SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830 840 850 860 870 880

Cry1Ac 900 910 920 930 940 950
KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELS
gi|598 KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELS
890 900 910 920 930 940

Cry1Ac 960 970 980 990 1000 1010
VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVL
gi|598 VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVL
950 960 970 980 990 1000

Cry1Ac 1020 1030 1040 1050 1060 1070
VVEWEAEVVSQEVVRCVCPGRGYILRV TAYKEGYGEGCVTIEIENNTDELKFSNCVVEEIIY
gi|598 VVEWEAEVVSQEVVRCVCPGRGYILRV TAYKEGYGEGCVTIEIENNTDELKFSNCVVEEIIY
1010 1020 1030 1040 1050 1060

Cry1Ac 1080 1090 1100 1110 1120
PNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|598 PNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC



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gi|160 VVPEWEAEVSEVRVCPGRGYILRVTAAYKEGYEGCVTTHEIENNTDELKFSNCVEEEVY
1010 1020 1030 1040 1050 1060

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
1080 1090 1100 1110 1120

gi|160 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRDRNPC
1070 1080 1090 1100 1110 1120

Cry1Ac EFNRYGRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170 1180

gi|160 ESNRYGDDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

>>gi|412688|emb|CAA00485.1| bt18 [synthetic construct] (1171 aa)
initn: 4651 initl: 3153 opt: 5381 Z-score: 6336.1 bits: 1184.4 E(): 0
Smith-Waterman score: 5433; 71.765% identity (84.454% similar) in 1190 aa overlap
(5-1182:1-1171)

Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50 60

gi|412 MEIVNNQNCVYPYNCLNPNENEIILDIERSNST-VATNIALEISRLLASA-TPIGGI
10 20 30 40 50

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|412 LLGLFDAIWGSIGPSQWDLFLEQIELLIDQKIEEFARNQAI SRLEGISLQYIYEAQFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVS
130 140 150 160 170 180

gi|412 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYQAAHLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS---RDWIRYNQFR
190 200 210 220 230

gi|412 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180 190 200 210 220 230

Cry1Ac RELTLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNVPLENFDGSRGSAQGIEGS-IR
240 250 260 270 280 290

gi|412 RELTISVLDIISFFRNYSRTPYPIPTSSQLTREVYTDVINITDYRVGSPFENIENSAIR
240 250 260 270 280 290

Cry1Ac SPHLMIDLNSITITDAHRGEYYSWGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVA
300 310 320 330 340 350

gi|412 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFTG-SSQVITTPQYGITANAEPRTIAP
300 310 320 330 340 350

Cry1Ac QLGQGV---YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDS
360 370 380 390 400 410

gi|412 STFPGLNLFYRTLSNPFRRSENI-TPTLGINVVQGVGFI---QPNAEVLRYRSRGTVDS
360 370 380 390 400

Cry1Ac LDEIIPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASD
420 430 440 450 460 470

gi|412 LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFVWTHHSATNTNTINPD
410 420 430 440 450 460

Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
480 490 500 510 520 530

gi|412 IITQIPLVKGFRLLGGTSTVIKGPFTGGDILRRNTIGEFVS---LQVNINSPITQ-RYR
470 480 490 500 510

Cry1Ac VVRVYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
540 550 560 570 580 590

gi|412 LRFVYASSRDARITVAIGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSPFRANPDII
520 530 540 550 560 570

Cry1Ac GVRNFSGTAG--VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
600 610 620 630 640

gi|412 RIAEELPIRGGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580 590 600 610 620 630

Cry1Ac IDQVSNLVTYLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGS
650 660 670 680 690 700

gi|412 IDQVSNLVECLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFRGINRQPDGRWGS
640 650 660 670 680 690

Cry1Ac GITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIY
710 720 730 740 750 760

gi|412 DITIQQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYELRGIYEDSQDLEIY
700 710 720 730 740 750

Cry1Ac SIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
770 780 790 800 810 820

gi|412 LIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
760 770 780 790 800 810

Cry1Ac SHHFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
830 840 850 860 870 880

gi|412 SHHFSLDIDVGCTDLNEDLGVWVIFKIKTQDGYARLGNLEFLEEKPLLGEALARVKRAEK
820 830 840 850 860 870

Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYL
890 900 910 920 930 940

gi|412 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRQLQADTNIAMIHAADKRVHSIREAYL
880 890 900 910 920 930

Cry1Ac PELSVIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNQ
950 960 970 980 990 1000

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.....
gi|412 PELSIVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNH
940 950 960 970 980 990

1010 1020 1030 1040 1050 1060
Cry1Ac RSVLVVPEWEAEVVSQEV RVCPGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCVE
.....
gi|412 RSVLVVPEWEAEVVSQEV RVCPGRGYILRV TAYKEGYGEGCVT IHEIEDNTDELKFSNCVE
1000 1010 1020 1030 1040 1050

1070 1080 1090 1100 1110 1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN P
.....
gi|412 EEVYPNNTVTCNNYTATQEEHEGTYTSRNRGYDEAYESNSSVHASVYEEKSYTDRREN P
1060 1070 1080 1090 1100 1110

1130 1140 1150 1160 1170 1180
Cry1Ac CEFNRGRDYTPPLVGVYTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
.....
gi|412 CESNRGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120 1130 1140 1150 1160 1170

>>gi|142752|gb|AAA22345.1| cryIE(a) (1171 aa)
initn: 4645 initl: 3147 opt: 5375 Z-score: 6329.1 bits: 1183.1 E(): 0
Smith-Waterman score: 5427; 71.681% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10 20 30 40 50 60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLSEFVPGAGF
.....
gi|142 MEIVNNQNCQVPYNCNLPENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
.....
gi|142 LLGLFDAIWGSIGPSQWDLFLEQIEILLIDQKIEEFARNQAISRLEGISLYGIYTEAFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.....
gi|142 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS--RDWIRYNQFR
.....
gi|142 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNGFR
180 190 200 210 220 230

240 250 260 270 280 290
Cry1Ac RELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIEGS-IR
.....
gi|142 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVINITDYRVGSPFENIENSAIR
240 250 260 270 280 290

300 310 320 330 340 350
Cry1Ac SPHLMIDLNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA

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.....
gi|142 SPHLMDFLNNTLIDTDLIRGVHYWAGHRVTSHTFG-SSQVITTPQYGITANAEPRTIAP
300 310 320 330 340 350

360 370 380 390 400 410
Cry1Ac QLGGQV---YRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVD
.....
gi|142 STFPGLNLFYRTLSNPFRRSENI-TPTLGINVVQVGF---QPNAAEVLYRSRGTVD
360 370 380 390 400

420 430 440 450 460 470
Cry1Ac LDEIIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNLIASD
.....
gi|142 LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFFVWTHHSATNTNTINPD
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
.....
gi|142 IITQIPLVKGFRLLGGGTSVIKGPFTGGDILRRNTIGEFVS----LQVNINSPITQ-RYR
470 480 490 500 510

540 550 560 570 580 590
Cry1Ac VRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
.....
gi|142 LRFRYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSPFSFRANPDI
520 530 540 550 560 570

600 610 620 630 640
Cry1Ac GVRNFSGTAG--VIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
.....
gi|142 RIAEELPIRGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580 590 600 610 620 630

650 660 670 680 690 700
Cry1Ac IDQVSNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
.....
gi|142 IDQVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGGST
640 650 660 670 680 690

710 720 730 740 750 760
Cry1Ac GITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSODLEIY
.....
gi|142 DITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSODLEIY
700 710 720 730 740 750

770 780 790 800 810 820
Cry1Ac SIRYNKHEHTVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
.....
gi|142 LIRYNKHEHTVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
760 770 780 790 800 810

830 840 850 860 870 880
Cry1Ac SHHFLSDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
.....
gi|142 SHHFLSDIDVGCTDLNEDLGWVWIFKIKTQDGYARLGNLEFLEEKPLVGEALARVKRAEK
820 830 840 850 860 870

890 900 910 920 930 940

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Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVSIREAYL
gi|142 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVSIREAYL
880 890 900 910 920 930

950 960 970 980 990 1000
Cry1Ac PELSVPVGNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQ
gi|142 PELSVPVGNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNH
940 950 960 970 980 990

1010 1020 1030 1040 1050 1060
Cry1Ac RSVLVVPEWEAEVSVQEVVCPGRGYILRVVTAYKEGYEGECVTIHEIENNTDELKFSNCVE
gi|142 RSVLVVPEWEAEVSVQEVVCPGRGYILRVVTAYKEGYEGECVTIHEIEDNTDELKFSNCVE
1000 1010 1020 1030 1040 1050

1070 1080 1090 1100 1110 1120
Cry1Ac EEIYPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRENPN
gi|142 EEVYPNNTVTCDNYTVNQEEYGGAYTSRNRGYDEAYESNSSVHASVYEEKSYTDRRRENPN
1060 1070 1080 1090 1100 1110

1130 1140 1150 1160 1170 1180
Cry1Ac CEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|142 CESNRYGDTPLPVAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120 1130 1140 1150 1160 1170

>>gi|58397442|gb|AAW72936.1| insecticidal delta endotoxi (1171 aa)
initn: 4645 initl: 3147 opt: 5375 Z-score: 6329.1 bits: 1183.1 E(): 0
Smith-Waterman score: 5427; 71.681% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10 20 30 40 50 60
Cry1Ac CMQAMNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|583 MEIVNQNQCVPYNCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|583 LLGLFDIAIWSIGSPQWDLFLEQIEILLIDQKIEEFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|583 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGPDS--RDWIRYNQFR
gi|583 VFGQAWGFDIATINSRYNDLTRLIPYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180 190 200 210 220 230

240 250 260 270 280 290

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Cry1Ac RELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGS-IR
gi|583 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREYVYTDVINITDYRVGSPFENIENSAIR
240 250 260 270 280 290

300 310 320 330 340 350
Cry1Ac SPHLMIDLNSITTYDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVA
gi|583 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG-SSQVITTPQYGITANAEPRRTIAP
300 310 320 330 340 350

360 370 380 390 400 410
Cry1Ac QLGQGV---YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYKRSKGTVDS
gi|583 STFPGLNLFYRTLSPFFRRSENI--TPTLGINVVQGVGFI---QPNNAEVLRSRGTVDS
360 370 380 390 400

420 430 440 450 460 470
Cry1Ac LDEIPPQNNVPPRQGFSHRSLHVMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASD
gi|583 LNELPIDGEN--SLVGYSHRSLHVTLTRSLYNTNITSL--PTFWVTHHSATNTNTINPD
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|583 IITQIPLVKGFRLLGGTGVKIKGPGFTGGDILRRNTIGEFVS---LQVNNISPIQ-RYR
470 480 490 500 510

540 550 560 570 580 590
Cry1Ac VRVRYASVTPIHNLNVWNGNSSIFSNVVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
gi|583 LRFYASSRDARITVAIGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSPFSFRANPDII
520 530 540 550 560 570

600 610 620 630 640
Cry1Ac GVRNFGSTAG--VIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|583 RIAEELPIRGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580 590 600 610 620 630

650 660 670 680 690 700
Cry1Ac IDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|583 IDQVSNLVECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGGST
640 650 660 670 680 690

710 720 730 740 750 760
Cry1Ac GITIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQLEIY
gi|583 DITIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGIYEDSQLEIY
700 710 720 730 740 750

770 780 790 800 810 820
Cry1Ac SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
gi|583 LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
760 770 780 790 800 810

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830 840 850 860 870 880
Cry1Ac SHHFSLDIDVGC...
gi|583 SHHFSLDIDVGC...

890 900 910 920 930 940
Cry1Ac KWRDKREKLEWETN...
gi|583 KWRDKCEKLEWETN...

950 960 970 980 990 1000
Cry1Ac PELSVIPGVNAAI...
gi|583 PELSVIPGVNAAI...

1010 1020 1030 1040 1050 1060
Cry1Ac RSVLVVPEWEAEV...
gi|583 RSVLVVPEWEAEV...

1070 1080 1090 1100 1110 1120
Cry1Ac EEIYPNNTVTCND...
gi|583 EEVYPNNTVTCN...

1130 1140 1150 1160 1170 1180
Cry1Ac CEFNRGRDYTP...
gi|583 CESNRGVDYTP...

>>gi|1610413|gb|AAB13385.1| Sequence 2 from patent US 55 (1171 aa)
initn: 4645 initl: 3147 opt: 5375 Z-score: 6329.1 bits: 1183.1 E(): 0
Smith-Waterman score: 5427; 71.681% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10 20 30 40 50 60
Cry1Ac CMQAMDNNPNINE...
gi|161 MEIVNNQNCVP...

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGI...
gi|161 LLGLFDAIWS...

130 140 150 160 170 180
Cry1Ac WEADPTNPALRE...
gi|161 WEADPTNPAL...

190 200 210 220 230
Cry1Ac VFGQRWGFDAAT...
gi|161 VFGQAWGFDI...

240 250 260 270 280 290
Cry1Ac RELTTLTVLDIV...
gi|161 RELTISVLDI...

300 310 320 330 340 350
Cry1Ac SPHLM DILNSIT...
gi|161 SPHLMDFLNN...

360 370 380 390 400 410
Cry1Ac QLGQGV---YR...
gi|161 STFPGLNLFY...

420 430 440 450 460 470
Cry1Ac LDEIPPQNNVPP...
gi|161 LNELPIDGEN...

480 490 500 510 520 530
Cry1Ac SITQIPAVKGN...
gi|161 IITQIPLVKG...

540 550 560 570 580 590
Cry1Ac VVRVYASVTP...
gi|161 LRFYASSRDAR...

600 610 620 630 640
Cry1Ac GVRNFGTAG--...
gi|161 RIAEELPIRG...

650 660 670 680 690 700
Cry1Ac IDQVSNLVTYL...
gi|161 IDQVSNLVCL...

710 720 730 740 750 760
Cry1Ac GITIQGGDVFK...
gi|161 DITIQQGDDV...



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640      650      660      670      680      690
Cry1Ac  GITIQGGDDVFKENYVTLPGTDFDECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
gi|161  DITIQQGDDVFKENYVTLPGTDFDECYPTLYLQKIDESKLFKAYTRYELRGYIEDSQDLEIY
700      710      720      730      740      750

770      780      790      800      810      820
Cry1Ac  SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
gi|161  LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
760      770      780      790      800      810

830      840      850      860      870      880
Cry1Ac  SHHFSLDIDVGCITDLNEDLGWVVIKIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEK
gi|161  SHHFSLDIDVGCITDLNEDLGWVVIKIKITQDGYARLGNLEFLEEKPLVGEALARVKRAEK
820      830      840      850      860      870

890      900      910      920      930      940
Cry1Ac  KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYL
gi|161  KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYL
880      890      900      910      920      930

950      960      970      980      990      1000
Cry1Ac  PELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQ
gi|161  PELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNH
940      950      960      970      980      990

1010     1020     1030     1040     1050     1060
Cry1Ac  RSVLVVPEWEAEVVSQEVVRCVPCGRGYILRVYAYKEGYGECVTVIHEIENNTDELKFSNCVE
gi|161  RSVLVVPEWEAEVVSQEVVRCVPCGRGYILRVYAYKEGYGECVTVIHEIENNTDELKFSNCVE
1000     1010     1020     1030     1040     1050

1070     1080     1090     1100     1110     1120
Cry1Ac  EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN
gi|161  EEVYPNNTVTCNNTATQEEHEGYTSRNRGYDEAYESNSSVHASVYEEKSYTDRREN
1060     1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac  CEFNRGRYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|161  CESNRGYDGYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120     1130     1140     1150     1160     1170

>>gi|17979619|gb|AAL50330.1|AF202531_1 Cry032 [Bacillus (1171 aa)
  initn: 4645 initl: 3147 opt: 5375 Z-score: 6329.1 bits: 1183.1 E(): 0
Smith-Waterman score: 5427; 71.681% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|179  MEIVNQNQCVPYINCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI

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10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
gi|179  LGLFDAIWGSIGSPQWDLFLEQIELLIDQKIEEFARNQAIISRLGLSNLYQIYIYAFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|179  WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS---RDWIRYNQFR
gi|179  VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180     190     200     210     220     230

240     250     260     270     280     290
Cry1Ac  RELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGS-IR
gi|179  RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVPVINITYRVGSPFENIENSAIR
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  SPHLMIDLNSITITYDAHRGEYYSWGHQIMASVGVGSGPEFTFPLYGTMGNAAPQQRIVA
gi|179  SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFTG-SSQVITTPQYGITANAEPRTIAP
300     310     320     330     340     350

360     370     380     390     400     410
Cry1Ac  QLGGQV---YRTLSSTLYRPPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDS
gi|179  STFPGLNLFYTRLSNPFRRSENI-TPTLGINVVQGVGFI---QPNAEVLVYRSRGTVDS
360     370     380     390     400

420     430     440     450     460     470
Cry1Ac  LDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|179  LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWWTHSATNTNTINPD
410     420     430     440     450     460

480     490     500     510     520     530
Cry1Ac  SITQIPAVKGNFLNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYR
gi|179  IITQIPLVKGFRGGTSSVIKGPFTGGDILRRNTIGEFVS----LQVNINSPIQ-RYR
470     480     490     500     510

540     550     560     570     580     590
Cry1Ac  VRRVYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
gi|179  LRFYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPFSSFRANPDII
520     530     540     550     560     570

600     610     620     630     640
Cry1Ac  GVRNFGTAG--VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH

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Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|593 IITQIPLVKGFRLLGGTGVKIPGPGFTGGDILRRNTIGEFVSV---LQVNSIPITQ-RYR
      470      480      490      500      510

      540      550      560      570      580      590
Cry1Ac VRRVRYASVTPIHLLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLG-NIV
gi|593 LRFVRYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSPFSFRANPDII
      520      530      540      550      560      570

      600      610      620      630      640
Cry1Ac GVRNFSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|593 RIAEELPIRGGELYIDKIELLLADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
      580      590      600      610      620      630

      650      660      670      680      690      700
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|593 IDQVSNLVECLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRWRGST
      640      650      660      670      680      690

      710      720      730      740      750      760
Cry1Ac GITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
gi|593 DITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSDLEIY
      700      710      720      730      740      750

      770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
gi|593 LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
      760      770      780      790      800      810

      830      840      850      860      870      880
Cry1Ac SHHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
gi|593 SHHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGYARLGNLEFLEEKPLVGEALARVKRAEK
      820      830      840      850      860      870

      890      900      910      920      930      940
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYL
gi|593 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYL
      880      890      900      910      920      930

      950      960      970      980      990      1000
Cry1Ac PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQ
gi|593 PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNH
      940      950      960      970      980      990

      1010      1020      1030      1040      1050      1060
Cry1Ac RSVLVVPEWEAEVSVQEVRCVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFSNCVE
gi|593 RSVLVVPEWEAEVSVQEVRCVCPGRGYILRVTA YKEGYGEGCVTIHEIEDNTDELKFSNCVE
      1000      1010      1020      1030      1040      1050

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      1070      1080      1090      1100      1110      1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN
gi|593 EEVYPNNTVTCNNYATQEEHEGTYTSRNRGYDEAYESNSSVHASVYEEKSYTDRRREN
      1060      1070      1080      1090      1100      1110

      1130      1140      1150      1160      1170      1180
Cry1Ac CEFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|593 CESNRGYGDTPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120      1130      1140      1150      1160      1170

>>gi|1946622|gb|AAD04732.1| Cry1Ea4 [Bacillus thuringien (1171 aa)
  initn: 4645 init1: 3147 opt: 5373 Z-score: 6326.7 bits: 1182.6 E(): 0
Smith-Waterman score: 5425; 71.681% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|194 MEIVNNQNCVYPYNCNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|194 LLGLFDIWSIGPSQWDLFLEQIELLIDQKIEEFARNQAISRLEGISSLYGIYTEAFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|194 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS---RDWIRYNQFR
gi|194 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
      180      190      200      210      220      230

      240      250      260      270      280      290
Cry1Ac RELTLTVLDDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIEGS-IR
gi|194 RELTISVLDIISFFRNYSRLYPIPTSSQLTREYVYTDVINITDYRVGSPFENIENSAIR
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac SPHLMIDLNSITITYDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVA
gi|194 SPHLMDFLNLTDITDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGN SQNAEPRTIAP
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac QLQGV---YRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKS GTVDS
gi|194 STFPGLNLFYRTLSNPFRRSENI--TPTLGINVVQGVGFI---QPNAEVL YRSRGTVDS
      360      370      380      390      400

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420      430      440      450      460      470
Cry1Ac LDEIIPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFWIHRSAEFNNIIASD
gi|194 LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFVWTHHSATNTINTINPD
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYR
gi|194 IITQIPLVKGFRLGGGTSVIKGGTGGDILRRNTIGEFVS---LQVNIINSPIQ-RYR
470      480      490      500      510

540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLG-NIV
gi|194 LRFYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPFSPANPDI
520      530      540      550      560      570

600      610      620      630      640
Cry1Ac GVRNFSGTAG--VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|194 RIAEELPIRGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580      590      600      610      620      630

650      660      670      680      690      700
Cry1Ac IDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|194 IDQVSNLVLECLDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGST
640      650      660      670      680      690

710      720      730      740      750      760
Cry1Ac GITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
gi|194 DITIQQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIY
700      710      720      730      740      750

770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
gi|194 LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
760      770      780      790      800      810

830      840      850      860      870      880
Cry1Ac SHHFSLDIDVGTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
gi|194 SHHFSLDIDVGTDLNEDLGWVVIKIKTQDGYARLGNLEFLEEKPLVGEALARVKRAEK
820      830      840      850      860      870

890      900      910      920      930      940
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYL
gi|194 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYL
880      890      900      910      920      930

950      960      970      980      990      1000
Cry1Ac PELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQ
gi|194 PELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNH
940      950      960      970      980      990

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1010      1020      1030      1040      1050      1060
Cry1Ac RSVLVVPEWEAEVSVQEVVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVE
gi|194 RSVLVVPEWEAEVSVQEVVCPGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCVE
1000      1010      1020      1030      1040      1050

1070      1080      1090      1100      1110      1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN
gi|194 EEVYPNNTVTCNNYATQEEHEGTYTSRNRGYDEAYESSNVHASVYEEKSYDGRREN
1060      1070      1080      1090      1100      1110

1130      1140      1150      1160      1170      1180
Cry1Ac CEFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|194 CESNRGYDYTPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120      1130      1140      1150      1160      1170

>>gi|3990784|gb|AAC84211.1|AR000634 Sequence 4 from pate (1171 aa)
initn: 4639 initl: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0
Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|399 MEIVNNQNCQVPYNCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
gi|399 LGLFLDAIWGSIGSPQWDLFLEQIELLIDQKIEEFARNQAISRLEGLISSLYGIYTAFAFRE
60      70      80      90      100      110

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|399 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS---RDWIRYNQFR
gi|399 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180      190      200      210      220      230

240      250      260      270      280      290
Cry1Ac RELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGS-IR
gi|399 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVPINITYRVGSPFENIENSAIR
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac SPHLMDILNSITTYDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|399 SPHLMDFLNLLTIDTDLIRGVHYWAGHRVTSHTFTG-SSQVITTPQYGITANAEPRTIAP
300      310      320      330      340      350

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360      370      380      390      400      410
Cry1Ac  QLGQGV---YRFLSSTLYRRFPNIGINNQQLSVLDGTFEAYGTSSNLPSSAVVRKSGTVD
gi|399  STFPGLNLFYRFLSNPFRRSENI--TPTLGINVVQGVGI---QPNNAEVLYRSRGTVD
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac  LDEIIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASD
gi|399  LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFWVTHHSATNTNTINPD
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|399  IITQIPLVKGFRLLGGGTSVIKGPFGFTGGDILRRNTIGEFVS----LQVNIINSPIQ-RYR
470      480      490      500      510

540      550      560      570      580      590
Cry1Ac  VRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLG-NIV
gi|399  LRFYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPPSFRANPDI
520      530      540      550      560      570

600      610      620      630      640
Cry1Ac  GVRNFSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|399  RIAEELPIRGELYIDKIELILADATFEEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580      590      600      610      620      630

650      660      670      680      690      700
Cry1Ac  IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|399  IDQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGGST
640      650      660      670      680      690

710      720      730      740      750      760
Cry1Ac  GITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
gi|399  DITIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSDLEIY
700      710      720      730      740      750

770      780      790      800      810      820
Cry1Ac  SIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
gi|399  LIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
760      770      780      790      800      810

830      840      850      860      870      880
Cry1Ac  SHHFLSLDIVGCTDLNEDLGVVVFIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
gi|399  SHHFLSLDIVGCTDLNEDLGVVVFIFKIKTQDGYARLGNLEFLEENPLLGEALARVKRAEK
820      830      840      850      860      870

890      900      910      920      930      940
Cry1Ac  KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYL
gi|399  KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYL

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880      890      900      910      920      930
Cry1Ac  PELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQ
gi|399  PELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNH
940      950      960      970      980      990

1010     1020     1030     1040     1050     1060
Cry1Ac  RSVLVVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVE
gi|399  RSVLVVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVE
1000     1010     1020     1030     1040     1050

1070     1080     1090     1100     1110     1120
Cry1Ac  EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRENP
gi|399  EEVYPNNTVTCNNYTATQEEHEGTYTSRNRGYDEAYESNSSVHASVYEEKSYTDRREN
1060     1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac  CEFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|399  CESNRGYDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120     1130     1140     1150     1160     1170

>>gi|53984833|gb|AAV26509.1| Sequence 4 from patent US 6 (1171 aa)
initn: 4639 initl: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0
Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|539  MEIVNNQNCQVPYNCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|539  LLGLFDAIWGSIGPSQWDLFLEQIELLIDQKIEEFARNQAISRLEGISSLYGIYTEAFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539  WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSS---RDWIRYNQFR
gi|539  VFGQANGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180     190     200     210     220     230

240     250     260     270     280     290
Cry1Ac  RELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDDGSRGSAQGIEGS-IR
gi|539  RELTISVLDIISFFRNYDSRLYPIPTSSQLTREYVYTDVINITYRVGSPFENIENSAIR

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      240      250      260      270      280      290
Cry1Ac 300      310      320      330      340      350
SPHLMIDLNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFLPYLGTMGNAAPQQRIVA
gi|539 SPHLMDFLNNLTIDTLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRTIAP
      300      310      320      330      340      350
Cry1Ac 360      370      380      390      400      410
QLGQGV---YRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQTVDS
gi|539 STFPGLNLFYRTLSPFFRRSENI--TPTLGINVVQGVGI---QPNAEVLYRSRGTVDS
      360      370      380      390      400
Cry1Ac 420      430      440      450      460      470
LDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASD
gi|539 LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFWVTHHSATNTNTINPD
      410      420      430      440      450      460
Cry1Ac 480      490      500      510      520      530
SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYR
gi|539 IITQIPLVKGFRLLGGGTSVIKGGFTGGDILRRNTIGEFVS---LQVNIINSPIQ-RYR
      470      480      490      500      510
Cry1Ac 540      550      560      570      580      590
VRVRYASVTPPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
gi|539 LRFYASSRDARITVAIGQIRVDMTELEKTMEIGESLTSRTFSYTNFSPNPFSSFRANPDI
      520      530      540      550      560      570
Cry1Ac 600      610      620      630      640
GVRNFSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|539 RIAEELPIRGELYIDKIELLADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
      580      590      600      610      620      630
Cry1Ac 650      660      670      680      690      700
IDQVSNLVITYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|539 IDQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQDRGWRGST
      640      650      660      670      680      690
Cry1Ac 710      720      730      740      750      760
GITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
gi|539 DITIQQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYELRGYIEDSDLEIY
      700      710      720      730      740      750
Cry1Ac 770      780      790      800      810      820
SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGEKCAHH
gi|539 LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGEKCAHH
      760      770      780      790      800      810
Cry1Ac 830      840      850      860      870      880
SHHFLSDIDVGCCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK

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gi|539 SHHFLSDIDVGCCTDLNEDLGVVWVIFKIKTQDGYARLGNLEFLEENPLLGEALARVKRAEK
      820      830      840      850      860      870
Cry1Ac 890      900      910      920      930      940
KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYL
gi|539 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYL
      880      890      900      910      920      930
Cry1Ac 950      960      970      980      990      1000
PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVEEQNNQ
gi|539 PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVEEQNNH
      940      950      960      970      980      990
Cry1Ac 1010     1020     1030     1040     1050     1060
RSVLVPEWAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVE
gi|539 RSVLVPEWAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIEDNTDELKFSNCVE
      1000     1010     1020     1030     1040     1050
Cry1Ac 1070     1080     1090     1100     1110     1120
EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN
gi|539 EEVYPNNTVTCNNYATQEEHEGTYTSRNRGYDEAYESSNVSHASVYEEKSYTDRRREN
      1060     1070     1080     1090     1100     1110
Cry1Ac 1130     1140     1150     1160     1170     1180
CEFNRGYRDYTPPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|539 CESNRGYGDTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120     1130     1140     1150     1160     1170
>>gi|15105603|gb|AAE66197.1| Sequence 4 from patent US 6 (1171 aa)
      initn: 4639 initl: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0
Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|151  MEIVNQNQCVPYNCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIE EFARNQAISRLEGLSNLYQIYAESFRE
gi|151  LLGLFDIWSIGGPSQWDLFLEQIELLIDQKIEEFARNQAISRLEGISLGYIYTAFARE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151  WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac 190     200     210     220     230
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS---RDWIRYNQFR

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gi|151 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
      180      190      200      210      220      230
      240      250      260      270      280      290
Cry1Ac RELTLTVLDIVSLFPNYSRTPYPIRTVSQTLREIYTNVPLENFDGSRGSAQGIIEGS-IR
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVPIVINITDYRVGSPFENIENSAIR
      240      250      260      270      280      290
      300      310      320      330      340      350
Cry1Ac SPHLMIDILNSITITDAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRTIAP
      300      310      320      330      340      350
      360      370      380      390      400      410
Cry1Ac QLGQGV---YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDS
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 STFPGLNLFYRTLSPFFRRSENI--TPTLGINVVQGVGFI---QPNNAEVLYRSRGTVDS
      360      370      380      390      400
      420      430      440      450      460      470
Cry1Ac LDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASD
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFVWTHHSATNTNTINPD
      410      420      430      440      450      460
      480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 IITQIPLVKGFRLGGTGVKPGFTGGDILRRNTIGEFVS----LQVNSPITQ-RYR
      470      480      490      500      510
      540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHNNVWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSLG-NIV
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LRFRYASSRDARITVAIGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPFSSFRANPDII
      520      530      540      550      560      570
      600      610      620      630      640
Cry1Ac GVRNFSGTAG--VIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 RIAEELPIRGELYIDKIELLLADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
      580      590      600      610      620      630
      650      660      670      680      690      700
Cry1Ac IDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 IDQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGRST
      640      650      660      670      680      690
      710      720      730      740      750      760
Cry1Ac GITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 DITIQQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIY
      700      710      720      730      740      750
      770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHH

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      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHH
      760      770      780      790      800      810
      830      840      850      860      870      880
Cry1Ac SHHFSLDIDVGCCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 SHHFSLDIDVGCCTDLNEDLGWVWIFKIKTQDGYARLGNLEFLEENPLLGEALARVKRAEK
      820      830      840      850      860      870
      890      900      910      920      930      940
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYL
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADNTIAMIHAADKRVHSIREAYL
      880      890      900      910      920      930
      950      960      970      980      990      1000
Cry1Ac PELSVIPGVNAAIFFELEGRIPTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQ
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 PELSVIPGVNAAIFFELEGRIPTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNH
      940      950      960      970      980      990
      1010      1020      1030      1040      1050      1060
Cry1Ac RSVLVVPEWAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 RSVLVVPEWAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIEDNTDELKFSNCVE
      1000      1010      1020      1030      1040      1050
      1070      1080      1090      1100      1110      1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRRREN
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 EEVYPNNTVTCNNYATQEEHEGTYTSRNRGYDEAYESSNVSHASVYEEKSYDRRREN
      1060      1070      1080      1090      1100      1110
      1130      1140      1150      1160      1170      1180
Cry1Ac CEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 CESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120      1130      1140      1150      1160      1170
>>gi|2298886|emb|CAA02750.1| unnamed protein product [Ba (1171 aa)
      initn: 4639 initl: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0
      Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap
      (5-1182:1-1171)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|229 MEIVNNQNCQVYPYNCLNPNENEILDERSNST-VATNIALEISRLLASA-TPIGGI
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|229 LLGLFDIANGSIGSPQWDLFLEQIELLIDQKIEEFARNQAIISRLEGISSLYGIYTEAFRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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gi|229 WEADPTNPALKKEEMRTQFNDMNSILVTAIPLFVQNYQVPPFVSVVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS--RDWIRYNQFR
gi|229 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
180 190 200 210 220 230

Cry1Ac 240 250 260 270 280 290
RELTLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVLENFDGSRFRGSAQIEGS-IR
gi|229 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREYVYTDVINITDYRVGSPFENIENSAIR
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350
SPHLMIDILNSITTYDAHRGEYYWSGHQIMASVPGFSGPEFTPLYGTMGNAAPQORIVA
gi|229 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRTIAP
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400 410
QLGQGV--YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDS
gi|229 STFPGLNLFYRFLSNPFFRRSENI--TPTLGINVVGQVGF--QPNNAEVLYRSRGTVDS
360 370 380 390 400

Cry1Ac 420 430 440 450 460 470
LDEIPPQNNVPPRQGFSHRLSHVMFRSGFNSVSIIRAPMFSWIHRSAEFNIIASD
gi|229 LNELPIDGEN--SLVGSHRLSHVTLTRSLYNTNITSL--PTFVWTHSATNTINTINPD
410 420 430 440 450 460

Cry1Ac 480 490 500 510 520 530
SITQIPAVKGNFLFNG--SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYR
gi|229 IITQIPLVKGFRLLGGTGVKIGPGFTGGDILRRNTIGEFVS---LQVNSIPITQ--RYR
470 480 490 500 510

Cry1Ac 540 550 560 570 580 590
VRVRYASVTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLG-NIV
gi|229 LRFYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPFSTRANPDII
520 530 540 550 560 570

Cry1Ac 600 610 620 630 640
GVRNFSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|229 RIAEELPIRGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
580 590 600 610 620 630

Cry1Ac 650 660 670 680 690 700
IDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|229 IDQVSNLVECLDSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRGWRGST
640 650 660 670 680 690

Cry1Ac 710 720 730 740 750 760

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Cry1Ac GITIQQGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
gi|229 DITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIY
700 710 720 730 740 750

Cry1Ac 770 780 790 800 810 820
SIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
gi|229 LIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHH
760 770 780 790 800 810

Cry1Ac 830 840 850 860 870 880
SHHFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
gi|229 SHHFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGYARLGNLEFLEENPLLGEALARVKRAEK
820 830 840 850 860 870

Cry1Ac 890 900 910 920 930 940
KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYL
gi|229 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAKRVHSIREAYL
880 890 900 910 920 930

Cry1Ac 950 960 970 980 990 1000
PELSVIPGVNAALFEFELEGRIPTAFSLYDARNVIKNGDFNNGLSWVKGHVDEVEQNNQ
gi|229 PELSVIPGVNAALFEFELEGRIPTAFSLYDARNVIKNGDFNNGLSWVKGHVDEVEQNNH
940 950 960 970 980 990

Cry1Ac 1010 1020 1030 1040 1050 1060
RSVLVPEWEAEVSVQEVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVE
gi|229 RSVLVVPEWEAEVSVQEVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIEDNTDELKFSNCVE
1000 1010 1020 1030 1040 1050

Cry1Ac 1070 1080 1090 1100 1110 1120
EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRENPN
gi|229 EEVYPNNTVTCNNYTATQEEHEGTYTSRNRGYDEAYESNSVHASVYEEKSYTDRRENPN
1060 1070 1080 1090 1100 1110

Cry1Ac 1130 1140 1150 1160 1170 1180
CEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|229 CESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120 1130 1140 1150 1160 1170

>>gi|40257|emb|CAA37933.1| crystal protein [Bacillus thu (1171 aa)
initn: 4639 init1: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0
Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap
(5-1182:1-1171)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|402 MEIVNNQNCVQPNYNCLNPNENEILDIERSNST-VATNIALEISRLLASA-TPIGGI
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120

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Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
gi|402 LLGLFDAIWGSIGPSQWDLFLEQIELLIDQKIEEFARNQAISRLEGISSLYGIYTEAFRE  
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|402 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS--RDWIRYNQFR  
gi|402 VFGQAWGFDAIATINSRYNDLTRLIPITYDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR  
180 190 200 210 220 230

Cry1Ac RELTLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLNFDGSRFGSAQGIIEGS-IR  
gi|402 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVINITDYRVGSPFENIENSAIR  
240 250 260 270 280 290

Cry1Ac SPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVA  
gi|402 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRTIAP  
300 310 320 330 340 350

Cry1Ac QLGQGV--YRTLSSTLYRRPFIINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDV  
gi|402 STFPGLNLFYRTLSNPFRRSENI--TPTLGINVVQGVGFI---QPNNAEVLYRSRGTVDV  
360 370 380 390 400

Cry1Ac LDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNI IASD  
gi|402 LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFVWTHHSATNTINPD  
410 420 430 440 450 460

Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR  
gi|402 IITQIPLVKGFRLGGGTSVIKPGPGFTGGDILRRNTIGEFVS----LQVNNINSPITQ-RYR  
470 480 490 500 510

Cry1Ac VRVRYASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLG-NIV  
gi|402 LRFYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPPFSFRANPDII  
520 530 540 550 560 570

Cry1Ac GVRNFSGTAG--VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKLTNVTDYH  
gi|402 RIAEELPIRGELYIDKIELILADATFEEEDLERAQKAVNALFTSTNQLGLKLTVDYDHY  
580 590 600 610 620 630

650 660 670 680 690 700  
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST  
gi|402 IDQVSNLVECLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWGST  
640 650 660 670 680 690

710 720 730 740 750 760  
Cry1Ac GITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY  
gi|402 DITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIY  
700 710 720 730 740 750

770 780 790 800 810 820  
Cry1Ac SIRYNKHEHTVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH  
gi|402 LIRYNKHEHTVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH  
760 770 780 790 800 810

830 840 850 860 870 880  
Cry1Ac SHHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK  
gi|402 SHHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGYARLGNLEFLEENPLLGEALARVKRAEK  
820 830 840 850 860 870

890 900 910 920 930 940  
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYL  
gi|402 KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYL  
880 890 900 910 920 930

950 960 970 980 990 1000  
Cry1Ac PELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQ  
gi|402 PELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNH  
940 950 960 970 980 990

1010 1020 1030 1040 1050 1060  
Cry1Ac RSVLVVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVCE  
gi|402 RSVLVVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIEDNTDELKFSNCVCE  
1000 1010 1020 1030 1040 1050

1070 1080 1090 1100 1110 1120  
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRENPE  
gi|402 EEVYPNNTVTCNNYATQEEHEGTYTSRNRGYDEAYESNSVHASVYEEKSYTDRRENPE  
1060 1070 1080 1090 1100 1110

1130 1140 1150 1160 1170 1180  
Cry1Ac CEFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|402 CESNRGYDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
1120 1130 1140 1150 1160 1170

>>gi|40282|emb|CAA39609.1| crystal protein [Bacillus thu (1171 aa)  
initn: 4639 initl: 3141 opt: 5369 Z-score: 6322.0 bits: 1181.8 E(): 0  
Smith-Waterman score: 5421; 71.597% identity (84.370% similar) in 1190 aa overlap  
(5-1182:1-1171)



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1120      1130      1140      1150      1160      1170
>>gi|160221245|gb|ABX11258.1| Cry1Ea [Bacillus thuringie (1171 aa)
  initn: 4631 initl: 3138 opt: 5353 Z-score: 6303.1 bits: 1178.3 E(): 0
Smith-Waterman score: 5405; 71.513% identity (84.118% similar) in 1190 aa overlap
(5-1182:1-1171)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . . . . .
gi|160  MEIVNQNQCVPYINCLNPNENEIILDIERSNST-VATNIALEISRPLASA-TPIGGI
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      . . . . .
gi|160  LLGLFDAIWGSIGPSQWDLFLQIELLIDQKIEEFARNQAIISRLEGLSSLYGIYTEAFRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi|160  WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

      190     200     210     220     230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS--RDWIRYNQFR
      . . . . .
gi|160  VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
      180     190     200     210     220     230

      240     250     260     270     280     290
Cry1Ac RELTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPLENFDGFSFRGSAQIEGS-IR
      . . . . .
gi|160  RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVINITDYRVGSPFENIENSAR
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac SPHLMIDILNSITITDAHRGEYIYWSGHQIMASPVGFSGPEPTFPFYGTMGNAAPQQRIVA
      . . . . .
gi|160  SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG-SSQVITTPQYGITANAEPRTIAP
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac QLQGV---YRLLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSNLSAVYRKSQTVDS
      . . . . .
gi|160  STFPGLNLFYRSLNPFRRSENI-TPTLGINVVQGVGFI---QPNAEVLVRSRGTVDVS
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac LDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASD
      . . . . .
gi|160  LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFVWTHHSATNTINPD
      410     420     430     440     450     460

      480     490     500     510     520     530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYR
      . . . . .
gi|160  IITQIPLVKGFRLLGGTTSVIKPGFTGGDILRRNTIGFVS----LQVNSINPITQ-RYR

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      470      480      490      500      510
Cry1Ac VVRVRYASVTPIHLNVNWNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
      . . . . .
gi|160  LRFRYASSRDARITVAIGGQIRVDMTLEKTMEIGESLTSRFTSYTNFNSPFRANPDII
      520     530     540     550     560     570

      600     610     620     630     640
Cry1Ac GVRNFGSTAG--VIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
      . . . . .
gi|160  RIAEELPIRGGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
      580     590     600     610     620     630

      650     660     670     680     690     700
Cry1Ac IDQVSNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGS
      . . . . .
gi|160  IDQVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGGS
      640     650     660     670     680     690

      710     720     730     740     750     760
Cry1Ac GITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKILKAFTRYQLRGIYEDSQDLEIY
      . . . . .
gi|160  DITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKILKAYTRYELRGIYEDSQDLEIY
      700     710     720     730     740     750

      770     780     790     800     810     820
Cry1Ac SIRYNKHEHTVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
      . . . . .
gi|160  LIRYNKHEHTVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
      760     770     780     790     800     810

      830     840     850     860     870     880
Cry1Ac SHHFLSDIDVGTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
      . . . . .
gi|160  SHHFLSDIDVGTDLNEDLGVVWIFKIKTQDGYARLGNLEFLEEKPLVGEALARVKRAEK
      820     830     840     850     860     870

      890     900     910     920     930     940
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYL
      . . . . .
gi|160  KWRDKCEKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYL
      880     890     900     910     920     930

      950     960     970     980     990     1000
Cry1Ac PELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEQNNQ
      . . . . .
gi|160  PELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEQNNH
      940     950     960     970     980     990

      1010    1020    1030    1040    1050    1060
Cry1Ac RSVLVVPEWAEVSEQEVRVCPGRGYILRVTAIYKEGYGEGCVTTHEIENNTDELKFSNCV
      . . . . .
gi|160  RSVLVVPEWAEVSEQEVRGCPGRGYILRVTAIYKEGYGEGCVTTHEIEDNTDELKFSNCV
      1000    1010    1020    1030    1040    1050

      1070    1080    1090    1100    1110    1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA-PSVPADYASVYEEKSYTDGRREN
      . . . . .

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Cry1Ac YLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHDVVEEQN
gi|598 YLPELSVIPGVNVDIFEEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNKGVHDVVEEQN
950 960 970 980 990 1000

1010 1020 1030 1040 1050 1060
Cry1Ac NQRSVLVVPWEAEVSEVVRVCPGRGYILRVITAYKEGYEGCVTIIHEIENNTDELKFSNC
gi|598 NHRSLVVPWEAEVSEVVRVCPGRGYILRVITAYKEGYEGCVTIIHEIENNTDELKFSNC
1010 1020 1030 1040 1050 1060

1070 1080 1090 1100 1110 1120
Cry1Ac VEEIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDG
gi|598 VEEIYPNNTVTCNDYTANQEYGGAYTSRNRGYDEYGSNSVADYASVYEEKSYTDG
1070 1080 1090 1100 1110 1120

1130 1140 1150 1160 1170 1180
Cry1Ac RRENPCFNRYRDTYPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|598 RRDNPCESNRYGDTYPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170 1180

>>gi|5987863|gb|AAE17028.1| Sequence 25 from patent US 5 (1174 aa)
initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|598 MENNIQ-NQCVPNCLNNEPEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGV
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIWIWGFQPSQWDAFLVQIEQLINQRIEIEFARNQAI SRLEGLSNLYQIYAESPFE
gi|598 AFGLFDLIWGFITPDSWLSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLSVYVQAANLHLSVLRDVS
gi|598 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVA
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|598 SPGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRRD
180 190 200 210 220 230

250 260 270 280 290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLEN--FDGSRFGSAQGIIEGSIKRS
gi|598 TLTVLDIVALFPNVDVRYPIQTSSQLTREIYTSVIEDSPVSAINPNGFNRAEFGVRRP
240 250 260 270 280 290

300 310 320 330 340 350

Cry1Ac HLMIDLNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQL
gi|598 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRRINFPSYGVF-NPGGAIWIADDE
300 310 320 330 340 350

360 370 380 390 400 410
Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQLLSV-LDGTEFAYGTSSNLPASAVYRKSQVTVDSLDEI
gi|598 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360 370 380 390 400

420 430 440 450 460 470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|598 PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTINTIDPERITQ
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVR
gi|598 IPLVKAHTLQSGTTVVRGPGFTGGDLILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
470 480 490 500 510 520

540 550 560 570 580 590
Cry1Ac YASVTPIHNLVNWGNSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|598 YASTTNLRIVYTVAGRIRIFAGQFNKMTMDTGDPLTFQSFYATINTAFTFPMQSSFTVGA
530 540 550 560 570 580

600 610 620 630 640 650
Cry1Ac RNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTINQLGLKTNVTDYHIDQV
gi|598 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQV
590 600 610 620 630 640

660 670 680 690 700 710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|598 SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
650 660 670 680 690 700

720 730 740 750 760 770
Cry1Ac QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|598 QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLRIRY
710 720 730 740 750 760

780 790 800 810 820 830
Cry1Ac NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|598 NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
770 780 790 800 810 820

840 850 860 870 880 890
Cry1Ac SLDIDVGCITDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|598 SLDIDVGCITDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830 840 850 860 870 880

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900 910 920 930 940 950  
 Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELS  
 gi|598 KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHRIREAYLPELS  
 890 900 910 920 930 940

960 970 980 990 1000 1010  
 Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNQRSVL  
 gi|598 VIPGVNVDIFEELKGRIFTAFLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNHRSVL  
 950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070  
 Cry1Ac VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIY  
 gi|598 VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIVY  
 1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120  
 Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRRNPC  
 gi|598 PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNP  
 1070 1080 1090 1100 1110 1120

1130 1140 1150 1160 1170 1180  
 Cry1Ac EFNRYGRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|598 ESNRYGYDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1130 1140 1150 1160 1170

>>gi|53932146|gb|AAV00428.1| Sequence 8 from patent US 6 (1174 aa)  
 initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0  
 Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap  
 (5-1182:1-1174)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|539 MENNIQ-NQCVPINCLNNEPEVEILNEER-STGRPLDLSLSTRFLLESEFVPGVGV  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFIPSPQWDAFLVQIEQLINQRIEFAFNQAIISRLEGLSNLYQIYAESFRE  
 gi|539 AFGLFDLIWGFITPSDWLFLQIEQLIEQRLETLENRRAITTLRGLADSYEIIYIEALRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|539 WEANPNNAQLREDVRIQFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 gi|539 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDITYNQGLLENLRGTNTRQWARFNQFRRLD  
 180 190 200 210 220 230

250 260 270 280 290  
 Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--PDGSFRGSAQGLEGSIRSP  
 gi|539 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFGVRRP  
 240 250 260 270 280 290

300 310 320 330 340 350  
 Cry1Ac HLMMDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL  
 gi|539 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPYSYGVF-NPGGAIWAIED  
 300 310 320 330 340 350

360 370 380 390 400 410  
 Cry1Ac GQGVYRTLSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI  
 gi|539 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI  
 360 370 380 390 400

420 430 440 450 460 470  
 Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ  
 gi|539 PPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHR SATPTNTIDPERITQ  
 410 420 430 440 450 460

480 490 500 510 520 530  
 Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR  
 gi|539 IPLVKAHTLQSGTIVVRGPGFTGGDILRRTSGGFAYT--IVNINGQLPQ---RYRARIR  
 470 480 490 500 510 520

540 550 560 570 580 590  
 Cry1Ac YASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV  
 gi|539 YASTTNLRIYVTVAGERIFAGQFNKTMDDTGLTFQSFYATINTAFTFPMSQSSFTVGA  
 530 540 550 560 570 580

600 610 620 630 640 650  
 Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV  
 gi|539 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV  
 590 600 610 620 630 640

660 670 680 690 700 710  
 Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI  
 gi|539 SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINQLDRGRGSDTITI  
 650 660 670 680 690 700

720 730 740 750 760 770  
 Cry1Ac QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY  
 gi|539 QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRY  
 710 720 730 740 750 760

780 790 800 810 820 830  
 Cry1Ac NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHSHF  
 gi|539 NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHSHF  
 770 780 790 800 810 820



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710      720      730      740      750      760
Cry1Ac  780      790      800      810      820      830
NAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
gi|160  NAKHETVNVLTGTSGLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|160  SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS
gi|160  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS
890      900      910      920      930      940

960      970      980      990      1000     1010
Cry1Ac  VIPGVNAAIFFELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVL
gi|160  VIPGVNVDIFFEELKGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNHRSVL
950      960      970      980      990      1000

1020     1030     1040     1050     1060     1070
Cry1Ac  VVPEWEAEVSEVVRVCPGRGYLLRVYTAYKEGYGEGCVTIEIENNTDELKFSNCVVEEYIY
gi|160  VVPEWEAEVSEVVRVCPGRGYLLRVYTAYKEGYGEGCVTIEIENNTDELKFSNCVVEEYIY
1010     1020     1030     1040     1050     1060

1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
gi|160  PNNTVTCNDYTVNQEEYGGAYTSRNRGYDETYGSSNVPADYASVYEEKSYTDGRRDNPC
1070     1080     1090     1100     1110     1120

1130     1140     1150     1160     1170     1180
Cry1Ac  EFNRYGDRYDTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|160  ESNRGGYDTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130     1140     1150     1160     1170

>>gi|3012932|gb|AAC11775.1|I76778 Sequence 8 from patent (1174 aa)
  initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|301  MENNIQ-NQCVPYNCLNNEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGV
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|301  AFGLFDLIWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSVEIYIEALRE

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60      70      80      90      100     110
Cry1Ac  130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|301  WEANPNNAQLREDRVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFREL
gi|301  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTRQWARFNQFRDL
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRFGSAQGIEGSIRSP
gi|301  TLTVLDIVSLFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFVVRPP
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSYGVF-NPGGAIWADED
gi|301  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSYGVF-NPGGAIWADED
300      310      320      330      340      350

360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSTLYRRPFNIGINQQLSV-LDGTEFAYGTSNNLPSAVYRKSGTVDSLDEI
gi|301  PRPFYRTLSSTLYRRPFNIGINQQLSV-LDGTEFAYGTSNNLPSAVYRKSGTVDSLDEI
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|301  PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTIDPERITQ
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
gi|301  IPLVKAHTLQSGTIVVRGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  YASVTPHILNVNWNSSIFSNTPATATSLDLQSSDFGYFESANAFTSSLGN---IVGV
gi|301  YASTTNLRIVTVAGERIFAGQFNKTMDTGDPDLPQSFYSYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|301  DTFSSGNEVYIDRFELIPVPTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI

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gi|301 SNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
650 660 670 680 690 700

Cry1Ac QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
720 730 740 750 760 770

gi|301 QRGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKPYTRYQLRGYIEDSQDLEIYLIRY
710 720 730 740 750 760

Cry1Ac NAKHETVNVPGTGLSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
780 790 800 810 820 830

gi|301 NAKHETVNVLTGSLWPLSVQSPIRKCCEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
770 780 790 800 810 820

Cry1Ac SLDIDVGCCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
840 850 860 870 880 890

gi|301 SLDIDVGCCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830 840 850 860 870 880

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS
900 910 920 930 940 950

gi|301 KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHRIREAYLPELS
890 900 910 920 930 940

Cry1Ac VIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGVHVDVEEQNNQRSVL
960 970 980 990 1000 1010

gi|301 VIPGVNVDIFEEELKGRIFTAFFLYDARNVIKNGDFNNGLSWCNVKGVHVDVEEQNNHRSVL
950 960 970 980 990 1000

Cry1Ac VVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIY
1020 1030 1040 1050 1060 1070

gi|301 VVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVY
1010 1020 1030 1040 1050 1060

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPNP
1080 1090 1100 1110 1120

gi|301 PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNP
1070 1080 1090 1100 1110 1120

Cry1Ac EFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170 1180

gi|301 ESNRGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

>>gi|1610951|gb|AAB13930.1| Sequence 25 from patent US 5 (1174 aa)
initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFQLLESEFVPGAGF
10 20 30 40 50 60

gi|161 MENNIQ-NQCVYPNCLNNPEVEILNEER-STGRLLPLDISLSLTRFLLSEFVPGVGV
10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|161 AFGLFDLIWGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSIEIYIEALRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|161 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
190 200 210 220 230 240

gi|161 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRTNTRQWARFNQFRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQIEGSIKSP
250 260 270 280 290

gi|161 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFVGRPP
240 250 260 270 280 290

Cry1Ac HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF--NPGGAIWIADSD
300 310 320 330 340 350

gi|161 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF--NPGGAIWIADSD
300 310 320 330 340 350

Cry1Ac GQGVYRTLSTLYRRPFNIGINQQLSV-LDGTEFAYGTSSNLPASAVYRKSQGTVDLDEI
360 370 380 390 400 410

gi|161 PRPFYRTLSDPVEVVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360 370 380 390 400

Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
420 430 440 450 460 470

gi|161 PPQDNGSAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410 420 430 440 450 460

Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVR
480 490 500 510 520 530

gi|161 IPLVKAHTLQSGTTVVRGPGFTGGDLRLRTSGGPFAYT--IVNINGQLPQ---RYRARIR
470 480 490 500 510 520

Cry1Ac YASVTPIHLLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
540 550 560 570 580 590

gi|161 YASTTNLRIVYTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMQSSFTVGA
530 540 550 560 570 580

Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
600 610 620 630 640 650



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Cry1Ac YASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|118 YASTNLRIRYVTVAGERIFAGQFNKMTDGLTQSFYSYATINTAFTFPMSSQSSFTVGA
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|118 DTFSSGNEVVIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|118 SNLVDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY
gi|118 QRGDDVFKENYVTLPGTDFDECYPTLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLRIRY
      710      720      730      740      750      760

      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHSHHF
gi|118 NAKHETVNVPGTGSWPLSVQSPIRKCCEPNRCAPHLEWNPDLDCSCRDGEKCAHHSHHF
      770      780      790      800      810      820

      840      850      860      870      880      890
Cry1Ac SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|118 SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      830      840      850      860      870      880

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELS
gi|118 KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHRIREAYLPELS
      890      900      910      920      930      940

      960      970      980      990      1000      1010
Cry1Ac VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEQNNQRSVL
gi|118 VIPGVNVDFEELKGRIFTAFFLYDARNVIKNGDFNNGLSWVNVKGVHDVVEQNNHRSVL
      950      960      970      980      990      1000

      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGECVTHIEIENNTDELKFSNCVVEEVIY
gi|118 VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGECVTHIEIENNTDELKFSNCVVEEVIY
      1010      1020      1030      1040      1050      1060

      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRRENPC
gi|118 PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSSNVPADYASVYEEKSYTDGRRDNPC
      1070      1080      1090      1100      1110      1120

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      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRRGYRDTPLPVGYVTKELEYFPETDKVWVIEIGETEGTFIVDSVELLLMEE
gi|118 ESNRRGYDYDTPLPAGYVTKELEYFPETDKVWVIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170

>>gi|142758|gb|AAA22348.1| insecticidal crystal protein (1174 aa)
  initn: 4718 init1: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|142 MENNIQ-NQCVPYNCLNNPEVEILNEER-STGRRLPLDISLSLTLRFLLEFVPGVGV
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|142 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|142 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|142 SFGQWGLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLLENLRGTNTRQWARFNQFRDL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLEN--FDGSFRGSAQGIIEGSIKSP
gi|142 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSNANIPNGFNRAEFVRRPP
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVGVF-NPGGAIWADEAD
gi|142 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVGVF-NPGGAIWADEAD
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQLSV-LDGTFAFGTSSNLPSAVYRKSQGVVDSLDEI
gi|142 PRPFYRTLSLSDPVFVRG---GFGNPHYVGLRGLVAFQVQ-TGTN-HTRFTNRSQGVVDSLDEI
      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|142 PPQDMSGAPWNVDYSHVLNHVTVFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460

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480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR
gi|142  IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  YASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|142  YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|142  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
gi|142  SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY
gi|142  QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKPYTRYQLRGIYEDSQDLEIYLYRY
710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|142  NAKHETVNVLTGSLWPLSVQSPIRKCCEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
gi|142  SLDIDVGCTDLNEDLDVWVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS
gi|142  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHRIREAYLPELS
890      900      910      920      930      940

960      970      980      990      1000      1010
Cry1Ac  VIPGVNAAFEELEGRIPTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVL
gi|142  VIPGVNVDIFEEELKGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNHRSVL
950      960      970      980      990      1000

1020     1030     1040     1050     1060     1070
Cry1Ac  VVPEWEAEVVSQEVVRCPRGYILLRVYAYKEGYGECVTHIEIENNTDELKFSNCVVEEVIY
gi|142  VVPEWEAEVVSQEVVRCPRGYILLRVYAYKEGYGECVTHIEIENNTDELKFSNCVVEEVIY
1010     1020     1030     1040     1050     1060

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1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCP
gi|142  PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNCP
1070     1080     1090     1100     1110     1120

1130     1140     1150     1160     1170     1180
Cry1Ac  EPNRGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|142  ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130     1140     1150     1160     1170

>>gi|34423559|gb|AAQ68988.1| Sequence 8 from patent US 5 (1174 aa)
initn: 4718 init1: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|344  MENNIQ-NQCVPNCLNNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGVG
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
gi|344  AFGLFDLIWGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIYIALRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|344  WEANPNNAQLREDRVIRFANTDDALITAINNFTLTSEIPLLSVYVQAAANLHLSLRLDAV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
gi|344  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRTNTRQWARFNQFRRLD
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRFGSAQIEGSIKRS
gi|344  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFVGRVP
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  HLMDDILNSITITYDAHRGEYYWSGHQIMASPVGFGSGPEFTFPYLGTMGNAAPQQRIVAQL
gi|344  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADSD
300     310     320     330     340     350

360     370     380     390     400     410
Cry1Ac  GQGVRVYRSLSTLYRPFNIGINNQLSV-LDGTFAFGTSSNLPSAVYRKSQGVDSLDEI
gi|344  PRPFYRSLSDPVPVVRG--GFGNPHYVLGLRGVAFQQ-TGTN-HTRFTFRNSGTDLSLDEI
360     370     380     390     400

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420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRSLHVMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|344  PPQDNSGAPWNDYSHVLNHVTFVVRWPGELSGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR
gi|344  IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPAYT--IVNINGQLPQ--RYRARIR
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGFESANAFTSSLGN--IVGV
gi|344  YASTTNLRIYVTVAGERIFAGQFNKTMDDPLTFQSFYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac  RNFVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|344  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDVTDYHIDQV
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
gi|344  SNLVDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY
gi|344  QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKPYTRYQLRGIYEDSQDLEIYLIRY
710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
gi|344  NAKHETVNVLTGTGLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|344  SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELS
gi|344  KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHRIREAYLPELS
890      900      910      920      930      940

960      970      980      990      1000      1010
Cry1Ac  VIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVL
gi|344  VIPGVNVDIFEELKGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNHRSVL

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950      960      970      980      990      1000
Cry1Ac  VVPEWEAEVSVQEVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEII
gi|344  VVPEWEAEVSVQEVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEII
1010     1020     1030     1040     1050     1060     1070

1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
gi|344  PNNTVTCNDYTVNQEEYGGAYTSRNRGYDETYGSNSVPADYASVYEEKSYTDGRRDNPC
1070     1080     1090     1100     1110     1120

1130     1140     1150     1160     1170     1180
Cry1Ac  EFNRGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|344  ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
1130     1140     1150     1160     1170

>>gi|12819676|gb|AAE47790.1| Sequence 8 from patent US 6 (1174 aa)
initn: 4718 init1: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128  MENNIQ-NQCVPYNCLNPEVEILNEER-STGRLLPDLISLSLTRLLEFVPGVGV
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFIPSPQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
gi|128  AFGLFDLIWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
gi|128  WEANPNNAQLREDRVIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLRLDVA
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWRIRYNQFRREL
gi|128  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLNLRGTNTRQWARFNQFRDL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIIEGSIKRP
gi|128  TLTVLDIVSLFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGVRPP
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPSTYGVF-NPGGAIWADED
gi|128  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPSTYGVF-NPGGAIWADED

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300      310      320      330      340      350
360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTAFYAGTSSNLPSAVYRKSQGTVDLSLDEI
gi|128  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360      370      380      390      400
420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|128  PPQDNMGAPWNDYSHVLNHNVTFRWRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410      420      430      440      450      460
480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR
gi|128  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470      480      490      500      510      520
540      550      560      570      580      590
Cry1Ac  YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|128  YASTNLRLIYVTVAGERIFAGQFNKTMDTGDLTFQSFYATINTAFTFPPMSQSSFTVGA
530      540      550      560      570      580
600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFFFIPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|128  DTFSSGNEVYIDRFEIIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQV
590      600      610      620      630      640
660      670      680      690      700      710
Cry1Ac  SNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|128  SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
650      660      670      680      690      700
720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|128  QRGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKPYTRYQLRGYIEDSQDLEIYLIRY
710      720      730      740      750      760
780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGSWPLSAQSPIKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHF
gi|128  NAKHETVNVLTGGSWPLSVQSPIKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHF
770      780      790      800      810      820
840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
gi|128  SLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
830      840      850      860      870      880
900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS

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gi|128  KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHRIREAYLPELS
890      900      910      920      930      940
960      970      980      990      1000      1010
Cry1Ac  VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQORSVL
gi|128  VIPGVNVDIFEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNHRSVL
950      960      970      980      990      1000
1020      1030      1040      1050      1060      1070
Cry1Ac  VVPEWAEVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEIY
gi|128  VVPEWAEVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEVY
1010      1020      1030      1040      1050      1060
1080      1090      1100      1110      1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|128  PNNTVTCNDYTVNQEEYGGAYTSRNRGYDETYGSNSVVPADYASVYEEKSYTDGRRDNPC
1070      1080      1090      1100      1110      1120
1130      1140      1150      1160      1170      1180
Cry1Ac  EFNRGYRDYTPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|128  ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1130      1140      1150      1160      1170
>>gi|1608057|gb|AAB11012.1| Sequence 25 from patent US 5 (1174 aa)
initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|160  MENNIQ-NQCVYINCLNNEVEILNEER-STGRPLDLSLSTRFLLESEFVPGVGV
10      20      30      40      50
70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|160  AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSSEIYIEALRE
60      70      80      90      100      110
130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|160  WEANPNNAQLREDVIRFANTDDALITAINNF'TLTSFEIPLLSVYVQAANLHLSLRDAV
120      130      140      150      160      170
190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
gi|160  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRDL
180      190      200      210      220      230
250      260      270      280      290
Cry1Ac  TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--PDGSFRGSAQGLEGSIRSP

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gi|160 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVSSVIEDSPVSANIPNGFNRAEFGVRPP
      240      250      260      270      280      290
      300      310      320      330      340      350
Cry1Ac HLM DILNSIT IYTD AHRGEY YW SGHQIMAS PVG FSGPEFT FPLYGTMGNAAPQQRIVAQL
      .....
gi|160 HLMDFMNSL FVTAET VRSQTVWGGH--LVSSRNTAGNRINFPSYGVF--NPGGAIWIADSD
      300      310      320      330      340      350
      360      370      380      390      400      410
Cry1Ac GQGVYRTL SSSLTYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKS GTVDSLDEI
      .....
gi|160 PRPFYRTL SDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGYN-HTRTFRNSGTIDSLDEI
      360      370      380      390      400
      420      430      440      450      460      470
Cry1Ac PPQNNVPPR QGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
      .....
gi|160 PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460
      480      490      500      510      520
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      .....
gi|160 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
      470      480      490      500      510      520
      540      550      560      570      580      590
Cry1Ac YASVTP IHLNWNWGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      .....
gi|160 YASTNLR IYVTVAGERIFAGQFNKMTDGDPLTFQSPSYATINTAFTFPMSQSSFTVGA
      530      540      550      560      570      580
      600      610      620      630      640      650
Cry1Ac RNFSGTAGVI IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      .....
gi|160 DTFSSGNEVY IDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
      590      600      610      620      630      640
      660      670      680      690      700      710
Cry1Ac SNLVTYL SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      .....
gi|160 SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
      650      660      670      680      690      700
      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTL SGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGIEDSQDLEIYSIRY
      .....
gi|160 QRGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKPYTRYQLRGIEDSQDLEIYLIRY
      710      720      730      740      750      760
      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGT GSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
      .....
gi|160 NAKHETVNVLTGSLWPLSVQSPIRKCCEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
      770      780      790      800      810      820
      840      850      860      870      880      890
Cry1Ac SLDIDVGC TDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD

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      830      840      850      860      870      880
gi|160 SLDIDVGC TDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELS
      .....
gi|160 KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHRIREAYLPELS
      890      900      910      920      930      940
      960      970      980      990      1000      1010
Cry1Ac VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVL
      .....
gi|160 VIPGVNVDIFEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVL
      950      960      970      980      990      1000
      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIY
      .....
gi|160 VVPEWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIY
      1010      1020      1030      1040      1050      1060
      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNDC
      .....
gi|160 PNNTVTCNDYTVNQEEYGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNC
      1070      1080      1090      1100      1110      1120
      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDYTPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|160 ESNRGYDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170
>>gi|33734265|gb|AAQ38646.1| Sequence 8 from patent US 6 (1174 aa)
      initn: 4718 init1: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
      Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
      (5-1182:1-1174)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      .....
gi|337 MENNIQ-NQCVPYNCLNNEVEILNEER-STGRPLDLSLSLTRFLLEFVPGVGV
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIE EFARNQAI SREGLSNLYQIYAESFRE
      .....
gi|337 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYI EALRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTN PALREEMRIQFNDMNSALTTAIP LFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|337 WEANPNNAQLRE DVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDH AVRWYNTGLERWGPDSRDWIRYNQFRREL

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Cry1Ac 70 80 90 100 110 120
VLGLVDIWIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|597 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|597 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRDL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLEN--FDGSFRGSAQIEGSI RSP
gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPP
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350
HLM DILNSITIIYTD AHRGEYIYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQL
gi|597 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF--NPGGAIWIADED
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400 410
GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEI
gi|597 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGNT-HTRTFRNSGTIDSLDEI
360 370 380 390 400

Cry1Ac 420 430 440 450 460 470
PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQ
gi|597 PPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410 420 430 440 450 460

Cry1Ac 480 490 500 510 520 530
IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVR
gi|597 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470 480 490 500 510 520

Cry1Ac 540 550 560 570 580 590
YASVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|597 YASTNLRILYVTVAGERIFAGQFNKTMDTGDPLTFQSF SYATINTAFTFPMSQSSFTVGA
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650
RNFSGTAGVVIDRFFPIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDVYHIDQV
gi|597 DTFSSGNEVYIDRFELIPVPTATFEAEYDLERAQKAVNALFTSINQIGIKTVDVTDVYHIDQV
590 600 610 620 630 640

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Cry1Ac 660 670 680 690 700 710
SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|597 SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITI
650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770
QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|597 QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRY
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830
NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHF
gi|597 NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHHF
770 780 790 800 810 820

Cry1Ac 840 850 860 870 880 890
SLDIDVGCTDLNEDLGWVVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|597 SLDIDVGCTDLNEDLDVWVVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830 840 850 860 870 880

Cry1Ac 900 910 920 930 940 950
KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELS
gi|597 KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHRIREAYLPELS
890 900 910 920 930 940

Cry1Ac 960 970 980 990 1000 1010
VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
gi|597 VIPGVNVDIFEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
950 960 970 980 990 1000

Cry1Ac 1020 1030 1040 1050 1060 1070
VPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIY
gi|597 VPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVY
1010 1020 1030 1040 1050 1060

Cry1Ac 1080 1090 1100 1110 1120
PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|597 PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSNSVPADYASVYEEKSYTDGRRDNPC
1070 1080 1090 1100 1110 1120

Cry1Ac 1130 1140 1150 1160 1170 1180
EFNRYGDRYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|597 ESNRYGDRYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

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>>gi|5973545|gb|AAE12825.1| Sequence 32 from patent US 5 (1174 aa)
initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

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Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|597 MENNIQ-NQCVPYNCLNPEVEILNEER-STGRPLDLSLSLFRLLSEFVPGVGV

Cry1Ac VLGLVDIWIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
gi|597 AFGLFDLWGFITPSDWSLFLQIEQLIEQRLETLELRNRAITTLRGLADSYEIIYIEALRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|597 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL  
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRRLD

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQIEGSIIRSP  
gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRP

Cry1Ac HLMIDLNSITIIYTDHRGEYVSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL  
gi|597 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSPYGVF-NPGGAIWADED

Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI  
gi|597 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI

Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQ  
gi|597 PPQNSGAPWINDYSHVLNHVTFVRWPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ

Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFSTSTRYRVRVR  
gi|597 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR

Cry1Ac YASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV  
gi|597 YASTNLRIRYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMQSSFTVGA

Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV  
gi|597 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQV

Cry1Ac SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTIT  
gi|597 SNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDTIT

Cry1Ac QGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY  
gi|597 QRGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRY

Cry1Ac NAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF  
gi|597 NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF

Cry1Ac SLDIDVGCITDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
gi|597 SLDIDVGCITDLNEDLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYPELS  
gi|597 KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHRIREAYPELS

Cry1Ac VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNRQSVL  
gi|597 VIPGVNVDIFEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNRHSVL

Cry1Ac VVPEWEAEVSQEVRRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYIY  
gi|597 VVPEWEAEVSQEVRRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYVY

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNDC  
gi|597 PNNTVTCNDYTVNQEEYGGAYTSRNRGYDETYGSNSVADYASVYEEKSYTDGRRDNPC

Cry1Ac EFNRRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|597

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gi|597 ESNRGGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1130      1140      1150      1160      1170

>>gi|42682716|gb|AAS28779.1| Sequence 6 from patent US 6 (1174 aa)
  inith: 4718 inilt: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      . . . . .
gi|426  MENNIQ-NQCVPNCLNNPEVEILNEER-STGRPLDISLSLTRLLESEFVPGVGV
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLESLNYQIYAESFRE
      . . . . .
gi|426  AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITLRLGLADSYEIIYIEALRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi|426  WGANPNNAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . . .
gi|426  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPLEN--FDGSRGSAQGIIEGSIRSP
      . . . . .
gi|426  TLTVLDIVALFPNVDVRYPIQTSSQLTREIYTSVIEDSPSANIPNGFNRAEFGVRRPP
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac HLMIDLNSITIIYTDHARGEYVWYSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      . . . . .
gi|426  HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPYGVF-NPGGAIWIAD
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQLSV-LDGTAFAYGTSSNLPASAVYRKSQTVDSLDEI
      . . . . .
gi|426  PRPFYRTLSDDPVFVRG---FGNPHYVLGLRGVAFQQ-TGTTN-HTRTFRNSGTIDSLDEI
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIIASDSITQ
      . . . . .
gi|426  PPQDMSGAPWNDYSHVLNHVTFVVRWPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410     420     430     440     450     460

      480     490     500     510     520     530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNLSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      . . . . .

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gi|426 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520

      540      550      560      570      580      590
Cry1Ac YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSLGN---IVGV
      . . . . .
gi|426  YASTTNLRIYVTVAGERIFAGQFNKMTDITGDPDLTFQSFYSATINTAFTFPMSQSSFTVGA
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      . . . . .
gi|426  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITI
      . . . . .
gi|426  SNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSTDITI
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLSGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
      . . . . .
gi|426  QRGDDVFKENYVTLPGTFDECYPTLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRY
      710      720      730      740      750      760

      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHSHF
      . . . . .
gi|426  NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHSHF
      770      780      790      800      810      820

      840      850      860      870      880      890
Cry1Ac SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      . . . . .
gi|426  SLDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      830      840      850      860      870      880

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS
      . . . . .
gi|426  KREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHRIREAYLPELS
      890      900      910      920      930      940

      960      970      980      990     1000     1010
Cry1Ac VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQRSVL
      . . . . .
gi|426  VIPGVNVDIFEELEKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNHRSVL
      950      960      970      980      990     1000

      1020     1030     1040     1050     1060     1070
Cry1Ac VVPEWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYI
      . . . . .
gi|426  VVPEWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYVY
      1010     1020     1030     1040     1050     1060

      1080     1090     1100     1110     1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVVEEKSYPDGRRENPC

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gi|426 PNNTVTCNDYTANQEEYGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNPC
      1070      1080      1090      1100      1110      1120

      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      : .....
gi|426 ESNRGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170

>>gi|142756|gb|AAA22347.1| cryIF (1174 aa)
  initn: 4718 initl: 3159 opt: 5301 Z-score: 6241.8 bits: 1166.9 E(): 0
Smith-Waterman score: 5301; 69.386% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1174)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      : .....
gi|142 MENNIQ-NQCVPNCLNNPEVEILNEER-STGRPLPLDISLSLRFLLSEFVPGVGV
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      : .....
gi|142 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : .....
gi|142 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
      : .....
gi|142 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRDDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLN--FDGSFRGSAQGIEGSIRSP
      : .....
gi|142 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPSANIPNGFNRAEFGVRRP
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac HLMIDLNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      : .....
gi|142 HLMDFMNSLFTAETVRSQTVWGGH--LVSSRNTAGNRINPFSYGVF--NPGGAIWADED
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac GQGVYRTLSSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPASVYRKSCTVDSLDEI
      : .....
gi|142 PRPFYRTLSDPVFVRG--FGFNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac PPQNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ

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.....
gi|142 PPQDNSGAPWNNDYSHVLNHTVFRWVPEISGSDSWRAPMFSWTHR.SATPNTIDPERITQ
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
      : .....
gi|142 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520

      540      550      560      570      580      590
Cry1Ac YASVTPIHNLVNWGNSIFSNVTPATATSLDNLQSSDFGYFESANAFSTSSLGN--IVGV
      : .....
gi|142 YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMQSSFTVGA
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      : .....
gi|142 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDQV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
      : .....
gi|142 SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGRWGSTDITI
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
      : .....
gi|142 QRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLPYTRYQLRGYIEDSQDLEIYLIRY
      710      720      730      740      750      760

      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF
      : .....
gi|142 NAKHETVNVLTGSLWPLSVQSPIRKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF
      770      780      790      800      810      820

      840      850      860      870      880      890
Cry1Ac SLDIDVGCTDLNEDLVVWVIFKIKTDGCHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      : .....
gi|142 SLDIDVGCTDLNEDLVVWVIFKIKTDGCHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      830      840      850      860      870      880

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYEKAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYLPELS
      : .....
gi|142 KREKLEWETNIVYEKAKESVDALFVNSQYDQLQADTNAMIHAADKRVHRIREAYLPELS
      890      900      910      920      930      940

      960      970      980      990     1000     1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
      : .....
gi|142 VIPGVNVDIFEEELKGRIFTAFFLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
      950      960      970      980      990     1000

      1020     1030     1040     1050     1060     1070

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Cry1Ac VVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEEBEY  
gi|142 VVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEEBEY  
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120  
Cry1Ac PNNTVTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC  
gi|142 PNNTVTCNDYTANQEYEGGAYTSRNRGYDETYGSNSSVPADYASVYEEKSYTDGRRDNPC  
1070 1080 1090 1100 1110 1120

1130 1140 1150 1160 1170 1180  
Cry1Ac EFNRYGRDYTPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|142 ESNRYGYDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1130 1140 1150 1160 1170

>>gi|5973549|gb|AAE12829.1| Sequence 36 from patent US 5 (1175 aa)  
initn: 4790 init1: 1664 opt: 5205 Z-score: 6128.5 bits: 1146.0 E(): 0  
Smith-Waterman score: 5205; 68.487% identity (83.529% similar) in 1190 aa overlap  
(5-1182:1-1175)

10 20 30 40 50 60  
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|597 MENNIQ-NQCVPNCLNPEVEILNEER-STGRPLDLSLSLTRFLLSEFVPGVGV  
10 20 30 40 50

70 80 90 100 110 120  
Cry1Ac VLGLVDIWIWIFGQSDAFVQIEQLINQRIEIEFARNQAI SRLEGLSNLYQIYAESPFE  
gi|597 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE  
60 70 80 90 100 110

130 140 150 160 170 180  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|597 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDVA  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDYNQGLLENLRGINTRQWARFNQFRRLD  
180 190 200 210 220 230

250 260 270 280 290  
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLN--FDGSRGSAQGIIEGSIKRS  
gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRP  
240 250 260 270 280 290

300 310 320 330 340 350  
Cry1Ac HLMIDLNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQL  
gi|597 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSYGVF-NPGGAIWIADED  
300 310 320 330 340 350

360 370 380 390 400 410

Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPASVYRKSQVTDVSLDEI  
gi|597 PRPFYRTLSDPVPFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI  
360 370 380 390 400

420 430 440 450 460 470  
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ  
gi|597 PPQNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ  
410 420 430 440 450 460

480 490 500 510 520 530  
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRV  
gi|597 IPLVKAHTLQSGTTVVRGPGFTGGDLRLRRTSGGPFAYT--IVNINGQLPQ---RYRIR  
470 480 490 500 510 520

540 550 560 570 580 590  
Cry1Ac YASVTPIHLNVNWGNSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV  
gi|597 YASTTNLRIYVTVAGERIFAGQFNKTMDTGDLPTFQSFYSATINTAFTFPMQSSFTVGA  
530 540 550 560 570 580

600 610 620 630 640 650  
Cry1Ac RNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV  
gi|597 DTFSSGNEVYIDRFELIPVTATLEAEYNLERAQEAVALFTSPNQLGIKTNVTDYHIDQV  
590 600 610 620 630 640

660 670 680 690 700 710  
Cry1Ac SNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITI  
gi|597 SNLVTVLSDEFCLDEKRELSEKVKHANGRLSDERNLLQDSNFKDINRQPRGGWGGSTGITI  
650 660 670 680 690 700

720 730 740 750 760 770  
Cry1Ac QGGDDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY  
gi|597 QRGDDVFKENYVTLGTFDECYLTLYQKIDESKLPYTRYELRGYIEDSQDLEIYLRIR  
710 720 730 740 750 760

780 790 800 810 820 830  
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF  
gi|597 NAKHETVNVLTGSLWRLSFESSIRKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF  
770 780 790 800 810 820

840 850 860 870 880 890  
Cry1Ac SLDIDVGCIDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEK-PLVGEALARVKRAEKKWR  
gi|597 SLDIDVGCIDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEGRAPLVGEALARVKRAEKKWR  
830 840 850 860 870 880

900 910 920 930 940 950  
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPEL  
gi|597 DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHTADKRVHRIQEAYLPEL  
890 900 910 920 930 940

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          960      970      980      990      1000      1010
Cry1Ac  SVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSV
gi|597  SVIPGVNVGIFEELEKGRIFTAFLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSV
          950      960      970      980      990      1000

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          1020     1030     1040     1050     1060     1070
Cry1Ac  LVVPEWEAEVVSQEVRCVPCGRGYILRVVTAYKEGYGECVTIHEIENNTDELKFSNCFVEEII
gi|597  LVVPEWEAEVVSQEVRCVPCGRGYILRVVTAYKEGYGTGCVTIHEIENNTDELKFSNFVEEIV
          1010     1020     1030     1040     1050     1060

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          1080     1090     1100     1110     1120
Cry1Ac  YPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEAP---SVPADYASVYEEKSYTDGRREN
gi|597  YPNNTVTCDNYTANQEEYGGAYTSCNRGYDETYGNSVVPADYASVYEEKAYTDGRRDNP
          1070     1080     1090     1100     1110     1120

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          1130     1140     1150     1160     1170     1180
Cry1Ac  CEFNRGYRDYTPPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|597  CESNRGYGDYTPPLPAGYVTKQLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1130     1140     1150     1160     1170

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>>gi|5987872|gb|AAE17037.1| Sequence 36 from patent US 5 (1175 aa)  
 initn: 4790 initl: 1664 opt: 5205 Z-score: 6128.5 bits: 1146.0 E(): 0  
 Smith-Waterman score: 5205; 68.487% identity (83.529% similar) in 1190 aa overlap  
 (5-1182:1-1175)

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          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSFVPGAGF
gi|598  MENNIQ-NQCVPYNCLNNEPEVEILNEER-STGRPLDISLSTRFLLESEFVPGVGV
          10      20      30      40      50

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          70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEFAFNQAIISRLEGLSNLYQIYAESFRE
gi|598  AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
          60      70      80      90      100     110

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          130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQANLHLSVLRDVS
gi|598  WEANPNNAQLREDVRIQFANTDDALITAINNFTLTSFEIPLLSVYVQANLHLSLLRDAV
          120     130     140     150     160     170

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          190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|598  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGNTNRQWARFNQFRRLD
          180     190     200     210     220     230

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          250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLEN--FDGSRFGSAQIEGSIKRS
gi|598  TLTVLDIVALFPNVDVRYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRPP
          240     250     260     270     280     290

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          300      310      320      330      340      350
Cry1Ac  HLMDDILNSITITDAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|598  HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPPGAIWIAD
          300      310      320      330      340      350

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          360      370      380      390      400      410
Cry1Ac  GQGVYRTLSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI
gi|598  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
          360      370      380      390      400

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          420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRSLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|598  PPQDNGAPWNDYSHLVNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
          410      420      430      440      450      460

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          480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVR
gi|598  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGFAYT--IVNINGQLPQ---RYRARIR
          470      480      490      500      510      520

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          540      550      560      570      580      590
Cry1Ac  YASVTPIHNLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|598  YASTTNLRIVYTVAGERIFAGQFNKMTDGTPLTFQSFYSATINTAFTFPMSSQSFYVGA
          530      540      550      560      570      580

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          600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|598  DTFSSGNEVYIDRFELIPVTATLEAEYNLERAQEAVALFTSPNQLGIKTNVTDYHIDQV
          590      600      610      620      630      640

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          660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITI
gi|598  SNLVTCLSDEFCLDEKRELSEKVKHANGLSDERNLLQDSNFKDINRQPDGRGGWGGSTGITI
          650      660      670      680      690      700

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          720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|598  QRGDDVFKENYVTLGTFDECYLYLYQKIDESKLFKPYTRYELRGYIEDSQDLEIYLIRY
          710      720      730      740      750      760

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          780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHF
gi|598  NAKHETVNVLTGSLWRLSFESSIRKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHHF
          770      780      790      800      810      820

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          840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLVWVIFKIKTQDGHARLGNLEFLEEK-PLVGEALARVKRAEKKWR
gi|598  SLDIDVGCIDLNEDLVWVIFKIKTQDGHARLGNLEFLEEK-PLVGEALARVKRAEKKWR
          830      840      850      860      870      880

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760      770      780      790      800      810
Cry1Ac  820      830      840      850      860      870
CSCRDGKCAHSHHFLSLDIVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLV
gi|151  820      830      840      850      860      870
CSCRDGKCAHSHHFTLIDVGCSDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLL

880      890      900      910      920      930
Cry1Ac  GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
gi|151  GEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAA

880      890      900      910      920      930
Cry1Ac  880      890      900      910      920      930
DKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNV
gi|151  DKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNGLLCWNV

940      950      960      970      980      990
Cry1Ac  DKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNV
gi|151  DKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNGLLCWNV

1000     1010     1020     1030     1040     1050
Cry1Ac  KGHVDVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVYTAYKEGYGEGCVTIHEIEN
gi|151  KGHVDVEEQNNHRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVYTAYKEGYGEGCVTIHEIED

1060     1070     1080     1090     1100     1110
Cry1Ac  NTDELKFSNCVVEEYIPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYAS
gi|151  NTDELKFSNCVVEEYIPNNVTVCNNYTGQEEYEGYTSRNQGYDEAYGNNSVPADYAS

1120     1130     1140     1150     1160     1170
Cry1Ac  VYEEKSYTDGRENPCFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVD
gi|151  VYEEKSYTDGRENPCESNRGYGDYTPPLVAGYVTKDLEYFPETDKVWIEIGETEGTFIVD

1180
Cry1Ac  SVELLLMEE
gi|151  SVELLLMEE
1180

>>gi|2298888|emb|CAA02751.1| unnamed protein product [un (1186 aa)
  initn: 4599 initl: 3093 opt: 5176 Z-score: 6094.2 bits: 1139.6 E(): 0
Smith-Waterman score: 5423; 70.954% identity (83.734% similar) in 1205 aa overlap
(5-1182:1-1186)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|229  MEIVNQNQCVPYNCLNPNENEILDIERSNST-VATNIAEISRLLASA-TPIGGI

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|229  LLGLFDAIWGSIQPSQWDLFLEQIEELLIDQKIEEFARNQAISRLEGISSLYGIYTEAFRE

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60      70      80      90      100     110
Cry1Ac  130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|229  WEADPTNPALKEEMRTQFNDMNSILVTAIPLFVQNYQVPLLSVYVQAANLHLSVLRDVS

120      130      140      150      160      170
Cry1Ac  190      200      210      220      230
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS---RDWIRYNQFR
gi|229  VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR

180      190      200      210      220      230
Cry1Ac  240      250      260      270      280      290
RELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDFGSRGSAQIEGS-IR
gi|229  RELTISVLDIISFFRNYDSRLYPIPTSSQLTREYVYTDPVINITDYRVGSPFENIENSAIR

240      250      260      270      280      290
Cry1Ac  300      310      320      330      340      350
SPHLMIDLNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|229  SPHLMDFLNNLTDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRTIAP

300      310      320      330      340      350
Cry1Ac  360      370      380      390      400      410
QLGQGV---YRSLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDS
gi|229  STFPGLNLFYRSLSNFFRSENI--TPTLGINVVQGVGFI---QPNAEVLVRSRGTVDS

360      370      380      390      400
Cry1Ac  420      430      440      450      460      470
LDEIPPQNNVPPRGFSHRLSHVSMFRSGFSSSVSIIIRAPMFSWIHRSAEFNIIIASD
gi|229  LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWVTHHSATNTNTINPD

410      420      430      440      450      460
Cry1Ac  480      490      500      510      520      530
SITQIPAVKGNFLNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|229  IITQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFPDFVS----LQVNINSPIQ-RYR

470      480      490      500      510
Cry1Ac  540      550      560      570      580
VRVRYASVTPIHNLVNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTS
gi|229  LRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLOKTMIEIGENLTSRTFRYTDFFSNPFFS

520      530      540      550      560      570
Cry1Ac  590      600      610      620      630
SLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTN
gi|229  RANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSN

580      590      600      610      620      630
Cry1Ac  640      650      660      670      680      690
QLGLKTNVTDYHLDQVSNLVTYLSDEFCLDEKRELEKVKHAKRLSDEKRLNLLQDSNFKDI
gi|229  QLGLKTNVTDYHLDQVSNLVTYLSDEFCLDEKRELEKVKHAKRLSDEKRLNLLQDSNFKDI

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Cry1Ac LDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASD
gi|399 LNLELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWTHHSATNTNTINPD
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYR
gi|399 IITQIPLVKGFRVWGGSVITGPGFTGGDILRRNTFGDFVS----LQVNINSPITQ-RYR
470 480 490 500 510

540 550 560 570 580
Cry1Ac VRVRYASVTPIHLLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTS
gi|399 LRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYDFSNPFSF
520 530 540 550 560 570

590 600 610 620 630
Cry1Ac SLG-NIVGVRN---F---SGTAG-VIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTN
gi|399 RANPDIIGLISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSN
580 590 600 610 620 630

640 650 660 670 680 690
Cry1Ac QLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDI
gi|399 QIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGI
640 650 660 670 680 690

700 710 720 730 740 750
Cry1Ac NRQPERGGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLR
gi|399 NRQPDGRWGRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELR
700 710 720 730 740 750

760 770 780 790 800 810
Cry1Ac GYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|399 GYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL
760 770 780 790 800 810

820 830 840 850 860 870
Cry1Ac CSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLV
gi|399 CSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLL
820 830 840 850 860 870

880 890 900 910 920 930
Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
gi|399 GEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRQLQVDTNIAMIHAA
880 890 900 910 920 930

940 950 960 970 980 990
Cry1Ac DKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNV
gi|399 DKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNV
940 950 960 970 980 990

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1000 1010 1020 1030 1040 1050
Cry1Ac KGHVDVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVYAYKEGYEGCVTIHEIEN
gi|399 KGHVDVEEQNNHRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVYAYKEGYEGCVTIHEIED
1000 1010 1020 1030 1040 1050

1060 1070 1080 1090 1100 1110
Cry1Ac NTDELKFSNCVEEYIPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYAS
gi|399 NTDELKFSNCVEEYVNNVTVCNNYTGTEYEGTYTSRNQGYDEAYGNNPSVPADYAS
1060 1070 1080 1090 1100 1110

1120 1130 1140 1150 1160 1170
Cry1Ac VYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVD
gi|399 VYEEKSYTDGRENPCESNRGYDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVD
1120 1130 1140 1150 1160 1170

1180
Cry1Ac SVELLLMEE
gi|399 SVELLLMEE
1180

>>gi|15110440|gb|AAE68104.1| Sequence 15 from patent US (1156 aa)
initn: 6962 initl: 5108 opt: 5122 Z-score: 6030.7 bits: 1127.8 E(): 0
Smith-Waterman score: 7316; 93.909% identity (95.854% similar) in 1182 aa overlap
(5-1182:1-1156)

10 20 30 40 50 60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|151 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIE EFARNQAISRLEGLSNLYQIYAESFRE
gi|151 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIE EFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|151 TLTVLDIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

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          310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|151 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPPQ
gi|151 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|151 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
          420      430      440      450      460      470

          490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|151 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
          480      490      500      510      520      530

          550      560      570      580      590      600
Cry1Ac TPIHLNVNWGNSISFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|151 TPIHLNVNWGNSISFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
          540      550      560      570      580      590

          610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTLY
gi|151 GVIIDRFEFIPVTATLEAESDLERAKAVNALFTSSNQIGLKTVDYHIDRVSNLVECL
          600      610      620      630      640      650

          670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
gi|151 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGGDDVDF
          660      670      680      690      700      710

          730      740      750      760      770      780
Cry1Ac KENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
gi|151 KENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAKHETV
          720      730      740      750      760      770

          790      800      810      820      830      840
Cry1Ac NVPGTGSLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEGKCAHSHHSHSLDIDVG
gi|151 NVPGTGSLWPLSAPSPIGK-----AHSHHSHSLDIDVG
          780      790      800      810

          850      860      870      880      890      900
Cry1Ac CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|151 CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
          820      830      840      850      860      870

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          910      920      930      940      950      960
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
gi|151 ETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
          880      890      900      910      920      930

          970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQSVLVPWEWA
gi|151 AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNHRSVLVPWEWA
          940      950      960      970      980      990

          1030      1040      1050      1060      1070      1080
Cry1Ac EVSQEVRVCPGRGYLLRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVNNVTVC
gi|151 EVSQEVRVCPGRGYLLRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYVNNVTVC
          1000      1010      1020      1030      1040      1050

          1090      1100      1110      1120      1130
Cry1Ac NDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPFNRYR
gi|151 NDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESNRYG
          1060      1070      1080      1090      1100      1110

          1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|151 DYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1120      1130      1140      1150

>>gi|42682718|gb|AAS28781.1| Sequence 15 from patent US (1156 aa)
initn: 6962 init1: 5108 opt: 5122 Z-score: 6030.7 bits: 1127.8 E(): 0
Smith-Waterman score: 7316; 93.909% identity (95.854% similar) in 1182 aa overlap
(5-1182:1-1156)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|426 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLYQIYAESFRE
gi|426 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|426 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
gi|426 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWVRYNQFREL
          180      190      200      210      220      230

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                250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|426  TLTVLDIVALFPNYDSRRYPPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIERSIRSPHL
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVaQLGQ
gi|426  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVaQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac  GvYrTLsStLYRRPFNIGInnQQLsVLDGTEfAYGTSSnLPSAVYrKSGTVDsLDEIppQ
gi|426  GvYrTLsStLYRRPFNIGInnQQLsVLDGTEfAYGTSSnLPSAVYrKSGTVDsLDEIppQ
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFsHrLshVSMFRSGfSNSSVSIIRAPMfSWIHRSaEFNNIaASDSITQIPa
gi|426  NNNVPPRQGFsHrLshVSMFRSGfSNSSVSIIRAPMfSWIHRSaEFNNIaASDSITQIPa
                420      430      440      450      460      470

                490      500      510      520      530      540
Cry1Ac  VKGNfLfnGsvISGPGfTGdLVRlNssGnNIQnrgYIEVPIHfPSTsTrYrVrVRYaSV
gi|426  VKGNfLfnGsvISGPGfTGdLVRlNssGnNIQnrgYIEVPIHfPSTsTrYrVrVRYaSV
                480      490      500      510      520      530

                550      560      570      580      590      600
Cry1Ac  TPIHLNvNwGnSSIFsNTvPAtATsLdNLQSSDFGfYfESANaFTSSLGNIVGVRNfSGTAs
gi|426  TPIHLNvNwGnSSIFsNTvPAtATsLdNLQSSDFGfYfESANaFTSSLGNIVGVRNfSGTAs
                540      550      560      570      580      590

                610      620      630      640      650      660
Cry1Ac  GVIIDRFefIPvTATLEaEYNLERAQKAVNALFTSTnQLGLKtNvDyHIDQVSNLVtYL
gi|426  GVIIDRFefIPvTATLEaESDLERAQKAVNALFTSSnQIGLkTDvDyHIDrVSNLVECL
                600      610      620      630      640      650

                670      680      690      700      710      720
Cry1Ac  SDEfCLDEKRElSEKvKHAKRLSDERNLLQDSnFKDInRQPERGwGGSgtITiQGGdDVf
gi|426  SDEfCLDEKRElSEKvKHAKRLSDERNLLQDPNFRGInRQLDRGWRGStDITiQGGdDVf
                660      670      680      690      700      710

                730      740      750      760      770      780
Cry1Ac  KENyVtLsGtFDEcYPTyLQKIDeSkLkAFtrYQLrGyIEdSdLEIySIRyNAKHETV
gi|426  KENyVtLlGtFDEcYPTyLQKIDeSkLkAYtrYQLrGyIEdSdLEIyLIRyNAKHETV
                720      730      740      750      760      770

                790      800      810      820      830      840
Cry1Ac  NVPgTgSLwPLsAQSPiGKCGEPnRCAPhLEwnPDLDcSRDgEKCAHSHHfSLDIDVg
gi|426  NVPgTgSLwPLsAPSPiGK-----AHSHHfSLDIDVg

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                780      790      800      810
Cry1Ac  CTDLNEDLGVVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
gi|426  CTDLNEDLGVVVIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
                820      830      840      850      860      870

                880      890      900      910      920      930      940      950      960
Cry1Ac  ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
gi|426  ETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNA
                880      890      900      910      920      930

                970      980      990      1000      1010      1020
Cry1Ac  AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSLVVPWEWA
gi|426  AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVLVPEWEWA
                940      950      960      970      980      990

                1030      1040      1050      1060      1070      1080
Cry1Ac  EVSQEVRVCPGRGYILRVtAYKEGYGEGCVtIHEIENNTDELKfSNcVVEEYIPNNtVtC
gi|426  EVSQEVRVCPGRGYILRVtAYKEGYGEGCVtIHEIENNTDELKfSNcVVEEYIPNNtVtC
                1000      1010      1020      1030      1040      1050

                1090      1100      1110      1120      1130
Cry1Ac  NDYtVnQEEYEGGAYtSRnrgYNEA---PSVPADYASVVEEKsYtDGRenPCEfNRGyR
gi|426  NDYtATQEEYEGYtSRnrgYDgAYESnSSVPADYASAYEeKAYtDGRDnPCESnRGYg
                1060      1070      1080      1090      1100      1110

                1140      1150      1160      1170      1180
Cry1Ac  DYtPLPvGvYtKElEYfPEtDKVWIEIGETEGtFIVDSVellMEE
gi|426  DYtPLPAGvYtKElEYfPEtDKVWIEIGETEGtFIVDSVellMEE
                1120      1130      1140      1150

>>gi|3211608|gb|AAC21368.1|I83311 Sequence 2 from patent (1176 aa)
  initn: 4516 init1: 3101 opt: 5029 Z-score: 5920.9 bits: 1107.5 E(): 0
Smith-Waterman score: 5230; 67.195% identity (83.222% similar) in 1198 aa overlap
(5-1182:1-1176)

                10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINeCIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLEFVPAGAGF
gi|321  MENNIQ-NQCVPYnCLSNPEEILLDGERISTGNSSIDISLSLVQLLVSNFVPGGGF
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac  VLGLVDIIWIGfGpSQWDAFLVQIEQLINQRIEEFARNQAIrSLRGLSNLYQIYAESFRE
gi|321  LVGLLDFVWIGfGpSPWDAFLVQIEQLINERIAAYARSAAIrSLRGLGNFNLYVFAFKE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLsLVRDVS
gi|321  WEADPDNPVTRTRVDRFRILDGLLERDIPsFRiAGfEVPLLSVYAQAANLHLAILRDSS

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120      130      140      150      160      170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGPDSRDWIRYNQFRREL
gi|321  IFGARWGLTTINVNENYRNLIRHIDEYANHCADTYNRLGNLNPSTYQDWITYNLRRDL
180      190      200      210      220      230
Cry1Ac  TLTVLDIVSLFFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRFGSAQG----IEGS-
gi|321  TLTVLVDIAAFPPSYDNRRIPIQSVGLTREIYTDPLI--TFNPLQLQSVQLPTFNVMSNA
240      250      260      270      280      290
Cry1Ac  TLTVLDIVSLFFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRFGSAQG----IEGS-
gi|321  TLTVLVDIAAFPPSYDNRRIPIQSVGLTREIYTDPLI--TFNPLQLQSVQLPTFNVMSNA
300      310      320      330      340      350
Cry1Ac  IRSPHMLDILNSITIIYTDADR-GE--YVWSGHQIMASPVGFGPEFTFFPLYGTMGNAAPQQ
gi|321  IRTPHLFDVLLNLTIFTDFWFSVGRNFYWGHRVVISNRIG--GGNITSPLYGREANQPEPR
360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRSLTSLYR--RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|321  SFT--FNGPVPFRTLSNPTFRPLQQPWPAPPFN--LRGVEGVF---STPLNSFTYRGRG
410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|321  TVDSLTELPEPNSVPPREGYSHRLCHATFVQRSG---TPFLTTPGVFVSWTHRSATDRN
470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|321  IIPDVINQIPLVKAFNLTSGTSVVRGPGFTGGDIIRTNVNGS-----VLSMSLNFST
530      540      550      560      570      580
Cry1Ac  ST-RYRVRVRYASVTPHILNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFT
gi|321  TLQRYRVRVRYAASQTMVMSVTVGGSTTGNQGFPTMSANGALTSQSRFAEFPVVISAS
590      600      610      620      630      640
Cry1Ac  SSLGNIVGVRNFGTAGVIIDRFEPVITATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|321  GSQGASISISNNVGRQMFHLDRIEFLPVTSTFEEYDLERAQEAVALFTSTNQLGLKTD
650      660      670      680      690      700
Cry1Ac  VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|321  VTDYHIDQVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDRNFRSINGQLDRG
710      720      730      740      750      760
Cry1Ac  WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQ

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gi|321  WRGSTDITIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLSYTRYELRGYIEDSQ
700      710      720      730      740      750
Cry1Ac  DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|321  DLEIYLIRYNAKHEIVNVPGTGLWPLSIENSIGPCGEPNRCAPHLEWNPDLDCSCRDGE
760      770      780      790      800      810
Cry1Ac  KCAHSHHFLSDIDVCGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|321  KCAHSHHFLSDIDVCGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
820      830      840      850      860      870
Cry1Ac  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHRSI
gi|321  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNAMIHAADKRVHRSI
880      890      900      910      920      930
Cry1Ac  REAYLPELSVIPGVNAIIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVE
gi|321  REAYLPELSVIPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNGLCWNKGVHVDVE
940      950      960      970      980      990
Cry1Ac  EQNNQRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKPF
gi|321  EQNNHRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKPF
1000      1010      1020      1030      1040      1050
Cry1Ac  SNCVEEEIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|321  SNCVEEIVPNNITVTCNDYTATQEEYGGAYTSRNGYKSYESNSVQADYASVYEEKAD
1060      1070      1080      1090      1100      1110
Cry1Ac  TDGRENPCFNRYRDTYPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|321  TDGRRDNHCSNRYGDTYPLPAGYVTKLEYFPETDKVWVEIGETEGTFIVDSVELLLM
1120      1130      1140      1150      1160      1170
Cry1Ac  EE
gi|321  EE
>>gi|37540106|gb|AAG35409.1| insecticidal crystal protei (1176 aa)
initn: 4516 initl: 3101 opt: 5029 Z-score: 5920.9 bits: 1107.5 E(): 0
Smith-Waterman score: 5230; 67.195% identity (83.222% similar) in 1198 aa overlap
(5-1182:1-1176)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

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gi | 375      MENNIQ-NQCVPNCLSNPEEILLDGERISTGNSSIDISLSLVQLLVSNFVPGGGF
              10      20      30      40      50
              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 LVGLLDFVWGVGSPWDFAFLVQIEQLINERIAAARSAAISNLEGLGNNFNVIYVAFKE
              60      70      80      90      100     110
              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLRDVS
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 WEADPDNPVTRVRVDRFRILDGLLERDIPSFRIAGFEVPLLSVYAQAANLHLAILRDSS
              120     130     140     150     160     170
              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 IFGARWGLTTINVNENYRNLIRHIDEYANHCADTYNRLGNNLPKSTYQDWITYNRLRRDL
              180     190     200     210     220     230
              250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG----IEGS-
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 TLTVLDIAAFPPSYDNRRYPIQSVGQLTREIYTDPLI-TFNPQLQSVQALPTFNVMESNA
              240     250     260     270     280     290
              300     310     320     330     340     350
Cry1Ac IRSPHMLDILNSITIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 IRTPHLFDVLNLLTIFTDFWFSVGRNFYWGHRVVISNRIG--GGNITSPIYGREANQEPFR
              300     310     320     330     340     350
              360     370     380     390     400
Cry1Ac RIVAQLQGQVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
              .. ::::::::::: .. ::::::::::: .. ::::::::::: .. :::::::::::
gi | 375 SFT--FNGPVFRTLNSPTFRPLQQPWPAPPFN--LRGVEGVEF---STPLNSFTYRGRG
              360     370     380     390     400
              410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSG---TPFLTTPGVFVSWTHRSATDRN
              410     420     430     440     450     460
              470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 IIPVDVINQIPLVKAFNLTSGTSVVRGPGFTGGDIIRTNVNGS-----VLSMSLNFSTN
              470     480     490     500     510
              530     540     550     560     570     580
Cry1Ac ST-RYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFT
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 TLQRYRVRVRYAASQTMVMSVTVGGSTTGNQGFPSTMSANGALTSQSFRAEFPPVGISAS
              520     530     540     550     560     570
              590     600     610     620     630     640
Cry1Ac SSLGNIVGVRNFGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN

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              :: : ... : : ..:::.....: :::::::::::.....
gi | 375 GSQGASISISNNVGRQMFHLDRIEFLPVTSTFEEEYDLERAQEAVALNFTSTNQLGLKTD
              580     590     600     610     620     630
              650     660     670     680     690     700
Cry1Ac VTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 VTDYHIDQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDRNFRSINGQLDRG
              640     650     660     670     680     690
              710     720     730     740     750     760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
              : :: : ::::::::::: ::::::::::: ..:::.....:
gi | 375 WRGSTDITIQGGDDVFKENYVTLPGTFDECPYTYLYQKIDESKLFKSYTRYELRGYIEDSQ
              700     710     720     730     740     750
              770     780     790     800     810     820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
              ::::: ::::::::::: ::::::::::: .. : ::::::::::: ..:
gi | 375 DLEIYLIRYNAKHEIVNVPGTGLWPLSIENSIGPCGEPNRCAPHLEWNPDLDCSCRDGE
              760     770     780     790     800     810
              830     840     850     860     870     880
Cry1Ac KCAHSHHFFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 KCAHSHHFFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
              820     830     840     850     860     870
              890     900     910     920     930     940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSI
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHRI
              880     890     900     910     920     930
              950     960     970     980     990     1000
Cry1Ac REAYLPELSVIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWLVKGVHDVE
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 REAYLPELSVIPGVNAGIFELEGRIFTAYSLYDARNVIKNGDFNGLSCWLVKGVHDVE
              940     950     960     970     980     990
              1010     1020     1030     1040     1050     1060
Cry1Ac EQNNQRSVLVVPWEAEVSVQEVRCVPRGYILRVTAIYKEGYGEGCVTIHEIENNTDELKF
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 EQNNHRSVLVVPWEAEVSVQEVRCVPRGYILRVTAIYKEGYGEGCVTIHEIEDNTDELKF
              1000     1010     1020     1030     1040     1050
              1070     1080     1090     1100     1110     1120
Cry1Ac SNCVEEIEYPNNVTVCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 SNCVEEIEYPNNVTVCNDYATQEEYGGAYTSRNGYKGSYESNSSVQADYASVYEEKAD
              1060     1070     1080     1090     1100     1110
              1130     1140     1150     1160     1170     1180
Cry1Ac TDGRRENPCFNRYGRDYTPLPVGYVTKLEYFPETDKVWVIEIGETEGTFIVDSVELLLM
              ::::::::::: ::::::::::: ::::::::::: ::::::::::: :::::::::::
gi | 375 TDGRRDNHCSNRGYGDYTPLPAGYVTKLEYFPETDKVWVIEIGETEGTFIVDSVELLLM
              1120     1130     1140     1150     1160     1170

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Cry1Ac EE
gi|375 EE
>>gi|3939847|gb|AAC81580.1|I95377 Sequence 2 from patent (1176 aa)
initn: 4516 initl: 3101 opt: 5029 Z-score: 5920.9 bits: 1107.5 E(): 0
Smith-Waterman score: 5230; 67.195% identity (83.222% similar) in 1198 aa overlap
(5-1182:1-1176)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|393 MENNIQ-NQCVPNCLSNPEEILLDGERISTGNSSIDISLSLVQLLVSNFVPGGGF
70 80 90 100 110 120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|393 LVGLLDFWGIWGFPSQWDAFLVQIEQLINERIAAYARSAAISNLEGLGNPNFYVEAFKE
130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|393 WEADPDNPVTRVRFRILDGLLERDIPSFRIAGFEVPLLSVYQAANLHLAALTRDSS
190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
gi|393 IFGARWGLTTINVENYNRILRHIDEYANHCADTYNRLNLPKSTYQDWITYNRLRRDL
250 260 270 280 290
Cry1Ac TLTVDLIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG-----IEGS-
gi|393 TLTVDLIAAFPSYDNRRIYQISVGLTREIYTDPLI-TFNPQLQSVQALPTFNVMSNA
300 310 320 330 340 350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQ
gi|393 IRTPHLFDVLNLLTIFTDFWVSGRNFYWGGRHVISNRIG--GGNITSPIYGREANQPEPR
360 370 380 390 400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSNNLPSAVYRKSG
gi|393 SFT--FNGPVFRTLNSPTFRPLQQPWPAPPFN--LRGVEGVF---STPLNSFTYRGRG
410 420 430 440 450 460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|393 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSG---TPFLTGTGVPVSWTHRSATDRN
470 480 490 500 510 520

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFST
gi|393 IIPVDVINIPLVKAFNLTSGTSVVRGPGFTGGDIIRTNVNGS-----VLSMSLNFNSNT
470 480 490 500 510
530 540 550 560 570 580
Cry1Ac ST-RYRVRVRYASVTP IHLNVNWNSSIFSNTV PATATSLDNLQSSDFGY--FESANAFT
gi|393 TLQRYRVRVRYAASQTMVMSVTGGSTTGNQGF PSTMSANGALTSQSFRAEFPVGISAS
520 530 540 550 560 570
590 600 610 620 630 640
Cry1Ac SSLGNIVGVNRVSGTAGVI IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|393 GSQGASISISNNVGRQMFHLDRIEFLPVSTFEEEDLERAQAVNALFTSTNQLGLKTD
580 590 600 610 620 630
650 660 670 680 690 700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|393 VTDYHIDQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDRNFRSINGQLDRG
640 650 660 670 680 690
710 720 730 740 750 760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKLLKAFTRYQLRGYIEDSQ
gi|393 WRGSTDITIQGGDDVFKENYVTLPGTFDECPYTYLYQKIDESKLLKSYTRYELRGYIEDSQ
700 710 720 730 740 750
770 780 790 800 810 820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|393 DLEIYLIRYNAKHEIVNVPGTGLWPLSIENSIGCGEPNRCAPHLEWNPDLDCSCRDGE
760 770 780 790 800 810
830 840 850 860 870 880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|393 KCAHSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
820 830 840 850 860 870
890 900 910 920 930 940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSI
gi|393 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNAMIHAADKRVHRI
880 890 900 910 920 930
950 960 970 980 990 1000
Cry1Ac REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVE
gi|393 REAYLPELSVIPGVNAGIFEELEGRIFTAYSLYDARNVIKNGDFNGLLSCWNLKGVHDVE
940 950 960 970 980 990
1010 1020 1030 1040 1050 1060
Cry1Ac EQNNQRSVLVVPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKF
gi|393 EQNNHRSVLVVPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKF
1000 1010 1020 1030 1040 1050

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1070      1080      1090      1100      1110      1120
Cry1Ac  SNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|393  SNCVEEEVYPNNTVTCNDYATQEEYGGAYTSRNRHGYSKSYESNSSVQADYASVYEEKAD
1060      1070      1080      1090      1100      1110

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1130      1140      1150      1160      1170      1180
Cry1Ac  TDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|393  TDGRRDNHCSNRGYDYTPLPAGYVTKELEYFPETDKVWVEIGETEGTFIVDSVELLLM
1120      1130      1140      1150      1160      1170

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Cry1Ac  EE
gi|393  EE

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>>gi|56642302|gb|AAW12020.1| Sequence 59 from patent US (1189 aa)
  in1tn: 4557 in1t1: 3093 opt: 5011 Z-score: 5899.6 bits: 1103.6 E(): 0
Smith-Waterman score: 5282; 68.264% identity (83.306% similar) in 1210 aa overlap
(5-1182:1-1189)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIIDISLSLTQFLLEFVPGAGF
gi|566  MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNYQIYAESFRE
gi|566  LVGLIDFVWGIWVQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|566  WEEDPNNPATRTRVIDRFRILDGLLERDIPSFASGFVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFRREL
gi|566  IFGERWGLTTINVENYNRILRHIDEYADHCANTYNRGLNMLPASTYQDWTYRRLRRDL
180     190     200     210     220     230

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250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG----IEGS-
gi|566  TLTVLIDIAAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNPQLQSVQALPTFVMESSA
240     250     260     270     280     290

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300     310     320     330     340     350
Cry1Ac  IRSPHLMILNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|566  IRNPHLFDILNNTIFTDWFVSVGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
300     310     320     330     340     350

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360      370      380      390      400
Cry1Ac  RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQQLSVLDTGTEFAYGTSNLSVAVYRKSG
gi|566  SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

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410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSTATLTN
410      420      430      440      450      460

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470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|566  TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
470      480      490      500      510

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530      540      550      560      570      580
Cry1Ac  STRYRVVRYASVTPPIHLNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566  Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMLPQKTEIGENLTSRTFRYTDPS
520      530      540      550      560      570

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590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566  NPFSTRANPDIIGISQPLFAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

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640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566  FTSSNQLGLKTDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

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700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKPKAFT
gi|566  NFRGINRQPRDGRWGGSTDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKPKAYT
700      710      720      730      740      750

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760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNKHEIVNVPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566  RYELRGYIEDSQDLEIYLIRYNKHEIVNVPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

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820      830      840      850      860      870
Cry1Ac  NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|566  NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

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880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566  EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

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760      770      780      790      800      810
Cry1Ac  820      830      840      850      860      870
NPDLDCSCRDGEKCAHSHSHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
gi|233  NPDLDCSCRDGEKCAHSHSHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|233  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|233  MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGVHDVVEEQNNQSRVSVLVPWEAEVSVQEVRCVCPGRGYILRVYTAYKEGEGCVTI
gi|233  LCWNVKGVHDVVEEQNNHRSVSVLVIPEWEAEVSVQEVRCVCPGRGYILRVYTAYKEGEGCVTI
1000     1010     1020     1030     1040     1050

1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|233  HEIEDNTDELKFSNCVVEEIVPNNVTTCNNYTGTEYEGYTSRNRQYDEAYGNNPSVP
1060     1070     1080     1090     1100     1110

1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
gi|233  ADYASVYEEKSYTDGRRENPCESNRYGDTPLPAGYVTKLEYPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170

1170     1180
Cry1Ac  TFIIVDSVELLLMEE
gi|233  TFIIVDSVELLLMEE
1180

>>gi|56664669|gb|AAW18094.1| Sequence 59 from patent US (1189 aa)
  initn: 4557 initl: 3093 opt: 5011 Z-score: 5899.6 bits: 1103.6 E(): 0
Smith-Waterman score: 5282; 68.264% identity (83.306% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566  MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|566  LVGLIDFVWVIGVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE

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60      70      80      90      100     110
Cry1Ac  130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566  WEEDPNNPATRTRVIDRFRILDGLLERDIPSPAISGFVPLLSVYAQAANLHLAALRDSV
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFREL
gi|566  IFGERWGLTTINVENYNRRLIRHIDEYADHCANTYNRGLNNLPASTYQDWITYNRRLRDL
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFSGAQQ----IEGS-
gi|566  TLTVLDIAAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNPQLQVAQLPTFNVMESSA
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac  IRSPHLMIDLNSITIYTDAGR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|566  IRNPHLFDILNNTLIFTDFWFSVGRNFYWGGRVVISLIG--GGNITSPYIGREANQEPFR
300      310      320      330      340      350

360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|566  SFT--FNGVPVFRTLNPTLRLQLQWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac  TVDSLDEIIPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRSGTPFLTGTGVV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|566  TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNSINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566  Q-RYRLRFYASRRDARVILVTGAASTGVGGQVSVNMLPQKMEIGENLTSRTFFRYTDFPS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566  NPFSTRANPDIIGIEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS

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gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAF
      . . . . .
gi|566 NFRGINRQPDGRGWGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      . . . . .
gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEGKCAHSHHSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      . . . . .
gi|566 NPDLDCSCRDEGKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIA
      . . . . .
gi|566 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      . . . . .
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQRSVLVPPEWAEVVSQEVVRCVCPGRGYILRVYTAYKEGYEGECVTI
      . . . . .
gi|566 LCWNVKGVHDVVEEQNNHRSVLVIPPEWAEVVSQEVVRCVCPGRGYILRVYTAYKEGYEGECVTI
      1000     1010     1020     1030     1040     1050

      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      . . . . .
gi|566 HEIEDNTDELKFSNCVVEEVYPNNTVTCNNYTGTEYEGTYTSRNQGYDEAYGNPSPVP
      1060     1070     1080     1090     1100     1110

      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
      . . . . .
gi|566 ADYASVYEEKSYTDGRENPCESNRGYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170

      1170     1180
Cry1Ac TFIVDSVELLLMEE
      . . . . .
gi|566 TFIVDSVELLLMEE
      1180

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>>gi|158456701|gb|ABW41374.1| Sequence 59 from patent US (1189 aa)  
 initn: 4557 initl: 3093 opt: 5011 Z-score: 5899.6 bits: 1103.6 E(): 0

Smith-Waterman score: 5282; 68.264% identity (83.306% similar) in 1210 aa overlap (5-1182:1-1189)

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      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . . . . .
gi|158 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi|158 LVGLIDFVWGVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi|158 WEEDPNPATRTRVIDRFRILDGLLERDIPSAISGFVEPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      . . . . .
gi|158 IPGERGLTTINVENYNRIRHIDEYADHCANTYNRGLNNLPASTYQDWIITYNRLRRLD
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGSAQG----IEGS-
      . . . . .
gi|158 TLTVLDIAAFFPNYDNRYPYIQVQGLTREVTDLPLI-NFNPQLQSVLQPLTFNVMESSA
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac IRSPHLMIDILNSITIYTDADR-GE-YYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQ
      . . . . .
gi|158 IRNPHLFDILNLTIFTDFWFSVGRNRYWGGHRSVSSLIIG--GGNITSPIYGREANQEPFR
      300     310     320     330     340     350

      360     370     380     390     400
Cry1Ac RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSG
      . . . . .
gi|158 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360     370     380     390     400

      410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFNSSSVSIIRAPMFSWIHRSAEFNN
      . . . . .
gi|158 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSATLTN
      410     420     430     440     450     460

      470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPST
      . . . . .
gi|158 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILLRNTFGDFVS---LQVNIINSPI
      470     480     490     500     510

      530     540     550     560     570     580
Cry1Ac STRYRVRVRYASVTPIHILNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA

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Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|179 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGLTTPFLTTGVV---FSWTHR SATLITN
      410      420      430      440      450      460

      470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHPST
gi|179 TIDPERINQIPLVKGFRVWGGTSTVITGPGFTGGDILRRNFTGDFVS---LQVNNISPIT
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLVNVGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|179 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKIMEIGENLTSRTFRYTDIFS
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|179 NFFSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERLLQDS
gi|179 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAYT
gi|179 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|179 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLLDCSCRDGKCAHSHHFFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
gi|179 NPDLLDCSCRDGKCAHSHHFFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|179 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|179 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

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      1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDEEQNNQRSVSVLVPWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI
gi|179 LCWNVKGHVDEEQNNHRSVSVLVIPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050

      1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|179 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNPNVSP
      1060      1070      1080      1090      1100      1110

      1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
gi|179 ADYASVYEEKSYTDGRRENPCESNRGYDYTPLPAGYVTKDLELYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIIVDSVELLLMEE
gi|179 TFIIVDSVELLLMEE
      1180

>>gi|56642267|gb|AAW11985.1| Sequence 2 from patent US 6 (1189 aa)
initn: 4555 initl: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0
Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566 MEEN-NQNQCIPYCNLSNPEVEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGFF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIQFVPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWGIQFVPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNINIVYEFAPKE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566 WEEDPNNPATRTRVDRFRILDGLLERDIPSAISGFVPLLSVYVQAANLHLLAIRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNLRRLD
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG----IEGS-
gi|566 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNQQLQSVLQPLTFNVMESSA
      240      250      260      270      280      290

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300      310      320      330      340      350
Cry1Ac  IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMTGNAAAPQQ
gi|566  IRNPHLFDILNLLTIFTDFWFSVGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

360      370      380      390      400
Cry1Ac  RIVAQLGGQVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|566  SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566  TVDSLTELPPEDNSVPPREGYSHRSLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|566  TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPI
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPIHNLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTIMEIGENLTSRTFRYTDFS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566  NPFSSFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|566  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGFDECYPTYLYQKIDESKCLKAFT
gi|566  NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKCLKAYT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYLRIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566  RYELRGYIEDSQDLEIYLRIRYNAKHEIVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac  NPDLDCSRDGEKCAHSHHFLSLDIDVGTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
gi|566  NPDLDCSRDGEKCAHSHHFLSLDIDVGTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

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880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566  EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHV DVEEQNNQRSV LVPWEAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTI
gi|566  LCWNVKGHV DVEEQNNHRSV LVPWEAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTI
1000     1010     1020     1030     1040     1050

1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCV EEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
gi|566  HEIEDNTDELKFSNCV EEEVYPNNTVTCNNYTGTEQEYEGYTSRNQGYDEAYGNPSPV
1060     1070     1080     1090     1100     1110

1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRRENPC EFNRYRDTYPLPVGYVTKELEYFPETDKVWIEIGETEG
gi|566  ADYASVYEEKSYTDGRRENPC ESNRYRDTYPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170

1170     1180
Cry1Ac  TFIVDSVELLLMEE
gi|566  TFIVDSVELLLMEE
1180

>>gi|17920870|gb|AAE86490.1| Sequence 2 from patent US 6 (1189 aa)
initn: 4555 init1: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0
Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|179  MEEN-NQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|179  VLGLIDFVWIGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|179  WEEDPNNPATRRVDIRFRILDGLLERDIPSPAISGFVPLLSVYAQAANLHLLAIRDVS
120     130     140     150     160     170

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          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|179  IFGERWGLTTINVNENYRNLIRRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRRDL
          180      190      200      210      220      230

          250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFRGSAQG----IEGS-
gi|179  TLTVLDIAAFPNYNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
          240      250      260      270      280      290

          300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITITYDAHR-GE-YWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|179  IRNPHLFDILNLTITFDWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQPEPPR
          300      310      320      330      340      350

          360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS
gi|179  SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGEVFS--TPTN--SFTYRGRG
          360      370      380      390      400

          410      420      430      440      450      460
Cry1Ac TVDSDLDEIPPNQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|179  TVDSDLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTN
          410      420      430      440      450      460

          470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|179  TIDPERINQIPLVKGRFVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
          470      480      490      500      510

          530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLVNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|179  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMPLOKQIMEIGENLTSRTFRYTDFS
          520      530      540      550      560      570

          590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|179  NPFSPFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
          580      590      600      610      620      630

          640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|179  FTSSNQIGLKTVDYHIDQVSNLVDCLDEFCLDEKRELSKVKHAKRLSDERNLLQDP
          640      650      660      670      680      690

          700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLPGTVDCEPTYLYQKIDESKPKAFT
gi|179  NFRGINRQPRDRGWRGSTDITIQGGDDVFKENYVTLPGTVDCEPTYLYQKIDESKPKAYT

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          700      710      720      730      740      750
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW
gi|179  RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW
          760      770      780      790      800      810

          820      830      840      850      860      870
Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
gi|179  NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
          820      830      840      850      860      870

          880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|179  EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
          880      890      900      910      920      930

          940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIPTAFSLYDARNVIKNGDFNNGL
gi|179  MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIPTAYSLYDARNVIKNGDFNNGL
          940      950      960      970      980      990

          1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGVHVDVEEQNNQSVLVVPEWEAEVSVQEVRCVCPGRGYLLRVYAYKEGYGECVTI
gi|179  LCWNVKGVHVDVEEQNNHRSVLVPEWEAEVSVQEVRCVCPGRGYLLRVYAYKEGYGECVTI
          1000      1010      1020      1030      1040      1050

          1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|179  HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGYTSRNQGYDEAYGNPSPV
          1060      1070      1080      1090      1100      1110

          1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
gi|179  ADYASVYEEKSYTDGRENPCESNRGYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
          1120      1130      1140      1150      1160      1170

          1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|179  TFIVDSVELLLMEE
          1180

>>gi|23325079|gb|AAN23779.1| Sequence 2 from patent US 6 (1189 aa)
  initn: 4555 init1: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0
Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFPVPGAGF
gi|233  MEEN-NQNCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF

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10      20      30      40      50
70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|233 LVGLIDFVWVIGVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100     110
130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|233 WEEDPNNPATRTRVDRFRILDGLLERDIPSAISGFVPLLSVYAQAANLHLAIRDVS
120     130     140     150     160     170
190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|233 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230
250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-
gi|233 TLTVLIDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVQQLPTFNMESSA
240     250     260     270     280     290
300     310     320     330     340     350
Cry1Ac IRSPHMLDILNSITITYTDAHR-GE-YYWSGHQIMASPVGFSGPEPTFFPLYGTMGNAAPQQ
gi|233 IRNPHLFDILNLTIFTDWFSVGRNFYWGHRVSSSLIG--GGNITSPIYGREANQEPFR
300     310     320     330     340     350
360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSG
gi|233 SFT--FNGPVFRTLNSPTLRLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
360     370     380     390     400
410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|233 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSQTPFLTTGVV----FSWTHRSATLTN
410     420     430     440     450     460
470     480     490     500     510     520
Cry1Ac IIASDSTIQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGIEVPIHFSPST
gi|233 TIDPERINQIPLVKGRFVWGGTTSVITGPGFTGGDLRRTFDFVS----LQVNNINSPIIT
470     480     490     500     510
530     540     550     560     570     580
Cry1Ac STRYRVRYASVTPIHNLNVNMGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|233 Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTFRYTDIFS
520     530     540     550     560     570
590     600     610     620     630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVVTATLEAEYNLERAQKAVNAL

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gi|233 NPFSFRANPDIIGISEQPLFGAGSISSEGLYIDKIEIILADATFEAESDLERAQKAVNAL
580     590     600     610     620     630
640     650     660     670     680     690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|233 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640     650     660     670     680     690
700     710     720     730     740     750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|233 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
700     710     720     730     740     750
760     770     780     790     800     810
Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
gi|233 RYELRGYIEDSDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
760     770     780     790     800     810
820     830     840     850     860     870
Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
gi|233 NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
820     830     840     850     860     870
880     890     900     910     920     930
Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|233 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880     890     900     910     920     930
940     950     960     970     980     990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|233 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940     950     960     970     980     990
1000    1010    1020    1030    1040    1050
Cry1Ac SCWNVKGVHDVEEQNNQRSVLPVPEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
gi|233 LCWNVKGVHDVEEQNNHRSVLPVPEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
1000    1010    1020    1030    1040    1050
1060    1070    1080    1090    1100
Cry1Ac HEIENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP
gi|233 HEIEDNTDELKFSNCVEEIEYPNNTVTCNNTYGTQEEYEGTYTSRNOGYDEAYGNMPSVP
1060    1070    1080    1090    1100    1110
1110    1120    1130    1140    1150    1160
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFETDKVWIEIGETEG
gi|233 ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPAGYVTKDLEYFETDKVWIEIGETEG
1120    1130    1140    1150    1160    1170
1170    1180
Cry1Ac TFIVDSVELLMEE

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gi|233 TFIVDSVELLLMEE
1180

>>gi|56664634|gb|AAW18059.1| Sequence 2 from patent US 6 (1189 aa)
  initn: 4555 initl: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0
Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . . . . .
gi|566  MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
          10      20      30      40      50

          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi|566  LVGLLIDFVWGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
          60      70      80      90      100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      . . . . .
gi|566  WEEDPNPATRTRVIRDRILDGLLERDIPSPFAISGFVPLLSVYAQAANLHLALLRDVS
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . . .
gi|566  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNLRRLRDL
          180     190     200     210     220     230

          250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQG----IEGS-
      . . . . .
gi|566  TLTVLDAIAAFPYNDRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
          240     250     260     270     280     290

          300     310     320     330     340     350
Cry1Ac IRSPHMLDILNSITIYTDADR-GE-YWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
      . . . . .
gi|566  IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVYSSSLIG--GGNITSPIYGREANQEPFR
          300     310     320     330     340     350

          360     370     380     390     400
Cry1Ac RIVAQLQGQVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
      . . . . .
gi|566  SFT--FNGPVFRTLNSPTRLRLQQPWAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
          360     370     380     390     400

          410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
      . . . . .
gi|566  TVDSLTELPPEDNSVPPREGYSHRSLCHATFVQSRGTPPLTTGVV---FSWTHR.SATLTN
          410     420     430     440     450     460

          470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNLSGNNIQNRGYIEVPIHFPST

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          470     480     490     500     510
gi|566  TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILLRRNTFGDFVS---LQVNNINSPIT
          470     480     490     500     510

          530     540     550     560     570     580
Cry1Ac STRYRVRVRYASVTPIHLMNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      . . . . .
gi|566  Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFRYTDPS
          520     530     540     550     560     570

          590     600     610     620     630
Cry1Ac NAFTSSLG-NIVGVRN--F--SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
      . . . . .
gi|566  NPF'SFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
          580     590     600     610     620     630

          640     650     660     670     680     690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
      . . . . .
gi|566  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
          640     650     660     670     680     690

          700     710     720     730     740     750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKCLKAFT
      . . . . .
gi|566  NFRGINRQPRDRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKCLKAYT
          700     710     720     730     740     750

          760     770     780     790     800     810
Cry1Ac RYQLRGIYIEDSQDLEIYSIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      . . . . .
gi|566  RYELRGIYIEDSQDLEIYLIRYNKAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
          760     770     780     790     800     810

          820     830     840     850     860     870
Cry1Ac NPDLDCSCRDGEKCAHSHHFLSDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
      . . . . .
gi|566  NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
          820     830     840     850     860     870

          880     890     900     910     920     930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      . . . . .
gi|566  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
          880     890     900     910     920     930

          940     950     960     970     980     990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      . . . . .
gi|566  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
          940     950     960     970     980     990

          1000    1010    1020    1030    1040    1050
Cry1Ac SCWNVKGHVDEEQNNQRSVLVVPEWAEVSVQEVRCVCPGRGYILRVTAAYKEGYGECVTI
      . . . . .
gi|566  LCWNVKGHVDEEQNNHRSVLVPEWAEVSVQEVRCVCPGRGYILRVTAAYKEGYGECVTI
          1000    1010    1020    1030    1040    1050

          1060    1070    1080    1090    1100

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Cry1Ac 940 950 960 970 980 990
MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|158 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL

Cry1Ac 1000 1010 1020 1030 1040 1050
SCWNVKGVHDVEEQNNQSVLVPVEWEAEVSVQEVRCVPCGRGYILRVYTAYKEGYGEGCVTI
gi|158 LCWNVKGVHDVEEQNNHRSVLVPEWEAEVSVQEVRCVPCGRGYILRVYTAYKEGYGEGCVTI

Cry1Ac 1060 1070 1080 1090 1100
HEIENNTDELKFSNCVVEEIIYNNVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|158 HEIEDNTDELKFSNCVVEEIVYNNVTTCNNYTGTEYEGYTSRNRQGYDEAYGNNPSPV

Cry1Ac 1110 1120 1130 1140 1150 1160
ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
gi|158 ADYASVYEEKSYTDGRRENPCSNRGYDYPPLPAGYVTKLELYFPETDKVWIEIGETEG

Cry1Ac 1170 1180
TFIVDSVELLMEE
gi|158 TFIVDSVELLMEE
1180

>>gi|14103734|gb|AAE55168.1| Sequence 2 from patent US 6 (1189 aa)
initn: 4555 initl: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0
Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|141 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|141 LVGLIDFVWGVGQPSQWDAFLVQIEQLINERIAEFARNAATAINLEGLGNPNFIYVEAFKE

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|141 WEEDPNNPATRTRVIDRFRILDGLLERDIPSPFAISGFVPLLSVYAQAANLHLAAILRDSV

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|141 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRRLRDL

Cry1Ac 250 260 270 280 290
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG-----IEGS-
gi|141 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA

Cry1Ac 300 310 320 330 340 350
IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|141 IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFR

Cry1Ac 360 370 380 390 400
RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLPASAVYRKSG
gi|141 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

Cry1Ac 410 420 430 440 450 460
TVDSLDEIIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQVRSRGTFFLTGTVV---FSWTHRSATLTN

Cry1Ac 470 480 490 500 510 520
IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPPST
gi|141 TIDPERINQIPLVKGFVRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIT

Cry1Ac 530 540 550 560 570 580
STRYRVRVRYASVTPIHNLVNWGNSSI-----FSNTVPPATATSL--DNLQSSDFGYFESA
gi|141 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTRFTDPS

Cry1Ac 590 600 610 620 630
NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
gi|141 NPFSFRANPDIIGIEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL

Cry1Ac 640 650 660 670 680 690
FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|141 FTSSNQIQLKTDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP

Cry1Ac 700 710 720 730 740 750
NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLPGTFCDECYPTYLYQKIDESKCLKAFT
gi|141 NFRGINRQPRDGRWGGSTDITIQGGDDVFKENYVTLPGTFCDECYPTYLYQKIDESKCLKAYT

Cry1Ac 760 770 780 790 800 810
RYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
gi|141 RYELRGIYEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW

Regulatory Product Characterization Team

820 830 840 850 860 870  
 Cry1Ac NPDDLDCSCRDGKCAHSHHFLDIDVGTDLNEDLGWVVIKIKTQDGHARLGNLEFLE  
 .....  
 gi|141 NPDDLDCSCRDGKCAHSHHFLDIDVGTDLNEDLGWVVIKIKTQDGHARLGNLEFLE  
 820 830 840 850 860 870

880 890 900 910 920 930  
 Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA  
 .....  
 gi|141 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA  
 880 890 900 910 920 930

940 950 960 970 980 990  
 Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL  
 .....  
 gi|141 MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL  
 940 950 960 970 980 990

1000 1010 1020 1030 1040 1050  
 Cry1Ac SCWNVKGHV DVEEQNNQRSVLVPEWEAEVVSQEVVCPGRGYILRVTA YKEGYGEGCVTI  
 .....  
 gi|141 LCWNVKGHV DVEEQNNQRSVLVPEWEAEVVSQEVVCPGRGYILRVTA YKEGYGEGCVTI  
 1000 1010 1020 1030 1040 1050

1060 1070 1080 1090 1100  
 Cry1Ac HEIENNTDELKFSNCEVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVP  
 .....  
 gi|141 HEIENNTDELKFSNCEVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVP  
 1060 1070 1080 1090 1100 1110

1110 1120 1130 1140 1150 1160  
 Cry1Ac ADYASVYEEKSYTDGRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG  
 .....  
 gi|141 ADYASVYEEKSYTDGRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG  
 1120 1130 1140 1150 1160 1170

1170 1180  
 Cry1Ac TFIVDSVELLLMEE  
 .....  
 gi|141 TFIVDSVELLLMEE  
 1180

>>gi|14112739|gb|AAE58154.1| Sequence 2 from patent US 6 (1189 aa)  
 initn: 4555 initl: 3093 opt: 5009 Z-score: 5897.2 bits: 1103.2 E(): 0  
 Smith-Waterman score: 5280; 68.264% identity (83.223% similar) in 1210 aa overlap  
 (5-1182:1-1189)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 .....  
 gi|141 MEEN-NQNQCIPYNCLSNPEVEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNAQISRLEGLSNLYQIYAESFRE  
 .....  
 gi|141 LVGLIDFVWGVQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi|141 WEEDPNNPATRTRVDRFRILDGLLERDIPSPFAISGFVPLLSVYVQAANLHLLALRDSV  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRFDWIRYNQFRREL  
 .....  
 gi|141 IPGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLLRDL  
 180 190 200 210 220 230

250 260 270 280 290  
 Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQG-----IEGS-  
 .....  
 gi|141 TLTVLDIAAFAFPNYDNRRYIQQVGLQTRVYTDPLI-NFNPQLQSVLQPLTFNVMESSA  
 240 250 260 270 280 290

300 310 320 330 340 350  
 Cry1Ac IRSPHMLDILNSITIIYTDADR-GE-YWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ  
 .....  
 gi|141 IRNPHLFDILNLLTIFTDWFSVGRNRYWGGHRVVISSLIG--GGNITSPYIGREANQEPFR  
 300 310 320 330 340 350

360 370 380 390 400  
 Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLPSSAVYRKS  
 .....  
 gi|141 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG  
 360 370 380 390 400

410 420 430 440 450 460  
 Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSSSVSIIIRAMPFSWIHRSAEFNN  
 .....  
 gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSATLTN  
 410 420 430 440 450 460

470 480 490 500 510 520  
 Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST  
 .....  
 gi|141 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT  
 470 480 490 500 510

530 540 550 560 570 580  
 Cry1Ac STRYRVRVRYASVTPIHLNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA  
 .....  
 gi|141 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTEMEIGENLTSRTFRYTDPS  
 520 530 540 550 560 570

590 600 610 620 630  
 Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL  
 .....  
 gi|141 NPFSSFRANPDIIGISEQLPFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL  
 580 590 600 610 620 630

640 650 660 670 680 690  
 Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS  
 .....  
 gi|141 FTSSNIGLKTVDYHIDQVSNLVDCSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP

Regulatory Product Characterization Team

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640      650      660      670      680      690
Cry1Ac  700      710      720      730      740      750
NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|141  NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

640      650      660      670      680      690
Cry1Ac  760      770      780      790      800      810
RYQLRGYIEDSQDLEIYSIRYNAKHETVNVVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
gi|141  RYELRGYIEDSQDLEIYLIRYNAKHEIVNVVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

640      650      660      670      680      690
Cry1Ac  820      830      840      850      860      870
NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
gi|141  NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

640      650      660      670      680      690
Cry1Ac  880      890      900      910      920      930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|141  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

640      650      660      670      680      690
Cry1Ac  940      950      960      970      980      990
MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|141  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

640      650      660      670      680      690
Cry1Ac  1000     1010     1020     1030     1040     1050
SCWNVKGHVDFVEEQNNRQSVLVVPEWEAEVVSQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|141  LCWNVKGHVDFVEEQNNRQSVLVVPEWEAEVVSQEVVCPGRGYILRVYAYKEGYGEGCVTI
1000     1010     1020     1030     1040     1050

640      650      660      670      680      690
Cry1Ac  1060     1070     1080     1090     1100
HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|141  HEIEDNTDELKFSNCVVEEIVPNNVTTCNNYTGTEYEGTYTSRNQGYDEAYGNNPSVP
1060     1070     1080     1090     1100     1110

640      650      660      670      680      690
Cry1Ac  1110     1120     1130     1140     1150     1160
ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|141  ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
1110     1120     1130     1140     1150     1160     1170

640      650      660      670      680      690
Cry1Ac  1170     1180
TFIVDSVELLMEE
gi|141  TFIVDSVELLMEE
1180

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>>gi|1612052|gb|AAB15032.1| Sequence 7 from patent US 55 (934 aa)  
 initn: 4518 init1: 2302 opt: 5007 Z-score: 5896.4 bits: 1102.7 E(): 0

Smith-Waterman score: 5007; 80.998% identity (90.234% similar) in 942 aa overlap (5-940:1-934)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|161  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|161  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|161  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFRREL
gi|161  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWRIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRGSAQIEGSIKRSRPHL
gi|161  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRGSAQIEGSIKRSRPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAPFLFGNAGNAAPPV-LVSLTGL
gi|161  MDILNRITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAPFLFGNAGNAAPPV-LVSLTGL
300     310     320     330     340     350

370     380     390     400     410
Cry1Ac  GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSQTVDSLDEIP
gi|161  GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTNLPSTIYRQRGTVDLSDVIP
360     370     380     390     400     410

420     430     440     450     460     470
Cry1Ac  PQNNVPPRQGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|161  PQDNSVPPRAGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQI
420     430     440     450     460     470

480     490     500     510     520     530
Cry1Ac  PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|161  PLTKSTNLGSGTSSVVKGPFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
480     490     500     510     520

540     550     560     570     580     590
Cry1Ac  ASVTPIHNLVNVGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR

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650      660      670      680      690      700
Cry1Ac  GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|551  GGDDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQDLEIYLIRYN
710      720      730      740      750      760      770
Cry1Ac  AKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHFHS
gi|551  AKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHFHS
770      780      790      800      810      820      830
Cry1Ac  LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|551  LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
830      840      850      860      870      880      890
Cry1Ac  REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSV
gi|551  REKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKR
890      900      910      920      930      940      950
Cry1Ac  IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNQRSVLV
gi|551  IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNQRSVLV

>>gi|23325115|gb|AAN23815.1| Sequence 61 from patent US (1189 aa)
  initn: 4550 initl: 3093 opt: 5004 Z-score: 5891.3 bits: 1102.1 E(): 0
Smith-Waterman score: 5275; 68.182% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|233  MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEAFARNQAIARLEGLSNLYQIYAESPFE
gi|233  LVGLIDFVWGVGPGSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|233  WEEDPNPATRTRVIDRFRILDGLLERDIPSPDISGFVPELLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|233  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRNLNLPASTYQDWITYNRLRRDL
180     190     200     210     220     230

250     260     270     280     290

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Cry1Ac  TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
gi|233  TLTVLDIAAFFPNYDNRRIYPIQVQGLTREVYTDPLI-NFNPQLQVAQLPTFNVMSSA
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|233  IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRVVISLIG--GGNITSPIYGREANQEPFR
300     310     320     330     340     350

360     370     380     390     400
Cry1Ac  RIVAQLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|233  SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360     370     380     390     400

410     420     430     440     450     460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRSLHVSFMF-RSGFNSSSVSIIRAMPFSWIHRSAEFNN
gi|233  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSRGTPLTGTGVV---FSWTHRSATLTN
410     420     430     440     450     460

470     480     490     500     510     520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
gi|233  TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDLRRNTFGDFVS---LQVNIINSPT
470     480     490     500     510

530     540     550     560     570     580
Cry1Ac  STRYRVRVRYASVTPPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|233  Q-RYRLRFYASSRDARVILVTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFFRYTDFS
520     530     540     550     560     570

590     600     610     620     630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|233  NPF'SFRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
580     590     600     610     620     630

640     650     660     670     680     690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|233  FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640     650     660     670     680     690

700     710     720     730     740     750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFT
gi|233  NFRGINRQDRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKCLKAYT
700     710     720     730     740     750

760     770     780     790     800     810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|233  RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
760     770     780     790     800     810

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Regulatory Product Characterization Team

820 830 840 850 860 870  
 Cry1Ac NPDDLDCSCRDKGEKCAHSHHFLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLE  
 gi|233 NPDDLDCSCRDKGEKCAHSHHFLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLE

880 890 900 910 920 930  
 Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA  
 gi|233 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

940 950 960 970 980 990  
 Cry1Ac MIHAADKRVHSIREAYLPESVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL  
 gi|233 MIHAADKRVHRIREAYLPESVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL

1000 1010 1020 1030 1040 1050  
 Cry1Ac SCWNVKGHV DVEEQNNQSVLVPVEWEAEVSVQEVVCPGRGYILRVYTAYKEGYEGECVTI  
 gi|233 LCWNVKGHV DVEEQNNHRSVLVPEWEAEVSVQEVVCPGRGYILRVYTAYKEGYEGECVTI

1060 1070 1080 1090 1100  
 Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEA---PSPV  
 gi|233 HEIEDNTDELKFSNCVVEEIVYPNNTVTNNYTGQEEYBGTYSRNRQGYDEAYGNMPSVP

1110 1120 1130 1140 1150 1160  
 Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG  
 gi|233 ADYASVYEEKSYTDGRENPCSNRQGYDTPLPAGYVTKDLEYFPETDKVWIEIGETEG

1170 1180  
 Cry1Ac TFIVDSVELLMEE  
 gi|233 TFIVDSVELLMEE

>>gi|56664670|gb|AAW18095.1| Sequence 61 from patent US (1189 aa)  
 initn: 4550 initl: 3093 opt: 5004 Z-score: 5891.3 bits: 1102.1 E(): 0  
 Smith-Waterman score: 5275; 68.182% identity (83.223% similar) in 1210 aa overlap  
 (5-1182:1-1189)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFLLSEFVPGAGF  
 gi|566 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
 gi|566 LVGLIDFVWGVGPGSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|566 WEEDPNPATRTRVIDRFRILDGLLERDIPSFDISGFEVPLLSVYAQAANLHLAILRDSV

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 gi|566 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNPLPASTYQDWITYNRLRDL

250 260 270 280 290  
 Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-  
 gi|566 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA

300 310 320 330 340 350  
 Cry1Ac IRSPHLM DILNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ  
 gi|566 IRNPHLFDILNLTIFTDWFVSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR

360 370 380 390 400  
 Cry1Ac RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSG  
 gi|566 SFT--FNGVVFRTLSNPTLRLQPPWAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

410 420 430 440 450 460  
 Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN  
 gi|566 TVDSLTELPEPNDVPPREGYSHRLCHATFVQRSGTFFLTGTVV---FSWTHRSATLTN

470 480 490 500 510 520  
 Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST  
 gi|566 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT

530 540 550 560 570 580  
 Cry1Ac STRYRVRYRYSVTPHILNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA  
 gi|566 Q-RYRLFRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFPS

590 600 610 620 630  
 Cry1Ac NAFTASSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL  
 gi|566 NPFSTRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL

640 650 660 670 680 690  
 Cry1Ac FTSTNQLGKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS  
 gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP

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      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGSGTITIQGGDDVFKENYVTLSPGTFDECPYTYLYQKIDESKLLKFT
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 NFRGINRQPDGRWGRSTDTITQGGDDVFKENYVTLPGTVDCEPYTYLYQKIDESKLLKAYT
      700      710      720      730      740      750

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      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 RYELRGYIEDSDLEIYLRIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

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      820      830      840      850      860      870
Cry1Ac NPDLDCSCRDGKCAHSHHFDLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 NPDLDCSCRDGKCAHSHHFDLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

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      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

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      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLEYDARNVIKNGDFNNGL
      940      950      960      970      980      990

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     1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNRQSVLVVPEWEAEVVSQEVRCVGRGYILRVYAYKEGYGEGCVTI
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 LCWNVKGVHDVVEEQNNRQSVLVVPEWEAEVVSQEVRCVGRGYILRVYAYKEGYGEGCVTI
     1000     1010     1020     1030     1040     1050

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     1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSNRNGYNEA---PSVP
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 HEIEDNTDELKFSNCVVEEIVPNNVTTCNNYTGTEYEGYTSRNQGYDEAYGNNSVSP
     1060     1070     1080     1090     1100

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     1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRENPCFENRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEG
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|566 ADYASVYEEKSYTDGRENPCESNRGYDYTPPLPAGYVTKLEYFPETDKVWIEIGETEG
     1120     1130     1140     1150     1160

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     1170     1180
Cry1Ac TFIVDVSELLMEE
      ::::::::::::::
gi|566 TFIVDVSELLMEE
     1180

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>>gi|17920906|gb|AAE86526.1| Sequence 61 from patent US (1189 aa)
  initn: 4550 initl: 3093 opt: 5004 Z-score: 5891.3 bits: 1102.1 E(): 0
Smith-Waterman score: 5275; 68.182% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

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      10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 MEEN-NQNQCIPYNCLSNPEEVLDDGERIETGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

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      70      80      90     100     110     120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESEFRE
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 LVGLIDFVWGIWGFPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKFE
      60      70      80      90     100     110

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     130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 WEEDPNPATRTRVIDRFRILDGLLERDIPSFDISGFVEVPLLSVYAQAANLHLAILRDSV
     120     130     140     150     160     170

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     190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDIRYQFREL
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLPASTYQDWITYNRLRDL
     180     190     200     210     220     230

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     250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 TLTVLDIAAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNQQLQSVLQPLTFNVMESSA
     240     250     260     270     280     290

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     300     310     320     330     340     350
Cry1Ac IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLLYGTMGNAAPQQ
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR
     300     310     320     330     340     350

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     360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSNLPASVYRKSG
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
     360     370     380     390     400

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```

     410     420     430     440     450     460
Cry1Ac TVDSLDEIIPQNNVPPRQGFVSHRSLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
     410     420     430     440     450     460

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     470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 TIDPERINQIPLVKGFVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
     470     480     490     500     510

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     530     540     550     560     570     580
Cry1Ac STRYRVRVRYASVTPHILNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      :::::::::::::: :::::::::::::: :::::::::::::: :::::::::::::: ::::::::::::::
gi|179 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDS

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520      530      540      550      560      570
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|179  NFFSFRANPDIIGISEQLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|179  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
640      650      660      670      680      690
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKPKAFT
gi|179  NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKPKAYT
700      710      720      730      740      750
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|179  RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810
Cry1Ac  NPDLDCSCRDEGKCAHSHHFLDIDVGCTDLNEDLGWVVIKFKIKTQDGHARLGNLEFLE
gi|179  NPDLDCSCRDEGKCAHSHHFTLDIDVGCTDLNEDLGWVVIKFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|179  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|179  MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
940      950      960      970      980      990
Cry1Ac  SCWNKGVHVDVEEQNNQSVLVPVEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTI
gi|179  LCWNKGVHVDVEEQNNHRSVLVPEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTI
1000     1010     1020     1030     1040     1050
Cry1Ac  HEIENNTDELKFSNCVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|179  HEIEDNTDELKFSNCVEEIVPNNTVT CNNTGTQEEYEGTYTSRNQGYDEAYGNPSPV
1060     1070     1080     1090     1100     1110
Cry1Ac  ADYASVYEEKSYTDGRRNPCEFNRGYRDYTP LVPGYVTKLELYFPETDKVWIEIGETEG
gi|179  ADYASVYEEKSYTDGRRNPCEFNRGYRDYTP LVPGYVTKLELYFPETDKVWIEIGETEG

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gi|179  ADYASVYEEKSYTDGRRNPCEFNRGYRDYTP LVPGYVTKLELYFPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170
1170     1180
Cry1Ac  TFIVDSVELLLMEE
gi|179  TFIVDSVELLLMEE
1180
>>gi|158456702|gb|ABW41375.1| Sequence 61 from patent US (1189 aa)
initn: 4550 init1: 3093 opt: 5004 Z-score: 5891.3 bits: 1102.1 E(): 0
Smith-Waterman score: 5275; 68.182% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFPVPGAGF
gi|158  MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
gi|158  LVGLIDFVWIGVSPQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVBAFKE
60      70      80      90      100     110
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|158  WEEDPNNPATRRVIDRFRILDGLLERRDIPSPDISGFVPLLSVYAQAANLHLLAIRLDSV
120     130     140     150     160     170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQRFREL
gi|158  IPGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPASTYQDWITYNRLRRDL
180     190     200     210     220     230
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-
gi|158  TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA
240     250     260     270     280     290
Cry1Ac  IRSPHLMIDLNSITITDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|158  IRNPHLFDILNLTIFTDFWFSVGRNFWYGGHVRVSSSLIG--GGNITSPYIGREANQEPFR
300     310     320     330     340     350
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNNLPSAVYRKSG
gi|158  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360     370     380     390     400
Cry1Ac  TVDSLDEIPPQNNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIIHRSAEFNN
gi|158  TVDSLDEIPPQNNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIIHRSAEFNN

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gi|566 300 310 320 330 340 350
Cry1Ac RIVAQLGQGVYRRLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|566 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
360 370 380 390 400
Cry1Ac TVDSDLDEIPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSDLTELPEDNSVPPREGYSHRLCHATFVQRSPTPLTTGGV----FSWTHRSATLTN
410 420 430 440 450 460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|566 TIDPERINQIPLVKGFRVWGGTTSVITGPGFTGGDILRRNTFGDFVS----LQVNIINSPI
470 480 490 500 510 520
Cry1Ac STRYRVRVRYASVTPIHNLVNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDS
530 540 550 560 570
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSPFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690
Cry1Ac NFKDINRQPERGWGSGTITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKPKAFT
gi|566 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKPKAYT
700 710 720 730 740 750
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810
Cry1Ac NPDLDCSCRDEKCAHSHHSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
gi|566 NPDLDCSCRDEKCAHSHHFTLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566 WEEDNNPATRFRVIDRFRILDGLLERDIPSPDISGFVPLLSVYAQAANLHLAILRDSV
880 890 900 910 920 930

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Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIFTAYSPLYDARNVIKNGDFNNGL
940 950 960 970 980 990
Cry1Ac SCWNVKGVHVDVEEQNNQRSVLPVPEWAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
gi|566 LCWNVKGVHVDVEEQNNHRSVLPVPEWAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
1000 1010 1020 1030 1040 1050
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP
gi|566 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEEYEGTYTSRNQGYDEAYGNPSPV
1060 1070 1080 1090 1100 1110
Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
gi|566 ADYASVYEEKSYTDGRENPCESNRGYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170
Cry1Ac TFIVDSVELLLMEE
gi|566 TFIVDSVELLLMEE
1170 1180
>>gi|158456667|gb|ABW41340.1| Sequence 4 from patent US (1189 aa)
initn: 4548 init1: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)
10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|158 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50
Cry1Ac VLGLVDIINGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|158 LVGLIDFVWGIVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|158 WEEDNNPATRFRVIDRFRILDGLLERDIPSPDISGFVPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|158 WEEDNNPATRFRVIDRFRILDGLLERDIPSPDISGFVPLLSVYAQAANLHLAILRDSV
180 190 200 210 220 230 240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|158 IPGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQG-----IEGS-
gi|158 TLTVLVDIAAAPPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPLQLQVAQLPTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHMLDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|158 IRNPHLFDILNLTIFTDFSVGRNFYWGHRVIVSSSLIG--GGNITSPYIGREANQPEPPR
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRSLTSLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSG
gi|158 SFT--FNGPVPFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVVFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|158 TVDSLTELPEPNSVPPREGYSHRLCHATFVQSRGTPLLTGVV---FSWTHR SATLITN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|158 TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
470 480 490 500 510 520

Cry1Ac STRYRVRVRYASVTPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|158 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDF'S
520 530 540 550 560 570

Cry1Ac NAFTASSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|158 NFFSFRANPDIIGISEQPLFGAGSISSEGLYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|158 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

Cry1Ac NFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTDFDECYPTYLYQKIDESKLAFT
gi|158 NFRGINRQPPDRGWRGSTDITIQGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLAFT
700 710 720 730 740 750

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Cry1Ac 760 770 780 790 800 810
RYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW
gi|158 760 770 780 790 800 810
RYELRGIYEDSQDLEIYLIRYNAKHEIVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW

Cry1Ac 820 830 840 850 860 870
NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|158 820 830 840 850 860 870
NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE

Cry1Ac 880 890 900 910 920 930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|158 880 890 900 910 920 930
EKPLLEGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

Cry1Ac 940 950 960 970 980 990
MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIPTAFSLYDARNVIKNGDFNNGL
gi|158 940 950 960 970 980 990
MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIPTAYSLYDARNVIKNGDFNNGL

Cry1Ac 1000 1010 1020 1030 1040 1050
SCWNVKGHVDEEQNNQRSVLPVPEWAEVSVQEVRCVPCGRGYLLRVTAKEGYGECVVTI
gi|158 1000 1010 1020 1030 1040 1050
LCWNVKGHVDEEQNNHRSVLPVPEWAEVSVQEVRCVPCGRGYLLRVTAKEGYGECVVTI

Cry1Ac 1060 1070 1080 1090 1100
HEIENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|158 1060 1070 1080 1090 1100 1110
HELEDNTDELKFSNCVEEIEYPNNTVTCNNYTGTEYEGTYTSRNQGYDEAYGNPNSVP

Cry1Ac 1110 1120 1130 1140 1150 1160
ADYASVYEEKSYTDGRENPCFNRGYRDYTPPLVGYVTKELEYFPETDKVWIEIGETEG
gi|158 1120 1130 1140 1150 1160 1170
ADYASVYEEKSYTDGRENPCSNRGYGDYTPPLPAGYVTKDLEYFPETDKVWIEIGETEG

Cry1Ac 1170 1180
TFIVDSVELLLMEE
gi|158 1170 1180
TFIVDSVELLLMEE

>>gi|56664635|gb|AAW18060.1| Sequence 4 from patent US 6 (1189 aa)
initn: 4548 init1: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|566 10 20 30 40 50 60
MEEN-NQMQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF

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Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|566 LVGLIDFVWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNVIYVEAFKE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS  
gi|566 WEEDPNNPATRTRVIDRFRILDGLLERDIPSFDISGFVPLLSVYAQAANLHLAILRDSV

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|566 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL

Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQTLREIYTNVLENFVDFGSAQ-----IEGS-  
gi|566 TLTVLVDIAAFFPNYDNRYPQIPVQQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA

Cry1Ac IRSPHMLDILNSITIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQ  
gi|566 IRNPHLFDILNLLTIFTDWFSVGRNFYWGHRVIVSSLI--GNITSPYIGREANQEPFR

Cry1Ac RIVAQLGGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS  
gi|566 SFT--FNGVVFRTLSTNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN  
gi|566 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGVV---FSWTHRSATLTN

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST  
gi|566 TIDPERINQIPLVKGRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNNISPT

Cry1Ac STRYRVVRYASVTP IHLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA  
gi|566 Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSNMPLQKTIMEIGENLTSRTFRYTFDS

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL  
gi|566 NPFSSFRANPDIIGISEQPLFGAGSISSEELYIDKIEIILADATFAESDLERAQKAVNAL

Cry1Ac FTSTNQLGLKTNVDYHIDQVSNLVTYLSDSEFLDDEKRELSEKVKHAKRLSDERNLLQDS  
gi|566 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFLDDEKRELSEKVKHAKRLSDERNLLQDP

Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLIKAFPT  
gi|566 NFRGINRQPRDGRWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLIKAYT

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW  
gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW

Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE  
gi|566 NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA  
gi|566 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL  
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAYSLYDARNVIKNGDFNNGL

Cry1Ac SCWNVKGHVDEEQQNQRSVLVPEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTI  
gi|566 LCWNVKGHVDEEQNHRSVLVIPEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTI

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP  
gi|566 HEIEDNTDELKFSNCVEEIVPNTVTCNNYTGTEYEGYTYTSRNOQGYDEAYGNPVSVP

Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG  
gi|566 ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG

Cry1Ac TFIVDSVELLLMEE  
gi|566 TFIVDSVELLLMEE

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1180
>>gi|14103735|gb|AAE55169.1| Sequence 4 from patent US 6 (1189 aa)
initn: 4548 initl: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|141 MEEN-NQNCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

Cry1Ac VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|141 LVGLIDFWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNPNFYVEAFKE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEEDPNNPATRTRVIDRFRILDGLLERDIPSPFDISGFVPLLSVYVQAANLHLAIRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|141 IFGERWGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRRLDL

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGSAQG----IEGS-
gi|141 TLTVLDIAAAPPNYNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA

Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQ
gi|141 IRNPHLFDILNLLTIFTDWFVSGRNFYWGGRHVIVSSLIG--GGNITSPIYGREANQPEPR

Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSNNLPSAVYRKSG
gi|141 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTTGVV---FSWTHRSATLTLN

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFST
gi|141 TIDPERINQIPLVKGRFVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT

470 480 490 500 510
530 540 550 560 570 580
Cry1Ac STRYRVRVRYASVTPHILNWNWGNSSI-----FSNTVVPATATSL--DNLQSSDFGYFESA
gi|141 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPKQKMEIGENLTSRTFRYTDIFS

590 600 610 620 630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVPTATLEAEYNLERAQKAVNAL
gi|141 NPFSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL

640 650 660 670 680 690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDS
gi|141 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDP

700 710 720 730 740 750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLAFT
gi|141 NFRGINRQDRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT

760 770 780 790 800 810
Cry1Ac RYQLRGIYIEDSDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIKCKGEPNRCAPHLEW
gi|141 RYELRGIYIEDSDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIKCKGEPNRCAPHLEW

820 830 840 850 860 870
Cry1Ac NPDLDSCDRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
gi|141 NPDLDSCDRDGEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE

880 890 900 910 920 930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|141 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

940 950 960 970 980 990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL

1000 1010 1020 1030 1040 1050
Cry1Ac SCWNVKGHVDEEQNNQSVLVVPEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
gi|141 LCWNVKGHVDEEQNNHRSVLVPEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI

1060 1070 1080 1090 1100
Cry1Ac HEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|141 HEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP

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gi|141 HEIEDNTDELKFSNCVVEEVYPNNTVTTCNNYTGTEEEYEGTYTSRNGQYDEAYGNNSVP
1060 1070 1080 1090 1100 1110

1110 1120 1130 1140 1150 1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG

gi|141 ADYASVYEEKSYTDGRRENPCSNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

1170 1180
Cry1Ac TFIVDSVELLMEE

gi|141 TFIVDSVELLMEE
1180

>>gi|18913153|gb|AAL79362.1| delta-endotoxin [Bacillus t (1189 aa)
initn: 4548 initl: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

gi|189 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFQPSQWDFAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFRE

gi|189 LVGLIDFVWGIWVQPSQWDFAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS

gi|189 WEEDPNNPATRTRIDFRILDLGLLERDIPSFRIISGFVPLLSVYAQAANLHLAHLRDSV
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

gi|189 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

250 260 270 280 290
Cry1Ac TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG----IEGS-

gi|189 TLTVLIDIAAFFPNYDNRYPQVPGQLTREYVTDPLI-NFNPQLQSVQAALPTFVMESSA
240 250 260 270 280 290

300 310 320 330 340 350
Cry1Ac IRSPHMDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ

gi|189 IRNPHLFDILNLTITFTDWFVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

360 370 380 390 400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAFGTSSNLPASVYRKSG

gi|189 SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

410 420 430 440 450 460
Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN

gi|189 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV----FSWTHRSATLTN
410 420 430 440 450 460

470 480 490 500 510 520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST

gi|189 TIDPERINQIPLVKGFRVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
470 480 490 500 510

530 540 550 560 570 580
Cry1Ac STRYRVRVRYASVTPPIHLNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA

gi|189 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLOKTEIGENLTSRTFRYTDPS
520 530 540 550 560 570

590 600 610 620 630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL

gi|189 NPFSTRANPDIIGISQPLFAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

640 650 660 670 680 690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDS

gi|189 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

700 710 720 730 740 750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKPKAFT

gi|189 NFRGINRQPRDGRWGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKPKAYT
700 710 720 730 740 750

760 770 780 790 800 810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW

gi|189 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

820 830 840 850 860 870
Cry1Ac NPDLDCSCRDEKCAHSHHFLDIDVGTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLE

gi|189 NPDLDCSCRDEKCAHSHHFTLDIDVGTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

880 890 900 910 920 930
Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA

gi|189 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930

940 950 960 970 980 990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAEIFEELGRIPTAFSLYDARNVIKNGDFNNGL

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gi|189 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLVDARNVKNKGNDFNNGL
    940    950    960    970    980    990
Cry1Ac SCWNVKGVHDVVEEQNNRQSVLVPVEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI
    1000    1010    1020    1030    1040    1050
gi|189 LCWNVKGVHDVVEEQNNRQSVLVPVEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI
    1000    1010    1020    1030    1040    1050
Cry1Ac HEIENNTDELKFSNCVEEIEYPNNTVTNNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
    1060    1070    1080    1090    1100
gi|189 HEIEDNTDELKFSNCVEEIEYPNNTVTNNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
    1060    1070    1080    1090    1100    1110
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
    1110    1120    1130    1140    1150    1160
gi|189 ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
    1110    1120    1130    1140    1150    1160
Cry1Ac TFIVDSVELLLMEE
    1170    1180
gi|189 TFIVDSVELLLMEE
    1180
>>gi|23325080|gb|AAN23780.1| Sequence 4 from patent US 6 (1189 aa)
  initn: 4548 initl: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
    10    20    30    40    50    60
gi|233 MEEN-NQNQCIPYNCLSNPEVEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
    10    20    30    40    50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
    70    80    90    100    110    120
gi|233 LVGLIDFVWVIGVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
    60    70    80    90    100    110
Cry1Ac WEADTPNAPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
    130    140    150    160    170    180
gi|233 WEEDPNPATRTRVDRFRILDGLLERDIPSPDISGFVPLLSVYVQAANLHLSVLRDVS
    120    130    140    150    160    170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
    190    200    210    220    230    240
gi|233 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
    180    190    200    210    220    230
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQG-----IEGS-
    250    260    270    280    290

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gi|233 TLTVLDIAAFFPNYDNRRIPIQFVGLTREVYTDPLI--NFNQQLQVAQLPTFNVMESSA
    240    250    260    270    280    290
Cry1Ac IRSPHLMIDLINSITIIYDADR-GE--YVWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQ
    300    310    320    330    340    350
gi|233 IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVSISSLIG--GGNITSPIYGREANQEPFR
    300    310    320    330    340    350
Cry1Ac RIVAQLGQVYRITLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQ
    360    370    380    390    400
gi|233 SPT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
    360    370    380    390    400
Cry1Ac TVDSLDEIPPNQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAMPFSWIHRSAEFNN
    410    420    430    440    450    460
gi|233 TVDSLDELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTGTGVV----FSWTHRSATLTN
    410    420    430    440    450    460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNYIEVPIHFPST
    470    480    490    500    510    520
gi|233 TIDPERINQIPLVKGFRVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
    470    480    490    500    510
Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
    530    540    550    560    570    580
gi|233 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMEIGENLTSRTFRYTDFS
    520    530    540    550    560    570
Cry1Ac NAFTASSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
    590    600    610    620    630
gi|233 NPFSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
    580    590    600    610    620    630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
    640    650    660    670    680    690
gi|233 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
    640    650    660    670    680    690
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLAFT
    700    710    720    730    740    750
gi|233 NFRGINRQPDWRGSTDITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLAFT
    700    710    720    730    740    750
Cry1Ac RYQLRGIYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
    760    770    780    790    800    810
gi|233 RYELRGIYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
    760    770    780    790    800    810
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQG-----IEGS-
    820    830    840    850    860    870

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Cry1Ac  NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
gi|233  NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|233  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|233  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGVHDVVEEQNNQSRVSVLVPWEAEVSVQEVVRCVPCGRGYILRVVTAYKEGYEGGCVTI
gi|233  SCWNVKGVHDVVEEQNNQSRVSVLVPWEAEVSVQEVVRCVPCGRGYILRVVTAYKEGYEGGCVTI
      1000     1010     1020     1030     1040     1050

      1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVEEIEYFNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|233  HEIENNTDELKFSNCVEEIEYFNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      1060     1070     1080     1090     1100     1110

      1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|233  ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170

      1170     1180
Cry1Ac  TFIIVDSVELLLMEE
gi|233  TFIIVDSVELLLMEE
      1180

>>gi|19880135|gb|AAM00264.1|AF362020_1 insecticidal prot (1189 aa)
  initn: 4548  initl: 3093  opt: 5002  Z-score: 5889.0  bits: 1101.7  E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|198  MEEN-NQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|198  VLGLIDFVWIVGQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNVIYVEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180

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Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|198  WEEDPNPATRTRVIDRFRILDGLLERRDIPSPFRISGFVPLLSVYVQAANLHAILRDSV
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFREL
gi|198  IPGERWGLTTINWENYRNLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG----IEGS-
gi|198  TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPLQLSVAQLPTFNVMESSA
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac  IRSPHLMIDLNSITIIYTDAGR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|198  IRNPHLFDILNLTIFTDFWVGRNRYFVGGHRVSSLIG--GGNITSPIYGREANQPPR
      300      310      320      330      340      350

      360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPYSAVYRKSG
gi|198  SFT--FNGVVFRTLSNPTLRLQLQPPWAPPFN--LRGVGVGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400

      410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPRQGFSHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|198  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGTVV---FSWTHRSATLTN
      410      420      430      440      450      460

      470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|198  TIDPERINQIPLVKGRVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac  STRYRVVRVRYASVTPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|198  Q-RYRLRFYASSRDARVILVTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFFYTFDS
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|198  NPFSSFRANPDIIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|198  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

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      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGSGTITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAFK
gi|198 NFRGINRQPDGRGWRGSDTITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYT
      700      710      720      730      740      750

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      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|198 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

```

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      820      830      840      850      860      870
Cry1Ac NPDLDCSRDEKCAHSHHFLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLE
gi|198 NPDLDCSRDEKCAHSHHFTLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

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      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|198 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

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      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|198 MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAYSLSYDARNVIKNGDFNNGL
      940      950      960      970      980      990

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     1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQRSVLVVPEWEAEVVSQEVVRCVCPGRGYILRVYTAYKEGYGEGCVTI
gi|198 LCWNVKGVHDVVEEQNNHRSVLVVPEWEAEVVSQEVVRCVCPGRGYILRVYTAYKEGYGEGCVTI
     1000     1010     1020     1030     1040     1050

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     1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|198 HEIEDNTDELKFSNCVVEEVYPNNTVTCNNYTGTEYEGYTSRNRQGYDEAYGNNSVSP
     1060     1070     1080     1090     1100     1110

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     1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
gi|198 ADYASVYEEKSYTDGRENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
     1120     1130     1140     1150     1160     1170

```

```

     1170     1180
Cry1Ac TFIVDSVELLLMEE
gi|198 TFIVDSVELLLMEE
     1180

```

>>gi|14112740|gb|AAE58155.1| Sequence 4 from patent US 6 (1189 aa)  
 initn: 4548 initl: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0  
 Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap  
 (5-1182:1-1189)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|141 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

```

```

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|141 LVGLIDFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAAI ANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110

```

```

     130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEEDPNNPATRTRVIDRFRILDGLLERDIPSPDISGFVPLLSVYAQAANLHLAILLRDVS
     120     130     140     150     160     170

```

```

     190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
gi|141 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRNLNLPKSTYQDWITYNRLRDL
     180     190     200     210     220     230

```

```

     250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-
gi|141 TLTVLDIAAFFPNYDNRRYPIQPVGQLTRVYTDPLI-NFNPLQLSVAQLPTFNVMESSA
     240     250     260     270     280     290

```

```

     300     310     320     330     340     350
Cry1Ac IRSPHLMIDILNSITIYTDADR-GE-YYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQ
gi|141 IRNPHLFDILNLTIFTDFWFSVGRNRYWGGHRVSSLIG--GGNITSPIYGREANQEPFR
     300     310     320     330     340     350

```

```

     360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSG
gi|141 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
     360     370     380     390     400

```

```

     410     420     430     440     450     460
Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSATLTN
     410     420     430     440     450     460

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```

     470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|141 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILLRNTFGDFVS---LQVNNISPIT
     470     480     490     500     510

```

```

     530     540     550     560     570     580
Cry1Ac STRYRVRYASVTPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|141 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDPS
     520     530     540     550     560     570

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          590          600          610          620          630
Cry1Ac NAFTSSLG-NIVGVNR---F---SGTAG-VIIDRFEPVPTATLBAEYNLERAQKAVNAL
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 NFFSFRANPDIIGIGEQPLFGAGSISSELYIDKLEIILADATFAESDLERAQKAVNAL
      580      590      600      610      620      630

```

```

          640          650          660          670          680          690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

```

```

          700          710          720          730          740          750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLKAF
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 NFRGINRQPDGRGWRGSDITITQGGDDVFKENYVTLPGTVDCEYPTYLYQKIDESKLKAY
      700      710      720      730      740      750

```

```

          760          770          780          790          800          810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

```

```

          820          830          840          850          860          870
Cry1Ac NPDLDCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

```

```

          880          890          900          910          920          930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

```

```

          940          950          960          970          980          990
Cry1Ac MIHAADKRVHSIREAYLPESVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 MIHAADKRVHRIREAYLPESVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

```

```

         1000         1010         1020         1030         1040         1050
Cry1Ac SCWNVKGHV DVEEQNNRSLVLPVEWEAEVSVQEVRCVGRGYILRVYAYKEGYEGECVTI
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 LCWNVKGHV DVEEQNNRSLVLPVEWEAEVSVQEVRCVGRGYILRVYAYKEGYEGECVTI
      1000      1010      1020      1030      1040      1050

```

```

         1060         1070         1080         1090         1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNTYGTQEEYEGYTSRNRQYDEAYGNPNSVP
      1060      1070      1080      1090      1100

```

```

         1110         1120         1130         1140         1150         1160
Cry1Ac ADYASVYEEKSYTDGRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 ADYASVYEEKSYTDGRENPCSNRYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG

```

```

          1120          1130          1140          1150          1160          1170
          1170          1180
Cry1Ac TFIVDSVELLLMEE
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|141 TFIVDSVELLLMEE
          1180

```

```

>>gi|37540181|gb|AAG50438.1| Cry1Ca [Bacillus thuringien (1189 aa)
  initn: 4548 init1: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

```

```

          10          20          30          40          50          60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
          10          20          30          40          50

```

```

          70          80          90          100          110          120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
          60          70          80          90          100          110

```

```

          130          140          150          160          170          180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  WEEDPNPATRTRVIDRFRILDLGLLERDIPSPRISGFVEVPLLSVYAQAANLHLAILRDSV
          120          130          140          150          160          170

```

```

          190          200          210          220          230          240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  IFGERWGLTTINVENYENRILIRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLRDL
          180          190          200          210          220          230

```

```

          250          260          270          280          290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  TLTVLDIAAFFPNYDNRRIPIQVQGLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA
          240          250          260          270          280          290

```

```

          300          310          320          330          340          350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  IRNPHLFDILNNTIFTDWFVSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR
          300          310          320          330          340          350

```

```

          360          370          380          390          400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLSAVYRKSG
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFES--TPTN--SFTYRGRG
          360          370          380          390          400

```

```

          410          420          430          440          450          460
Cry1Ac TVDSLDEIPPQNNVPPRQGFHSHLSVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|375  TVDSLTELPEPNSVPPRQGFHSHLSVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN

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410      420      430      440      450      460
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  TIDPERINQIPLVKGFVRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
      470      480      490      500      510
Cry1Ac  STRYRVRVRYASVTPPIHLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMP LQK TME IGENLTSRTFRYTD FS
      520      530      540      550      560      570
Cry1Ac  STRYRVRVRYASVTPPIHLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMP LQK TME IGENLTSRTFRYTD FS
      580      590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  NPFSSFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
      640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITTIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAYT
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  NFRGINRQPDGRWGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYT
      760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSDLEIYSLIRYNAKHETVNVPGTGLWPLSAQSPIGKCEPNRCAPHLEW
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  RYELRGYIEDSDLEIYSLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCEPNRCAPHLEW
      820      830      840      850      860      870
Cry1Ac  NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHV DVEEQNNRQSVLVVPEWAEVSVQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|375  LCWNVKGHV DVEEQNNRQSVLVVPEWAEVSVQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050
Cry1Ac  HEIENNTDELKFSNCEVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  HEIEDNTDELKFSNCEVEEIVPNNVTTCNNYTGTEQEEYEGTYTSRNRQGYDEAYGNNSVSP
      1060     1070     1080     1090     1100     1110
Cry1Ac  ADYASVYEEKSYTDGRRNPCEFNRYGDRDYTPPLVGYVTKELEYFPETDKVWIEIGETEG
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  ADYASVYEEKSYTDGRRNPCEFNRYGDRDYTPPLVGYVTKELEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170
Cry1Ac  TFIVDSVELLLMEE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  TFIVDSVELLLMEE
      1170     1180
Cry1Ac  TFIVDSVELLLMEE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|375  TFIVDSVELLLMEE
      1180

>>gi|34423558|gb|AAQ68987.1| Sequence 6 from patent US 5 (1189 aa)
  initn: 4548 initl: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQPLLESEFVPGAGF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|344  MEEN-NQNQCIPYCNLSNPEVEVLGGERISTGNSSIDISLSLVQPLVSNFVPGGGF
      70      80      90      100     110     120
Cry1Ac  VLGLVDIIVGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|344  LVGLIDFVWVIGVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|344  WEEDPNNPATRTRVIDRFRILDGLLERDIPSFRI SGFEVPLLSVYVQAANLHLLAILRDSV
      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|344  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWIITYNRLRRDL
      250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG-----IEGS-
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|344  TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNQLQSVLQPLTFNVMESSA
      300     310     320     330     340     350
Cry1Ac  IRSPHLMIDILNSITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|344 IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

          360      370      380      390      400
Cry1Ac RIVAQLGGQVYRTLSTLYR---RPFNIGINNQQLSVLDTGTEFAYGTSSNLPSAVYRKSQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
          360      370      380      390      400

          410      420      430      440      450      460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQVRSPTPLTTGVV---FSWTHRSATLTN
          410      420      430      440      450      460

          470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 TIDPERINQIPLVKGRVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNNISPTI
          470      480      490      500      510

          530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTIMEIGENLTSRTFRYTDFS
          520      530      540      550      560      570

          590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 NPFSSFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFAESDLERAQKAVNAL
          580      590      600      610      620      630

          640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
          640      650      660      670      680      690

          700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKDKAFT
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTDECYPTYLYQKIDESKDKAYT
          700      710      720      730      740      750

          760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
          760      770      780      790      800      810

          820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEKCAHSHHSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 NPDLDCSCRDEKCAHSHHFTLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
          820      830      840      850      860      870

          880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA

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          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 EKPLLGEALARVKRAEKKWRDKREKLEQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
          880      890      900      910      920      930

          940      950      960      970      980      990
Cry1Ac MIHAADKRVHSTIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 MIHAADKRVHSTIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLEYDARNVIKNGDFNNGL
          940      950      960      970      980      990

          1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDEVEEQNNQSRVSVLVPWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 LCWNVKGHVDEVEEQNNHRSVLPVPEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
          1000      1010      1020      1030      1040      1050

          1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEQEEYEGTYTSRNRQGYDEAYGNPSPV
          1060      1070      1080      1090      1100      1110

          1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYPETDKVWIEIGETEG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 ADYASVYEEKSYTDGRRENPCSNRQYDTPPLPAGYVTKDLEYPETDKVWIEIGETEG
          1120      1130      1140      1150      1160      1170

          1170      1180
Cry1Ac TFIVDSVELLLMEE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 TFIVDSVELLLMEE
          1180

>>gi|56642268|gb|AAW11986.1| Sequence 4 from patent US 6 (1189 aa)
initn: 4548 init1: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|566 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|566 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDSV
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|566 WEEDPNPATRTRVIDRFRILDGLLERDIPSPDISGFEVPLLSVYVQAANLHLLLRDSV
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

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gi|566 180 190 200 210 220 230
Cry1Ac 250 260 270 280 290
gi|566 240 250 260 270 280 290
Cry1Ac 300 310 320 330 340 350
gi|566 300 310 320 330 340 350
Cry1Ac 360 370 380 390 400
gi|566 360 370 380 390 400
Cry1Ac 410 420 430 440 450 460
gi|566 410 420 430 440 450 460
Cry1Ac 470 480 490 500 510 520
gi|566 470 480 490 500 510 520
Cry1Ac 530 540 550 560 570 580
gi|566 520 530 540 550 560 570
Cry1Ac 590 600 610 620 630
gi|566 580 590 600 610 620 630
Cry1Ac 640 650 660 670 680 690
gi|566 640 650 660 670 680 690
Cry1Ac 700 710 720 730 740 750
gi|566 700 710 720 730 740 750
Cry1Ac 760 770 780 790 800 810
gi|566 760 770 780 790 800 810

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Cry1Ac 820 830 840 850 860 870
gi|566 820 830 840 850 860 870
Cry1Ac 880 890 900 910 920 930
gi|566 880 890 900 910 920 930
Cry1Ac 940 950 960 970 980 990
gi|566 940 950 960 970 980 990
Cry1Ac 1000 1010 1020 1030 1040 1050
gi|566 1000 1010 1020 1030 1040 1050
Cry1Ac 1060 1070 1080 1090 1100
gi|566 1060 1070 1080 1090 1100
Cry1Ac 1110 1120 1130 1140 1150 1160
gi|566 1110 1120 1130 1140 1150 1160
Cry1Ac 1170 1180
gi|566 1170 1180
>>gi|17920871|gb|AAE86491.1| Sequence 4 from patent US 6 (1189 aa)
initn: 4548 init1: 3093 opt: 5002 Z-score: 5889.0 bits: 1101.7 E(): 0
Smith-Waterman score: 5273; 68.182% identity (83.140% similar) in 1210 aa overlap
(5-1182:1-1189)
Cry1Ac 10 20 30 40 50 60
gi|179 10 20 30 40 50
Cry1Ac 70 80 90 100 110 120
gi|179 70 80 90 100 110 120

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Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
gi|179 LVGLIDFVWIVGSPQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE  
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|179 WEEDPNPATRTRVIDRFRILDGLLERDIPSPDISGFVPLLSVYAQAANLHLAILRDSV  
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|179 IFGERWGLTTINVENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDL  
180 190 200 210 220 230

Cry1Ac TLTVDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQG-----IEGS-  
gi|179 TLTVDIAAFFPNYDNRYPQVQQLTREVYTDPLI-NFNPQLQSVQQLPTFNVMESSA  
240 250 260 270 280 290

Cry1Ac IRSPHMLDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEPTFFPLYGTMGNAAPQQ  
gi|179 IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVIVSSLI--GGNITSPIYGREANQEPFR  
300 310 320 330 340 350

Cry1Ac RIVAQLQGQVYRSLTSLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS  
gi|179 SFT--FNGFVFRSLNPTLRLLQQPWPAPPFN--LRGVEGVFVS--TPTN--SFTYRGRG  
360 370 380 390 400

Cry1Ac TVDSDLDEIPPQNNVPPRQGFHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN  
gi|179 TVDSDLTELPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGVV----FSWTHRSATLTN  
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST  
gi|179 TIDPERINQIPLVKGRFVWGGTSSVITGPGFTGGDLRRNTFGDFVS---LQVNIINSPI  
470 480 490 500 510 520

Cry1Ac STRYRVRVRYASVTPIHNLNVNMGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA  
gi|179 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFRYTD  
520 530 540 550 560 570

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL  
gi|179 NPFSTRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL  
580 590 600 610 620 630

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS  
gi|179 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP  
640 650 660 670 680 690

Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT  
gi|179 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT  
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW  
gi|179 RYELRGYIEDSDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW  
760 770 780 790 800 810

Cry1Ac NPDLCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE  
gi|179 NPDLCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE  
820 830 840 850 860 870

Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA  
gi|179 EKPLLGEALARVKRAEKKWRDKREKLELQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA  
880 890 900 910 920 930

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL  
gi|179 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNGL  
940 950 960 970 980 990

Cry1Ac SCWNVKGVHDVEEQNNQSRVSVLVPWEAEVSVQEVVCPGRGYILRVTAAYKEGYGEGCVTI  
gi|179 LCWNVKGVHDVEEQNNHRSVSVLVIPEWEAEVSVQEVVCPGRGYILRVTAAYKEGYGEGCVTI  
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP  
gi|179 HEIEDNTDELKFSNCVEEIVPNNTVTCNNYTGTEEEYEGTYTSRNOGYDEAYGNMPSVP  
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYYVTKLELYFPETDKVWIEIGETEG  
gi|179 ADYASVYEEKSYTDGRRENPCESNRGYGDTPLPAGYVTKDLYFPETDKVWIEIGETEG  
1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLLMEE  
gi|179 TFIVDSVELLLMEE  
1170 1180

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>>gi|56642272|gb|AAW11990.1| Sequence 12 from patent US (1189 aa)
initn: 4546 initl: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

Cry1Ac VLGLVDIWIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWGVGQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNVIYVAFKE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|566 WEEDPHNPATRTRVIDRFRILDGLLERDIPSPRISGFVPLLSVYAQAANLHLAILRDSV

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
gi|566 IFGERWGLTTINVENYENRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRDL

Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG----IEGS-
gi|566 TLTVLDAIAAFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNMESSA

Cry1Ac IRSPHLMIDLNSITIYTDahr-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|566 IRNPHLFDILNLLTIFTDFWVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFR

Cry1Ac RIVAQLQGQVYRTLSTLYR--RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS
gi|566 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPELTTGVV---FSWTHRSATLTN

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNLSGNNIQRNGYIEVPIHFPST
gi|566 TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRTFVDFVS---LQVNNISPTI

Cry1Ac STRYRVRVRYASVTPHILNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFFRYTDFFS

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPF'SFRANPDIIGISQQLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNAL

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP

Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLAFT
gi|566 NFRGINRQPRDGRWGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGYIEDSQDLEIYLIRYNKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEW

Cry1Ac NPDLDCSCRDEKCAHSHHFLDIDVGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
gi|566 NPDLDCSCRDEKCAHSHHFTLDIDVGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL

Cry1Ac SCWNVKGHVDEEQNNQSVLVVPEWAEVSVQEVRCVCPGRGYILRVTAAYKEGYGECVTI
gi|566 LCWNVKGHVDEEQNNHRSVLVPEWAEVSVQEVRCVCPGRGYILRVTAAYKEGYGECVTI

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|566 HEIEDNTDELKFSNCVEEIVPNNTVTCNNYTGTEYEGYTSRNRQYDEAYGNNPSVP

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1060      1070      1080      1090      1100      1110
1110      1120      1130      1140      1150      1160
Cry1Ac  ADYASVYEEKSYTDGRENPCFNRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEG
gi|566  ADYASVYEEKSYTDGRENPCFNRGYDYTPPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120      1130      1140      1150      1160      1170

1170      1180
Cry1Ac  TFIVDSVELLLMEE
gi|566  TFIVDSVELLLMEE
1180

>>gi|14103739|gb|AAE55173.1| Sequence 12 from patent US (1189 aa)
initn: 4546 init1: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|141  MEEN-NQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGIIFGSPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESPFE
gi|141  LVGLIDFVWIVGSPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|141  WEEDPHNPATRRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|141  IFGERWGLTTINVNENYRNLIRHIDEBYADHCANTYRNLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGFSFRGSAQG-----IEGS-
gi|141  TLTVLDIAAFFFNYDNRRYPIQPVGQLTREYVTDPLI-NFNPQLQSVQALPTFNVMESSA
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  IRSPHLMIDLINSITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQ
gi|141  IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRHVISSLIG--GNNITSPIYGREANQEPFR
300     310     320     330     340     350

360     370     380     390     400
Cry1Ac  RIVAQLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|141  SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG

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360      370      380      390      400
410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSSNSVSIIRAMPFSWIHRSAEFNN
gi|141  TVDSLTELPEDNSVPPREGYSHRLCHATFVQVRSRGTFFLTGGV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|141  TIDPERINQIPLVKGFVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|141  Q-RYRLFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTFRYTFDS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
gi|141  NPFSTRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|141  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLAFT
gi|141  NFRGINRQPRGWRGSTDITIQGGDDVFKENYVTLVPGTVDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKGCPEPNRCAPHLEW
gi|141  RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKGCPEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac  NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
gi|141  NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|141  EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL

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gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSPLYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac SCWNVKGHV DVEEQNNQRSVLVVPEWEAEVVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

gi|141 LCWNVKGHV DVEEQNNHRSVLVIPWEAEVVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
1060 1070 1080 1090 1100

gi|141 HEIEDNTDELKFSNCVVEEIVPNNTVTTCNNTGTQEEYEGYTSRNQGYDEAYGNNSPVP
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEG
1110 1120 1130 1140 1150 1160

gi|141 ADYASVYEEKSYTDGRRNPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLLMEE
1170 1180

gi|141 TFIVDSVELLLMEE
1180

>>gi|56664639|gb|AAW18064.1| Sequence 12 from patent US (1189 aa)
initn: 4546 initl: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

gi|566 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|566 LVGLIDFVWGI VGPSQWDAFLVQIEQLINERIAEFARNAAI ANLEGLGNPNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTN PALREEMRIQFNDMNSALTTAIP LFAVQNYQVPLLSVYQAANLHLSVLRDVS
130 140 150 160 170 180

gi|566 WEEDPHN PATRTRVIDRFRILDGLLERDIP SFRI SGFEVPLLSVYAQAANLH LAI LRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDH AVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|566 IFGERWGLTTIN VNNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTR EYITNPVLENFDGSRGSAQG-----IEGS-
250 260 270 280 290

gi|566 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFN PQLQSVAQLPTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHLM DILNSITIIYTD AHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
300 310 320 330 340 350

gi|566 IRNPHLFDILN NLTIFTDFWFSVGRNFYWG GHRVVISSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTL SSSLTYR---RPFNIGINNQQLSVLDGTEFAYGTSNLP SVAVYRKSG
360 370 380 390 400

gi|566 SFT--FNGPVFRTL SNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEI PPQNNVPPRQGF SHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
410 420 430 440 450 460

gi|566 TVDSLTELP PEDNSVPPREGYSHRLCHATFVQRSGT PFLTGTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFST
470 480 490 500 510 520

gi|566 TIDPERINQIPLVKGF RVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNI NSPIT
470 480 490 500 510

Cry1Ac STRYRVRYR YASVTPIH LNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|566 Q-RYRLRFRYAS SRDARVIVL TGAASTGVGGQVSNMPLQK TMEIGENLTSRTFRYTD FS
520 530 540 550 560 570

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
590 600 610 620 630

gi|566 NPF SFRANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
640 650 660 670 680 690

gi|566 FTSSNQIGLKT DVTDYHIDQVSNLV DCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL SGTDFDECYPTYLYQKIDESKCLKAFT
700 710 720 730 740 750

gi|566 NFRGINRQ PDRGWRGSTDITIQGGDDVFKENYVTL PGTVDECYPTYLYQKIDESKCLKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGS LWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGS LWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac NPDLDCSRDRGEKCAHSHHFSLDIDVGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

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gi|566 NPDLLDCSCRDGKCAHSHHFTLDIDVGCTDLNEDLVGVVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870
Cry1Ac 880      890      900      910      920      930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930
Cry1Ac 940      950      960      970      980      990
MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990
Cry1Ac 1000     1010     1020     1030     1040     1050
SCWNVKGHV DVEEQNNQRSVLVVPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTI
gi|566 LCWNVKGHV DVEEQNNHRSVLVPIPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050
Cry1Ac 1060     1070     1080     1090     1100
HEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|566 HEIEDNTDELKFSNCEVEEIVPNNVTTCNNYGTQEEYEGTYTSRNQGYDEAYGNNPSPV
      1060     1070     1080     1090     1100     1110
Cry1Ac 1110     1120     1130     1140     1150     1160
ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|566 ADYASVYEEKSYTDGRRNPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170
Cry1Ac 1170     1180
TFIVDSVELLLMEE
gi|566 TFIVDSVELLLMEE
      1180
>>gi|158456671|gb|ABW41344.1| Sequence 12 from patent US (1189 aa)
  initn: 4546 initl: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|158 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGFF
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNLYQIYAESFRE
gi|158 LVGLIDFVWGVGQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNIIYVEAFKE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVQAANLHLSVLRDVS

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gi|158 WEEDPHNPATRRVDIRFRILDGLLERDIPSPRISGFVEVPLLSVYAQAANLHLAILLRDSV
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRWDIYRQVFRREL
gi|158 IPGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG----IEGS-
gi|158 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA
      240      250      260      270      280      290
Cry1Ac 300      310      320      330      340      350
IRSPHLMIDLNSITITYTDAHR-GE-YWWSGHQIMASPVGFSGPEPTFPLYGTMGNAAPQQ
gi|158 IRNPHLFDILNLLTIFTDWFSVGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350
Cry1Ac 360      370      380      390      400
RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLPSPAVYRKSQ
gi|158 SFT--FNGPVFRTLSNPTLRLLQQPWAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400
Cry1Ac 410      420      430      440      450      460
TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|158 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSATLTN
      410      420      430      440      450      460
Cry1Ac 470      480      490      500      510      520
IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQRNGYIEVPIHPFST
gi|158 TIDPERINQIPLVKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
      470      480      490      500      510
Cry1Ac 530      540      550      560      570      580
STRYRVRVRYASVTPIHLNVNNGNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|158 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMP LQKTEMEIGENLTSRTFRYTDPS
      520      530      540      550      560      570
Cry1Ac 590      600      610      620      630
NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|158 NPFSTRANPDIIGISEQLPFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630
Cry1Ac 640      650      660      670      680      690
FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|158 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690
Cry1Ac 700      710      720      730      740      750

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Cry1Ac NFKDINRQPERGWGGSTGITIQQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKPKAFT
gi|158 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECPYTYLYQKIDESKPKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|158 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac NPDLDCSCRDKGEKCAHSHHFLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
gi|158 NPDLDCSCRDKGEKCAHSHHFTLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|158 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|158 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac SCWNVKGHVVDVEEQNNQSVLVPVEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|158 LCWNVKGHVVDVEEQNNHRSVLPVPEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTTCNDYTVNQEYEGAYTSRNRGYNEA---PSVP
gi|158 HEIEDNTDELKFSNCVEEIVPNNTVTTCNNTYGTQEYEGYTSRNRQGYDEAYGNPSPV
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYGDRYDTPPLVGYVTKLEYFPEYDVKWIEIGETEG
gi|158 ADYASVYEEKSYTDGRRNPCEFNRYGDRYDTPPLVGYVTKLEYFPEYDVKWIEIGETEG
1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLMEE
gi|158 TFIVDSVELLMEE
1180

>>gi|17920875|gb|AAE86495.1| Sequence 12 from patent US (1189 aa)
initn: 4546 initl: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10 20 30 40 50 60

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|179 MEEN-NQNQCIPYNCLSNPEVEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|179 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEAFARNAIANLEGLGNFNLYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|179 WEEDPHNPATRTFRVIDRFRILDGLLERRDIPSFRI SGFEVPLLSVYAQAANLHLLLRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|179 IFGERWGLTTINWENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQG-----IEGS-
gi|179 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPLQSVLQPLTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHMLDILNSITIYTDADR-GE-YWWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQ
gi|179 IRNPHLFDILNNTIFTDFWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTLSSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSG
gi|179 SPT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|179 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|179 TIDPERINQIPLVKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPI
470 480 490 500 510

Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|179 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMLQKTMIEIGENLTSRTFRYTDPS
520 530 540 550 560 570



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470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 TIDPERINQIPLVKGRVWGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIIT
      470      480      490      500      510

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530      540      550      560      570      580
Cry1Ac STRYRVRVRYAVTPIHLNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSVNMLQKTMIEIGENLTSRTFRYTDFFS
      520      530      540      550      560      570

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590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 NFFSFRANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

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640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

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700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGSGTITIQGGDDVFKENYVTLSTGTFDECPYTYLYQKIDESKLLKAPT
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 NFRGINRQPDGRWGSTDITIQGGDDVFKENYVTLPGTVDCEPYTYLYQKIDESKLLKAPT
      700      710      720      730      740      750

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760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 RYELRGYIEDSQDLEIYIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

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820      830      840      850      860      870
Cry1Ac NPDLDCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 NPDLDCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

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880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

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940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLEYDARNVIKNGDFNNGL
      940      950      960      970      980      990

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1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGHV DVEEQNNQRSV LVPWEAEV SQEVRVCPGRGYILRV TAYKEGYEGCVTI
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 LCWNVKGHV DVEEQNNHRSV LVPWEAEV SQEVRVCPGRGYILRV TAYKEGYEGCVTI

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1000     1010     1020     1030     1040     1050
Cry1Ac HEIENNTDELKFSNCV EEEIYPNNITVTCNDYTVNQEEYGGAYTSRRNGYNEA----PSVP
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 HELEDNTDELKFSNCV EEEVYPNNITVTCNNYTGQTQEEYEGTYTSRNGYDEAYGNPSPVP
      1060     1070     1080     1090     1100     1110
Cry1Ac ADYASVYEEKSYTDGRRENPC EFNRGYRDYTPPLVGVYTKLELYFPETDKVWIEIGETEG
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 ADYASVYEEKSYTDGRRENPC ESNRGYGDYTPPLPAGYVTKDLELYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170
Cry1Ac TFIVDSVELLLMEE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|141 TFIVDSVELLLMEE
      1170     1180

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>>gi|23325084|gb|AAN23784.1| Sequence 12 from patent US (1189 aa)  
initn: 4546 init1: 3093 opt: 5000 Z-score: 5886.6 bits: 1101.2 E(): 0  
Smith-Waterman score: 5271; 68.182% identity (83.058% similar) in 1210 aa overlap  
(5-1182:1-1189)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLLSEFVPGAGF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233  MEEN-NQNCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233 LVGLIDFVWGI FGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFN DMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233 WEEDPHNPATRTRVIDRFR ILDGLLERDIPSFRI SGFEVPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233 IFGERWGLTTINVENYNRIRIHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDL
      180     190     200     210     220     230

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250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG-----IEGS-
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMSSA
      240     250     260     270     280     290

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300     310     320     330     340     350
Cry1Ac IRSPHLM DILNSITIYTD AHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|233 IRNPHLFDILNNTIFTDWFVSGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR

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300      310      320      330      340      350
      360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSTLTYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
.. .. :.:.:. : .: . : : .: .: . : : : : : : : : : : : :
gi|233 SFT--FNGPVRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
      360      370      380      390      400
410      420      430      440      450      460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGGVV---FSWTHRSTATLTN
      410      420      430      440      450      460
470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 TIDPERINQIPLVKGFRVWGGTSSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
      470      480      490      500      510
530      540      550      560      570      580
Cry1Ac STRYRVVRYASVTPIHLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
. : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKIMEIGENLTSRTFRYTDIFS
      520      530      540      550      560      570
590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
: : . : . : . : : : : : : : : : : : : : : : : : : : : : :
gi|233 NFFSFRANPDIIGISEQPLFGAGSISSEELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630
640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRRLSDERNLLQDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRRLSDERNLLQDP
      640      650      660      670      680      690
700      710      720      730      740      750
Cry1Ac NFKDINRQPERGGSTGITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAYT
: : . : . : . : : : : : : : : : : : : : : : : : : : : : :
gi|233 NFRGINRQPDGRGWRGSTDITIQGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYT
      700      710      720      730      740      750
760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
. : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 RYELRGYIEDSQDLEIYLIRYNAKHHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810
820      830      840      850      860      870
Cry1Ac NPDLLDCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVIFKIKIQDGHARLGNLEFLE
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 NPDLLDCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVIFKIKIQDGHARLGNLEFLE
      820      830      840      850      860      870
880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
: : : : . : . : . : : : : : : : : : : : : : : : : : :

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gi|233 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930
      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990
1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDEEQNNQSRVSVLVPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTI
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 LCWNVKGHVDEEQNNHRSVSVLVIPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050
1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 HEIEDNTDELKFSNCVVEEIVPNTVTTCNNYTGTEYEGTYTSRNGQYDEAYGNPNSVP
      1060      1070      1080      1090      1100      1110
1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 ADYASVYEEKSYTDGRRENPCSNRYGDTPLPAGYVTKLELYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170
1170      1180
Cry1Ac TFIVDSVELLLMEE
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|233 TFIVDSVELLLMEE
      1180
>>gi|14103738|gb|AAE55172.1| Sequence 10 from patent US (1189 aa)
      initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)
10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: : . : . : . : : : : : : : : : : : : : : : : : : : : : :
gi|141 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGFF
      10      20      30      40      50
70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIQFVPSQWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE
. : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|141 LVGLIDFVWGIQFVPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNIVYEAFAKE
      60      70      80      90      100      110
130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: : : : . : . : . : : : : : : : : : : : : : : : : : :
gi|141 WEVDPNPGRTRTRVIDRFRILDGLLERDIPSRISGFVPLLSVYVQAANLHLAILRDSV
      120      130      140      150      160      170
190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
: : : : . : . : . : : : : : : : : : : : : : : : : : :

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gi|141 IFGERWGLTTINVENYENRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
      180      190      200      210      220      230
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQTLREIYTNPVENFDGSGFRGSAQG-----IEGS-
      250      260      270      280      290
gi|141 TLTVLDAIAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
      240      250      260      270      280      290
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
      300      310      320      330      340      350
gi|141 IRNPHLFDILNLLTIFTDFWFSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSG
      360      370      380      390      400
gi|141 SFT--FNGPVFRTLNSPTLRLQLQPPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
      410      420      430      440      450      460
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGVV---FSWTHRSATLITN
      410      420      430      440      450      460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
      470      480      490      500      510      520
gi|141 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
      470      480      490      500      510
Cry1Ac STRYRVRVRYASVTPIHNLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      530      540      550      560      570      580
gi|141 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDS
      520      530      540      550      560      570
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAAYNLERAQKAVNAL
      590      600      610      620      630
gi|141 NPFSFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDS
      640      650      660      670      680      690
gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRSLDERNLLQDP
      640      650      660      670      680      690
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLAFT
      700      710      720      730      740      750
gi|141 NFRGINRQPDGRWRGSDTITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
      700      710      720      730      740      750
Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW

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      760      770      780      790      800      810
gi|141 RYELRGYIEDSDLEIYLIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810
Cry1Ac NPDLDCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870
gi|141 NPDLDCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870
Cry1Ac EKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      880      890      900      910      920      930
gi|141 EKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      880      890      900      910      920      930
Cry1Ac MIHAADKRVHSIREAYLPELSVPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNG
      940      950      960      970      980      990
gi|141 MIHAADKRVHSIREAYLPELSVPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNG
      940      950      960      970      980      990
Cry1Ac SCWNVKGHVDEVEEQNNQSVLVVPEWAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050
gi|141 LCWNVKGHVDEVEEQNNHRSVLVPEWAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
      1060      1070      1080      1090      1100
gi|141 HEIEDNTDELKFSNCVVEEIIYPNNTVTCNNTYGTQEEYEGYTSRNRQGYDEAYGNNPSVP
      1060      1070      1080      1090      1100      1110
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
      1110      1120      1130      1140      1150      1160
gi|141 ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
      1110      1120      1130      1140      1150      1160
Cry1Ac TFIVDSVELLLMEE
      1170      1180
gi|141 TFIVDSVELLLMEE
      1180
>>gi|17920874|gb|AAE86494.1| Sequence 10 from patent US (1189 aa)
      initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
      Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
      (5-1182:1-1189)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      70      80      90      100      110      120
gi|179 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE

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>>gi|56664638|gb|AAW18063.1| Sequence 10 from patent US (1189 aa)
initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|566 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWIVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110
Cry1Ac WEADTPNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566 WEVDPNNGPTRVIRVDRFRILDGLLERDIPSFRIISGFVPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQG-----IEGS-
gi|566 TLTVLIDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVQQLPTFNMVMESSA
240 250 260 270 280 290
Cry1Ac IRSPHLMIDLNSITIYTDADR-GE-YYWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|566 IRNPHLFDILNLTIFTDWFVSVGRNFYWGHRVIVSSSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350
Cry1Ac RIVAQLGQGVYRTLSSTLYR--RPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKS
gi|566 SFT--FNGPVFRTLSNPTLRLLQPPWAPPFN--LRGVEGVFSS--TPTN--SFTYRGRG
360 370 380 390 400
Cry1Ac TVDSDLDEIPPNQNNVPPRQGFSHRLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSDLTELPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTLN
410 420 430 440 450 460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNLSGNNIQRNGYIEVPIHPFST
gi|566 TIDPERINQIPLVKGRFVWGGTTSVITGPGFTGGDLVRLNLSGNNIQRNGYIEVPIHPFST
470 480 490 500 510 520
Cry1Ac
gi|566

530 540 550 560 570 580
Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTFRYTD
520 530 540 550 560 570
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSFRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|566 NFRGINRQPDGRWGRGTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
700 710 720 730 740 750
Cry1Ac RYQLRGIYIEDSDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGIYIEDSDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810
Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
gi|566 NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870
Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940 950 960 970 980 990
Cry1Ac SCWNVKGVHVDVEEQNNQSVLVVPEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|566 LCWNVKGVHVDVEEQNNHRSVLVPEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSPV
gi|566 HEIENNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNNSVSP
1060 1070 1080 1090 1100 1110

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1110      1120      1130      1140      1150      1160
Cry1Ac  ADYASVYEEKSYTDGRRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|566  ADYASVYEEKSYTDGRRENPCFENRGYRDYTPLPAGYVTKLEYFPETDKVWIEIGETEG
1120      1130      1140      1150      1160      1170

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1170      1180
Cry1Ac  TFIVDSVELLLMEE
gi|566  TFIVDSVELLLMEE
1180

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>>gi|56642271|gb|AAW11989.1| Sequence 10 from patent US (1189 aa)  
 initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0  
 Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap  
 (5-1182:1-1189)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566  MEEN-NQNCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

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70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|566  LVGLIDFVWGVGQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNVIYEFKFE
60      70      80      90      100      110

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130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|566  WEVDPNNGPTRTRVLDLFRILDGLLERDIPFRISGFVPLLSVYAQAANLHLAIRDVS
120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRRDL
180      190      200      210      220      230

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250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQG-----IEGS-
gi|566  TLTVLDIAAFFPNYDNRRIYPIQVQQLTREVYTDPLI-NFNPLQVSAQLPTFNVMESSA
240      250      260      270      280      290

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```

300      310      320      330      340      350
Cry1Ac  IRSPHLMIDLNSITIYDADR-GE-YWWSGHQIMASPVGFSGPEPTFPPLYGTMGNAAPQQ
gi|566  IRNPHLFDILNLTIFTDFWVGRNFYWGHRVIVSSLIG--GGNITSPYIGREANQPEPPR
300      310      320      330      340      350

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```

360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRSLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|566  SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVFES--TPTN--SFTYRGRG
360      370      380      390      400

```

```

410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPPQNNVPPRQGFSHRLSHVSMF-RSGFNSSSVSIIRAPMFSWIHRSAEFNN
gi|566  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV----FSWTHRSTATLTN
410      420      430      440      450      460

```

```

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|566  TIDPERINQIPLVKGRVWGGT SVITGPGFTGGDLRRNTFGDFVS----LQVNIINSPIIT
470      480      490      500      510

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```

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTRFYTDPS
520      530      540      550      560      570

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590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566  NPFSSFRANPDIIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

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640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566  FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

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700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLKAYT
gi|566  NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLVPGTVDECYPTYLYQKIDESKLKAYT
700      710      720      730      740      750

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760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566  RYELRGYIEDSQDLEIYLIRYNKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

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820      830      840      850      860      870
Cry1Ac  NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|566  NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

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880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

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940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL

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Regulatory Product Characterization Team

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940      950      960      970      980      990
Cry1Ac  1000      1010      1020      1030      1040      1050
SCWNVKGVHDVVEEQNNQRSVLLVPEWEAEVVSQEVVRVCPGRGYILRVYTAYKEGYEGECVTII
gi|566  LCWNVKGVHDVVEEQNNHRSVLLVPEWEAEVVSQEVVRVCPGRGYILRVYTAYKEGYEGECVTII
1000      1010      1020      1030      1040      1050

1060      1070      1080      1090      1100
Cry1Ac  HEIENNTDELKFSNCVVEEIIYPNNVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|566  HEIEDNTDELKFSNCVVEEIVPNNVTTCNNYTGTEYEGYTSRNQGYDEAYGNNSVVP
1060      1070      1080      1090      1100      1110

1110      1120      1130      1140      1150      1160
Cry1Ac  ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|566  ADYASVYEEKSYTDGRRNPCESNRGYGDYTPLPAGYVTKIDLEYFPETDKVWIEIGETEG
1110      1120      1130      1140      1150      1160      1170

1170      1180
Cry1Ac  TFIIVDSVELLLMEE
gi|566  TFIIVDSVELLLMEE
1180

>>gi|7141141|gb|AAF37224.1|AF215647_1 toxin Cry1Ca6 [Bac (1189 aa)
initn: 4543 initl: 3090 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 67.934% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|714  MEEN-NQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGIQFQSDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESPFE
gi|714  LVGLIDFVWGIQFQSDAFLVQIEQLINERIAEFARNAIANLEGLGNNFNIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|714  WEEDPNNPATRTRVIDRFRILDGLLERDIPSRISGFVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDRDWRIRYNQFRREL
gi|714  IFGERWGVTTINVNENYRNLIRHIDEYADHCANTYRNLNLPKSTYQDWITYNLRRDL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGSRFRGSAQG-----IEGS-
gi|714  TLTVLDIAAFFPNYDNRYPYIQQVQGLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA

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240      250      260      270      280      290
Cry1Ac  300      310      320      330      340      350
IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVVFGSGPEFTFPLYGTMGNAAPQQ
gi|714  IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKS
gi|714  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRSLHVSMTF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|714  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTGVV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|714  TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDLRRNTFGDFVS---LQVNNSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPHILNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|714  Q-RYRLRFRYASSRDARVILVTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFRYTDPS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGV--RNFSGTAGV-----IIDRFEPVPTATLEAEYNLERAQKAVNAL
gi|714  NPF'SFRANPDIIGISERPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|714  FTSSNQLGLKTDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLAFT
gi|714  NFRGINRQPDWRGSGTDITIQGGDDVFKENYVTLVPGTVDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac  RYQLRGIYIEDSDLEIYSIRYNAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW
gi|714  RYELRGIYIEDSDLEIYLIRYNAKHEIVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac  NPDLDCSCRDGEKCAHSHHFLSLDIDVGCCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE

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gi|714 NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac 880 890 900 910 920 930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA

gi|714 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930

Cry1Ac 940 950 960 970 980 990
MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL

gi|714 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac 1000 1010 1020 1030 1040 1050
SCWNVKGHVDVEEQNNQSRVSVLVPWEAEVSVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTI

gi|714 LCWNVKGHVDVEEQNNHRSVSVLVPWEAEVSVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac 1060 1070 1080 1090 1100
HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP

gi|714 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGQEEYEGYSSRNQGYDEAFGNMPSVP
1060 1070 1080 1090 1100 1110

Cry1Ac 1110 1120 1130 1140 1150 1160
ADYASVYEEKSYTDGRENPCFENRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEG

gi|714 ADYASVYEEKSYTDGRENPCENRNGYDYPPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

Cry1Ac 1170 1180
TFIVDSVELLMEE

gi|714 TFIVDSVELVLMEE
1180

>>gi|14112743|gb|AAE58158.1| Sequence 10 from patent US (1189 aa)
initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

gi|141 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGIQFQSDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE

gi|141 LVGLIDFVWGIQFQSDAFLVQIEQLINERIAEFARNAAIANLEGLGNPNFYIEAFKE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNIPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDSV

gi|141 WEADPTNIPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDSV
130 140 150 160 170 180

gi|141 WEVDPNNGTRTRVIDRFRILDGLLERDIPSRISGFVPLLVSVAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

gi|141 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290
TLTVLVDIVSLFPNYDSRTYPIRTVSQTLREIYTNVPLENFDGSRFSAQG-----IEGS-

gi|141 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350
IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ

gi|141 IRNPHLFDILNLTIFTDWFVSVGRNFYWGHRVSSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400
RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSG

gi|141 SFT--FNGPVFRTLSNPTLRLQPPWAPPFN--LRGVEGVFES--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac 410 420 430 440 450 460
TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFNSNSVSIIRAPMFSWIHRSAEFNN

gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac 470 480 490 500 510 520
IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST

gi|141 TIDPERINQIPLVKGFVRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
470 480 490 500 510

Cry1Ac 530 540 550 560 570 580
STRYRVRVRYASVTPPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA

gi|141 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTDFS
520 530 540 550 560 570

Cry1Ac 590 600 610 620 630
NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL

gi|141 NPFSSFRANPDIIGISEQPLFAGSISSEGLYIDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac 640 650 660 670 680 690
FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDS

gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

Cry1Ac 700 710 720 730 740 750
NFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKFT

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gi|141 NFRGNIHQVDRGWRGSDTITQGGDDVFKENYVTLPGTVDECYPTLYLQKIDESLKKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

gi|141 RYELRGYIEDSDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac NPDDLDCSCRDGEKCAHSHHFLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

gi|141 NPDDLDCSCRDGEKCAHSHHFLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

gi|141 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

gi|141 MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac SCWNVKGVHDVVEEQNNQSVLVVPEWEAEVVSQEVRCVCPGRGYILRVYAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

gi|141 LCWNVKGVHDVVEEQNNHRSVLVPEWEAEVVSQEVRCVCPGRGYILRVYAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
1060 1070 1080 1090 1100 1110

gi|141 HEIEDNTDELKFSNCVEEIEYPNNTVTCNNYGTQEEYEGYTSRNQGYDEAYGNPNSVP
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

gi|141 ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLLMEE
1170 1180

gi|141 TFIVDSVELLLMEE
1170 1180

>>gi|23325083|gb|AAN23783.1| Sequence 10 from patent US (1189 aa)
initn: 4544 initl: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

gi|233 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|233 LVGLIDFVWGIWGFPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
130 140 150 160 170 180

gi|233 WEVDPNPNPGRTRVDIRFRILDGLLERDIPSPRISGFVEVPLLSVYQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|233 IFGERWGLTTINWVENYNRILRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG-----IEGS-
250 260 270 280 290

gi|233 TLTVLIDIAAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNQLQSVLQPLTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHLMIDILNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
300 310 320 330 340 350

gi|233 IRNPHLFDILNNTIFTDFWVGRNRYVWGGHRVSSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLPSSAVYRKSG
360 370 380 390 400

gi|233 SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
410 420 430 440 450 460

gi|233 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
470 480 490 500 510 520

gi|233 TIDPERINQIPLVKGFVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPT
470 480 490 500 510

Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|233 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDS
520 530 540 550 560 570

590 600 610 620 630

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Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|233 NPFSSFRANPDIIGISEQLFGAGSISSEGLYIDKIEIILADATFAESDLERAQKAVNAL

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|233 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP

Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKPKAFT
gi|233 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKPKAYT

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
gi|233 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEW

Cry1Ac NPDLDCSCRDGKCAHSHHFLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
gi|233 NPDLDCSCRDGKCAHSHHFLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|233 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|233 MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAYSLYDARNVIKNGDFNNGL

Cry1Ac SCWNVKGHVDVEEQNNQSRVSVLVPWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI
gi|233 LCWNVKGHVDVEEQNNHRSVSVLVPWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTI

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|233 HEIEDNTDELKFSNCVEEIVPNNTVTCCNYTGTQEEYEGYTSRNQGYDEAYGNNPSVP

Cry1Ac ADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|233 ADYASVYEEKSYTDGRENPCSNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEG

1170 1180
Cry1Ac TFIVDSVELLLMEE
gi|233 TFIVDSVELLLMEE
1180

>>gi|158456670|gb|ABW41343.1| Sequence 10 from patent US (1189 aa)
initn: 4544 init1: 3093 opt: 4998 Z-score: 5884.3 bits: 1100.8 E(): 0
Smith-Waterman score: 5269; 68.099% identity (83.223% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|158 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAEFSPRE
gi|158 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFAFNAAIANLEGLGNNFNIIYVEAFKE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|158 WEVDPNPGRTRFRVIDRFRILDGLLDRDIPFRISGFVPLLSVYVQAANLHLLAIRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|158 IPGERGLTTINVENYRNLIRHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRRLRDL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQG----IEGS-
gi|158 TLTVLDIAAFFPNYDNRRIYIQPVGQLTREVYTDPLI-NFNPQLQVAQLPTFNVMESSA

Cry1Ac IRSPHLMIDLNSITIYTDADR-GE-YWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ
gi|158 IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRVVISLIG--GGNITSPYGREANQEPFR

Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLPSSAVYRKSG
gi|158 SFT--FNGVVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

Cry1Ac TVDSLDEIPPQNNVPPRQGFHSHLSVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|158 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGVV----FSWTHRSTLTLN

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470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPST
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 TIDPERINQIPLVKGFVRVGGTTSVITGPGFTGGDILRRRTFGDFVS---LQVNSINSPIT
      470      480      490      500      510

530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDIFS
      520      530      540      550      560      570

590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 NPFSSFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKLKAF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 NFRGINRQPDGRWGGSTGITIQGGDDVFKENYVTLPGTDECPYTYLYQKIDESKLKAYT
      700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYIRYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 RYELRGYIEDSQDLEIYLIRYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEGKCAHSHHFFSLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 NPDLDCSCRDEGKCAHSHHFFSLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPESLVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 MIHAADKRVHRIREAYLPESLVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGHVDFVEEQNNQRSVLVPEWEAEVVSQEVRCVCPGRGYILRVVTAYKEGYGEGCVTI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 LCWNVKGHVDFVEEQNNHRSVLVPEWEAEVVSQEVRCVCPGRGYILRVVTAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050

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1060     1070     1080     1090     1100
Cry1Ac HELENTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSPV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 HELEDNDELKFSNCVVEEIVPNNTVTCNNYTGTEEEYEGTYTSRNRQGYDEAYGNNSVSP
      1060     1070     1080     1090     1100     1110

1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRGYRDYTPLPVGVYVTKLEYFPETDKVWIEIGETEG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 ADYASVYEEKSYTDGRRNPCESNRQYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170

1170     1180
Cry1Ac TFIVDSVELLLMEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 TFIVDSVELLLMEE
      1180

>>gi|40294|emb|CAA30396.1| unnamed protein product [Baci (1189 aa)
      initn: 4530 initl: 3093 opt: 4997 Z-score: 5883.1 bits: 1100.6 E(): 0
      Smith-Waterman score: 5256; 68.017% identity (82.975% similar) in 1210 aa overlap
      (5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 LVGLIDFVWVGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYEAFAKE
      60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 WEEDPNNPETRTRVIDRFRILDGLLERDIPSPRISGFVPLLSVYAQAANLHLAALLRDSV
      120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRIRYNQFRREL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 IPGERWGLTTINWVNNYRNLRIHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDL
      180     190     200     210     220     230

250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLENFDGSGFRGSAQG----IEGS-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSR
      240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac IRSPHMLDILNSITIYDADR-GE-YYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 IRNPHLFDILNLLTIFTDFWFSVGRNRYWGGHRVISSLIG--GGNITSPYIGREANQEPFR
      300     310     320     330     340     350

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          360      370      380      390      400
Cry1Ac RIVAQLGQGVYRRTLSSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 SFT--FNGPVRTLSNPTLRLQLQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
          360      370      380      390      400

          410      420      430      440      450      460
Cry1Ac TVDSDLDEIPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSSVSIIRAPMFSNLHRSAEFNN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 TVDSDLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGGVV---FSWTDRSATLTN
          410      420      430      440      450      460

          470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 TIDPERINQIPLVKGRFVWGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIIT
          470      480      490      500      510

          530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLNVWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMEIGENLTSRTFRYTDIFS
          520      530      540      550      560      570

          590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 NPFSPFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
          580      590      600      610      620      630

          640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
          640      650      660      670      680      690

          700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKPKAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 NFRGINRQPRDRWGSDITIQGGDDVFKENYVTLPGTVDECPYTYLYQKIDESKPKAYT
          700      710      720      730      740      750

          760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYLRIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 RYELRGYIEDSQDLEIYLRIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
          760      770      780      790      800      810

          820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 NPDLDCSCRDEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
          820      830      840      850      860      870

          880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

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          880      890      900      910      920      930
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIPTAFSLYDARNVIKNGDFNNGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIPTAYSLYDARNVIKNGDFNNGL
          940      950      960      970      980      990

          1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQRSVLPVPEWAEVSVQEVVPCPGRGYILRVTAKEGYGEGCVTI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 LCWNVKGVHDVVEEQNNHRSVLPVPEWAEVSVQEVVPCPGRGYILRVTAKEGYGEGCVTI
          1000     1010     1020     1030     1040     1050

          1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 HEIEDNTDELKFSNCVEEEVYPNNTVTCNNYTGQEEYEGTYTSRNQGYDEAYGNPSPV
          1060     1070     1080     1090     1100     1110

          1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYYTKLELYFPETDKVWIEIGETEG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|402 ADYASVYEEKSYTDGRRNPCESNRQYGDYTPLPAGYVTKDLELYFPETDKVWIEIGETEG
          1120     1130     1140     1150     1160     1170

          1170     1180
Cry1Ac TFIVDSVELLLMEE
      . . . . . : . . . . .
gi|402 TFIVDSVELLLMEE
          1180

>>gi|15105602|gb|AAE66196.1| Sequence 2 from patent US 6 (1189 aa)
      initn: 4542 initl: 3093 opt: 4996 Z-score: 5881.9 bits: 1100.3 E(): 0
      Smith-Waterman score: 5267; 68.099% identity (83.058% similar) in 1210 aa overlap
      (5-1182:1-1189)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
          10      20      30      40      50

          70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNIIYVEAFKE
          60      70      80      90      100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 WEEDNNPETRFRVIDRFRILDGLLDRDIPSPRISGFVPLLSVYAQAANLHLAIALRDSV
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 IFGERWGLTTINVENYNRILRHIDEYADHCANTYNRGLNPLKSTYQDWITYNRLRRDL

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180      190      200      210      220      230
Cry1Ac  250      260      270      280      290
TTLVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQG-----IEGS-
gi|151  240      250      260      270      280      290
TTLVLDIAAFPNYDNRRYPIQPVGQLTREYVTDPLI-NFNPLQSQVAQLPTFNVMESSA

300      310      320      330      340      350
Cry1Ac  IRSPHMLDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|151  IRNPHLFDILNLLTIFTDFSVGRNFWYGGHRVIVSSLIG--GGNITSPIYGREANQEPFR

360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSTSLYR--RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|151  SFT--FNGPVPFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVVEFS--TPTN--SFTYRGRG

410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|151  TVDSLTELPEPENSVPREGYSHRLCHATFVQRSGTFFLTTGVV---FSWTHRSATLTN

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|151  TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIIT

530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|151  Q-RYRLRFRYASSRDRVIVLTGAASTGVGGQVSNMPLQKTMEIGENLTSRTFRYTDFFS

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|151  NFFSFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDS
gi|151  FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRSLDERNLLQDP

700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKPKAFT
gi|151  NFRGINRQPDGRWGSTDITIQGDDVFKENYVTLPGTVDCEPTYLYQKIDESKPKAYT

760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW

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gi|151  760      770      780      790      800      810
RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW

820      830      840      850      860      870
Cry1Ac  NPDLDCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
gi|151  NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE

880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|151  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|151  MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNGL

1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHVDEEQNNQSVLVVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYGECVTI
gi|151  LCWNVKGHVDEEQNNHRSVLVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYGECVTI

1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|151  HELEDNTDELKFSNCVEEEVYPNNTVTCNNYTGTEYEGTYTSRNQGYDEAYGNPNSVP

1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRENPCENRNGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEG
gi|151  ADYASVYEEKSYTDGRENPCENRNGYGDYTPPLPAGYVTKDLELYFPETDKVWIEIGETEG

1170     1180
Cry1Ac  TFIVDSVELLLMEE
gi|151  TFIVDSVELLLMEE

1180
Cry1Ac  VLGLVDIIWGIQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFRE

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>>gi|3990783|gb|AAC84210.1|AR000633 Sequence 2 from pate (1189 aa)
initn: 4542 init1: 3093 opt: 4996 Z-score: 5881.9 bits: 1100.3 E(): 0
Smith-Waterman score: 5267; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

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gi|399 LVGLIDFVWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNFIYVEAFKE
      60      70      80      90      100     110
Cry1Ac WEADPTN PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|399 WEEDPNNPETRTRVIDRFRILDGLLERDIPSFRIISGFEVPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190     200     210     220     230     240
gi|399 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVENFDGSRGSAQG-----IEGS-
      250     260     270     280     290
gi|399 TLTVLDAIAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
      240     250     260     270     280     290
Cry1Ac IRSPHLM DILNSITTYTDAHR-GE-YWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
      300     310     320     330     340     350
gi|399 IRNPHLFDILNLLTFTDWFVSVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFR
      300     310     320     330     340     350
Cry1Ac RIVAQLGGQVYRTLSTLYR---RPFNIGINNQQLSVLDTGTEFAYGTSSNLPSAVYRKSG
      360     370     380     390     400
gi|399 SFT--FNGPVFRTLSPNPLRLQLQWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360     370     380     390     400
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
      410     420     430     440     450     460
gi|399 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTN
      410     420     430     440     450     460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
      470     480     490     500     510     520
gi|399 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
      470     480     490     500     510
Cry1Ac STRYRVVRYASVTPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      530     540     550     560     570     580
gi|399 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKIMEIGENLTSRTFRYTFDS
      520     530     540     550     560     570
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPFIPVTATLEAEYNLERAQAVNAL
      590     600     610     620     630
gi|399 NFFSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQAVNAL
      580     590     600     610     620     630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
      640     650     660     670     680     690

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gi|399 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640     650     660     670     680     690
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTDECYPTLYLQKIDESKLFKFT
      700     710     720     730     740     750
gi|399 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLVPGTVDECYPTLYLQKIDESKFKAYT
      700     710     720     730     740     750
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760     770     780     790     800     810
gi|399 RYELRGYIEDSQDLEIYLIRYNKAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760     770     780     790     800     810
Cry1Ac NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
      820     830     840     850     860     870
gi|399 NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
      820     830     840     850     860     870
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      880     890     900     910     920     930
gi|399 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880     890     900     910     920     930
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGL
      940     950     960     970     980     990
gi|399 MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIFTAYSLYDARNVIKNGDFNNGL
      940     950     960     970     980     990
Cry1Ac SCWNVKGVHVDVEEQNNQSVLVVPEWAEVSEVVRVCPGRGYILRVTA YKEGYGEGCVTI
      1000    1010    1020    1030    1040    1050
gi|399 LCWNVKGVHVDVEEQNNHRSVLVPEWAEVSEVVRVCPGRGYILRVTA YKEGYGEGCVTI
      1000    1010    1020    1030    1040    1050
Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      1060    1070    1080    1090    1100    1110
gi|399 HEIEDNTDELKFSNCVEEIVPNNTVTCNNYTGTEYEGYTYTSRNRQGYDEAYGNPNSVP
      1060    1070    1080    1090    1100    1110
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
      1110    1120    1130    1140    1150    1160
gi|399 ADYASVYEEKSYTDGRRENPCESNRGYGDTPLPAGYVTKDLELYFPETDKVWIEIGETEG
      1120    1130    1140    1150    1160    1170
Cry1Ac TFIVDSVELLLMEE
      1170    1180
gi|399 TFIVDSVELLLMEE
      1170    1180

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>>gi|2298884|emb|CAA02749.1| unnamed protein product [Ba (1189 aa)

Regulatory Product Characterization Team

initn: 4542 init1: 3093 opt: 4996 Z-score: 5881.9 bits: 1100.3 E(): 0
Smith-Waterman score: 5267; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFLLSEFVPGAGF
gi|229 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
Cry1Ac VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|229 LVGLIDFWGIVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|229 WEEDPNNPETRTRVIDRFRILDGLLERDIPSFRIISGFVPLLSVYAQAANLHLAII LRDSV
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|229 IFGERWGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRRLDL
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDFGSRGSAQG----IEGS-
gi|229 TLTVLDIAAFFPNYDNRRIYIQQVGLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
Cry1Ac IRSPHLM DILN SITYTDAHR-GE-YWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|229 IRNPHLFDILN NLTIFTDWFVSGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|229 SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
Cry1Ac TVDSDLDEIPPNQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|229 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGT PPLTTGVV---FSWTHRSATLTN
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|229 TIDPERINQIPLVKGRFVWGGTSVITGPGFTGGDLRLRNTFGDFVS---LQVNNISPIT

Cry1Ac STRYRVRVRYASVTPIHNLVNWGNSSI----FSNTVVPATATSL--DNLQSSDFGYFESA
gi|229 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYDFDS
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVPTATLEAEYNLERAQKAVNAL
gi|229 NPFSSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEEASDLERAQKAVNAL
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|229 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTDFDECYPTLYQKIDESKPKAFT
gi|229 NFRGINRQDRGWRGSTDITIQGGDDVFKENYVTLTSGTDFDECYPTLYQKIDESKPKAYT
Cry1Ac RYQLRGIYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIKCKGEPNRCAPHLEW
gi|229 RYELRGIYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIKCKGEPNRCAPHLEW
Cry1Ac NPDLDSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
gi|229 NPDLDSCDRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|229 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|229 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
Cry1Ac SCWNVKGHVDVEEQNNQSVLVVPEWAEVSEVVRVCPGRGYILRVTA YKEGYGEGCVTI
gi|229 LCWNVKGHVDVEEQNNHRSVLVPEWAEVSEVVRVCPGRGYILRVTA YKEGYGEGCVTI
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|229 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNNPSPV

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1110      1120      1130      1140      1150      1160
Cry1Ac  ADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLEYFPEPDKVWIEIGETEG
gi|229  ADYASVYEEKSYTDGRRENPCSNRGYGDYTPLPAGYVTKDLEYFPEPDKVWIEIGETEG
1120      1130      1140      1150      1160      1170

1170      1180
Cry1Ac  TFIVDSVELLLMEE
gi|229  TFIVDSVELLLMEE
1180

>>gi|53984832|gb|AAV26508.1| Sequence 2 from patent US 6 (1189 aa)
  in1tn: 4542 in1t1: 3093 opt: 4996 Z-score: 5881.9 bits: 1100.3 E(): 0
Smith-Waterman score: 5267; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|539  MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGLESLNYQIYAESFRE
gi|539  LVGLIDFVWGIWVQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
gi|539  WEEDPNNPETRRVIDRFRILDGLLERDIPSFRIISGFVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|539  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQTLREIYTNPVLENFDGSRFGSAQG----IEGS-
gi|539  TLTVLIDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVAVLPTFVVMESSA
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  IRSPHLMIDILNSITITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|539  IRNPHLFDILNLTIFTDWFVSVGRNFYWGHRVIVSSLIIG--GGNITSPYIGREANQPEPPR
300     310     320     330     340     350

360     370     380     390     400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS
gi|539  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360     370     380     390     400

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410      420      430      440      450      460
Cry1Ac  TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|539  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPFLTTGGV----FSWTHRSTATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPST
gi|539  TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  STRYRVRYASVTPPIHLNVNNGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|539  Q-RYRLRFYASSRDARIVLVTGAASTGVGGQVSNMPLQKTEIGENLTSRTFRYTDFS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|539  NPFSTRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|539  FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|539  NFRGINRQPRGWRGSTDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac  RYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
gi|539  RYELRGIYEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac  NPDLCSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
gi|539  NPDLCSCDRDGEKCAHSHHFTLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|539  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|539  MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

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1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGVHDVVEEQNNQSRVSVLVPWEAEVVSQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI
gi|539 LCWNVKGVHDVVEEQNNHRSVSVLVIPEWEAEVVSQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI
1000      1010      1020      1030      1040      1050

1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYNNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
gi|539 HEIEDNTDELKFSNCVVEEIVYNNNTVTCNNYTGTEYEGTYTSRNGYDEAYGNPSPV
1060      1070      1080      1090      1100      1110

1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|539 ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
1120      1130      1140      1150      1160      1170

1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|539 TFIVDSVELLLMEE
1180

>>gi|1247717|emb|CAA01886.1| bt15 [Bacillus thuringiensis (1189 aa)
  initn: 4542 initl: 3093 opt: 4996 Z-score: 5881.9 bits: 1100.3 E(): 0
Smith-Waterman score: 5267; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|124 MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|124 LVGLIDFVWVIGVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100      110

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|124 WEEDPNNPETRTRVDRFRILDGLLERDIPSFRIISGFVPLLSVYAQAANLHLAII LRDSV
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|124 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRNLNLPKSTYQDWITYNRLRRDL
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQ-----IEGS-
gi|124 TLTVLIDIAAFFPNYDNRYPQVQQLTREVYTDPLI-NFNQLQSVQALPTFNVMESSA
240      250      260      270      280      290

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300      310      320      330      340      350
Cry1Ac IRSPHMLDILNSITIIYTDADR-GE-YYWGGHQMSPVGFSGPEFTFPPIYGTMGNAAPQQ
gi|124 IRNPHLFDILNLLTIFTDFWFSVGRNRYWGGHRSVSLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQ
gi|124 SPT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFVS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNNSVSIIRAPMFSWIHRSAEFNN
gi|124 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPTPLTTGVV----FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQRNGYIEVPIHFPST
gi|124 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDLRLRNTFGDFVS---LQVNNINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPPIHLNWNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|124 Q-RYRLFRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTRFYTFDFS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|124 NPFSTRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|124 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLAFT
gi|124 NFRGINRQPDWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac RYQLRGIYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|124 RYELRGIYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|124 NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE

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      820      830      840      850      860      870
      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|124 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930
      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|124 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990
      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQSRVSVLVPVEWAEVSVQEVVRCVCPGRGYILRVVTAYKEGYGEGCVTI
gi|124 LCWNVKGVHDVVEEQNNHRSVSVLVIPEWAEVSVQEVVRCVCPGRGYILRVVTAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050
      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGAYTSRNRGYNEA---PSVP
gi|124 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGYTSRNRQYDEAYGNPNPSVP
      1060     1070     1080     1090     1100     1110
      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|124 ADYASVYEEKSYTDGRRENPCESNRGYDGYTPLPAGYVTKLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170
      1170     1180
Cry1Ac TFIVDSVELLLMEE
gi|124 TFIVDSVELLLMEE
      1180
>>gi|14103737|gb|AAE55171.1| Sequence 8 from patent US 6 (1189 aa)
  in1n: 4540 in1l: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|141 MEEN-NQNCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|141 LVGLIDFVWIVGQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEDDPHNPTTRTRVDRFRILDGLLDRDIPFRISGFVPLLSVYAQAANLHLAILLRDSV

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      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFREL
gi|141 IPGERWGLTTINVENYRNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWIITYNRLRRDL
      180      190      200      210      220      230
      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQG----IEGS-
gi|141 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQVAQLPTFNVMSSA
      240      250      260      270      280      290
      300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGSGPEFTFPYLYGTMGNAAPQQ
gi|141 IRNPHLFDILNNTLIFTDFWFSVGRNFWGGHRVSSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350
      360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSTLYR--RPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|141 SFT--FNGPVFRTLNSPTLRLQLQWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400
      410      420      430      440      450      460
Cry1Ac TVDSLDEIIPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNN
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSRGTPTLTTGVV---FSWTHRSATLTLN
      410      420      430      440      450      460
      470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|141 TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNSPIT
      470      480      490      500      510
      530     540     550     560     570     580
Cry1Ac STRYRVRVRYASVTPIHNLNVNNGNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|141 Q-RYRLRFYASSRDARVILVTGAASTGVGGQVSVNMPLQKTEIAGENLTSRTFRYTFDFS
      520     530     540     550     560     570
      590     600     610     620     630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|141 NPFSTRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
      580     590     600     610     620     630
      640     650     660     670     680     690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640     650     660     670     680     690
      700     710     720     730     740     750
Cry1Ac NFKDINRQPERGWGSGTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|141

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gi|141 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECPYTYLQKIDESKCLKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

gi|141 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

gi|141 NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

gi|141 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac SCWNVKGHV DVEEQNNQRSVLVPWEAEVVSQEVVRVCPGRGYILRVYTAYKEGYEGCVTI
1000 1010 1020 1030 1040 1050

gi|141 LCWNVKGHV DVEEQNNHRSVLVIPWEAEVVSQEVVRVCPGRGYILRVYTAYKEGYEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEA---PSVP
1060 1070 1080 1090 1100

gi|141 HEIENNTDELKFSNCVVEEIVPNNTVTCCNYTGTQEEYEGTYTSRNRQYDEAYGNNSPVP
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRENPCFENRGYRDYTPLVGYVTKLEYFPETDKVWIEIGETEG
1110 1120 1130 1140 1150 1160

gi|141 ADYASVYEEKSYTDGRENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
1110 1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLLMEE
1170 1180

gi|141 TFIVDSVELLLMEE
1180

>>gi|17920873|gb|AAE86493.1| Sequence 8 from patent US 6 (1189 aa)
initn: 4540 initl: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGF
10 20 30 40 50 60

gi|179 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGSLNLYQIYAESFRE
70 80 90 100 110 120

gi|179 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|179 WEDDPHNPTTRTRVIDRFRILDGLLERDIPSPRISGFVEVPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
190 200 210 220 230 240

gi|179 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNPLKSTYQDWITYNRLRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQG----IEGS-
250 260 270 280 290

gi|179 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVTDLPLI-NFNPQLQSVLQPLTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHLMIDILNSITIYTDADR-GE--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
300 310 320 330 340 350

gi|179 IRNPHLFDILNLTIFTDFWFSVGRNRYWGGHRVISSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSG
360 370 380 390 400

gi|179 SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLHVSMSF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
410 420 430 440 450 460

gi|179 TVDSLTELPEPNDSPREGYSHRLCHATFVQRSGTPTFLTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFST
470 480 490 500 510 520

gi|179 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDLLRRNTFGDFVS---LQVNNSPIT
470 480 490 500 510

Cry1Ac STRYRVRYASVTPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|179 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDPS
520 530 540 550 560 570

Cry1Ac NAFTASSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
590 600 610 620 630

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      : . . . . . : : . . . : . . . . . : . . . . . : . . . . . :
gi|179 NFFSFRANPDIIGISEQLFGAGSISSGELYIDKIEIILADATFAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDS
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRSLDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGGSTGITIQGGDDVFKENYVTLPGTVEDECYPTYLYQKIDESLKAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVEDECYPTYLYQKIDESLKAFT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGHVDVEEQNNRQSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 LCWNVKGHVDVEEQNNRQSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050

      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 HEIEDNTDELKFSNCVEEIEYPNNTVTCNNYTGTOEYEGYTSRNRQGYDEAYGNPNSVP
      1060     1070     1080     1090     1100     1110

      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 ADYASVYEEKSYTDGRRNPCESNRYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170

      1170     1180

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Cry1Ac TFIVDSVELLLMEE
      : . . . . . :
gi|179 TFIVDSVELLLMEE
      1180

>>gi|56664637|gb|AAW18062.1| Sequence 8 from patent US 6 (1189 aa)
      initn: 4540 initl: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
      Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
      (5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      : . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 MEEN-NQQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIQVPSQWDAFLVQIEQLINORIEEFARNQAISRLEGLSNLYQIYAESFRE
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 LVGLIDFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 WEDDPHNPTRTRVIDRFRILDLGLLERDIPSPFRISGFVEPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 IFGERWGLTTINVENYENRRLIRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLRDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 TLTVLVDIAAFFPNYDNRRYPIQPVGQLTREYVTDPLI-NFNPQLQSVLQPLTFNVMESSA
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAPQQ
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 IRNPHLFDILNLTIFTDFWFSVGRNRYWGGHRVSSLIG--GGNITSPIYGREANQEPFR
      300     310     320     330     340     350

      360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLSVAVYRKSG
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360     370     380     390     400

      410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSSNSSVSIIRAPMFSWIHRSAEFNN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|566 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
      410     420     430     440     450     460

      470     480     490     500     510     520

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Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|566 TIDPERINQIPLVKGRFVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHLMVNVGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMP LQK TMEIGENLTSRTFRYTD FS
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSSFRANPDIIGISEQLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAF
gi|566 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLKAYT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGYIEDSQDLEIYLRIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLE
gi|566 NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHV DVEEQNQRSVLVPVEWAEVVSQEV RVC PGRGYILRV TAYKEGYGEGCVTI
gi|566 LCWNVKGHV DVEEQNHRSVLVIPEWAEVVSQEV RVC PGRGYILRV TAYKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050

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      1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|566 HEIEDNTDELKFSNCVVEEIVPNNVTVCNNYTGTEQEEYEGTYTSRNRQGYDEAYGNNSVSP
      1060      1070      1080      1090      1100      1110

      1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYGDRDYTPPLVGYVTKLEYFPETDKVWIEIGETEG
gi|566 ADYASVYEEKSYTDGRRENPCSNRYGDRDYTPPLVGYVTKDLEYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|566 TFIVDSVELLLMEE
      1180

>>gi|56642270|gb|AAW11988.1| Sequence 8 from patent US 6 (1189 aa)
      initn: 4540 init1: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
      Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
      (5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|566 MEEN-NQNCQIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIBEFARNQAISRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWGI FGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566 WEDDPHNPTTRTRVIDRFRILDGLLERDIPSPRISGFVPLLSVYQAANLHLAILRDSV
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
gi|566 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPLQLSVAQLPTFNVMESSA
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac IRSPHLMIDILNSITITYTDAHR-GE-YWWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQ
gi|566 IRNPHLFDILNLTIFTDFWFSVGRNFWYGGHRVVISSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350

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360      370      380      390      400
Cry1Ac RIVAQLGGQVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQ
gi|566 SFT--FNGPVFRTLSTLNPTLRLQLQPPWAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|566 TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLNVNMGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDIFS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSSFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKPKAFT
gi|566 NFRGINRQPDGRWGRSTDITIQGGDDVFKENYVTLPGTVDCEPYTYLYQKIDESKPKAYT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSLSLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEKCAHSHHSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
gi|566 NPDLDCSCRDEKCAHSHHFTLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIA
gi|566 EKPLLVGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

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940      950      960      970      980      990
Cry1Ac MIHAADKRVHSTREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHSTREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHVDVEEQNNQSRVSVLVPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTI
gi|566 LCWNVKGVHVDVEEQNNHRSVSVLVPWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTI
1000     1010     1020     1030     1040     1050

1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNGYNEA---PSVP
gi|566 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNGQYDEAYGNNPSPV
1060     1070     1080     1090     1100     1110

1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
gi|566 ADYASVYEEKSYTDGRRENPCSNRYGDDYTPLPAGYVTKDLELYFPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170

1170     1180
Cry1Ac TFIVDSVELLLMEE
gi|566 TFIVDSVELLLMEE
1180

>>gi|158456669|gb|ABW41342.1| Sequence 8 from patent US (1189 aa)
initn: 4540 initl: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|158 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
gi|158 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNINLYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|158 WEDDPHNPTTRTRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLLAIRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|158 IPGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230

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                250      260      270      280      290
Cry1Ac  TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQG-----IEGS-
gi|158  TLTVLVDIAAFFPNYDNRRIYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
                240      250      260      270      280      290

                300      310      320      330      340      350
Cry1Ac  IRSPHLMIDLNSITITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|158  IRNPHLFDILNLLTIFTDFWFSVGRNFYWGGRHVISSSLIG--GGNITSPIYGREANQPEPPR
                300      310      320      330      340      350

                360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR--RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSAG
gi|158  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
                360      370      380      390      400

                410      420      430      440      450      460
Cry1Ac  TVDSDLDEIPPNVPPRQGFSHRLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNN
gi|158  TVDSDLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTN
                410      420      430      440      450      460

                470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|158  TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDLRRTFGDFVS---LQVNNISPIIT
                470      480      490      500      510

                530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPIHLNVNWNSSII-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|158  Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTFDFS
                520      530      540      550      560      570

                590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPFVPTATLEAEYNLERAQKAVNAL
gi|158  NPFSSFRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
                580      590      600      610      620      630

                640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|158  FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
                640      650      660      670      680      690

                700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESLKAFT
gi|158  NFRGINRQPRDGRWGSTDITIQGGDDVFKENYVTLPGTVDECPYTYLYQKIDESLKAFT
                700      710      720      730      740      750

                760      770      780      790      800      810
Cry1Ac  RYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|158  RYELRGIYEDSQDLEIYLIRYNAKHIEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW

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                760      770      780      790      800      810
Cry1Ac  NPDLDSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
gi|158  NPDLDSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
                820      830      840      850      860      870

                880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|158  EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
                880      890      900      910      920      930

                940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|158  MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNGL
                940      950      960      970      980      990

                1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHVDVEEQNNQRSVLVVPEWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|158  LCWNVKGHVDVEEQNNHRSVLVPEWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
                1000     1010     1020     1030     1040     1050

                1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVVEEIEYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP
gi|158  HEIEDNTDELKFSNCVVEEIEYPNNTVTTCNNYTGTEYEGYTSRNQGYDEAYGNPSPV
                1060     1070     1080     1090     1100     1110

                1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRENPCFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
gi|158  ADYASVYEEKSYTDGRENPCSNRYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
                1120     1130     1140     1150     1160     1170

                1170     1180
Cry1Ac  TFIVDSVELLLMEE
gi|158  TFIVDSVELLLMEE
                1180

>>gi|14112742|gb|AAE58157.1| Sequence 8 from patent US 6 (1189 aa)
initn: 4540 init1: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0
Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

                10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|141  MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
                10      20      30      40      50

                70      80      90      100     110     120
Cry1Ac  VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAIARLEGLSNLYQIYAESFRE
gi|141  LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEAFARNAIANLEGLGNFNFIYVEAFKE

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60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEDDPHNPTTRTRVDRFRILDGLLELDIPSPFRISGFEVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFRREL
gi|141 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230
Cry1Ac TLTVDLIVSLFPPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRFGSAQG-----IEGS-
gi|141 TLTVDLIAAFFPNYDNRRIPIQVPGQLTREVYTDPLI-NFNPQLQSVLQPTFNVMESSA
240     250     260     270     280     290
Cry1Ac IRSPHMLDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEPTFFPLYGTMGNAAPQQ
gi|141 IRNPHLFDILNLTIFTDFWFSVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFR
300     310     320     330     340     350
Cry1Ac RIVAQLQGQVYRSLTSLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
gi|141 SFT--FNGPVRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFSS--TPTN--SFTYRGRG
360     370     380     390     400
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPFLTTGVV---FSWTHRSATLTN
410     420     430     440     450     460
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|141 TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIIT
470     480     490     500     510     520
Cry1Ac ISTRYRVRVRYASVTPIHNLVNVGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|141 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTFRYTDFFS
520     530     540     550     560     570
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
gi|141 NPFSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580     590     600     610     620     630
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|141 FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS

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gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
640     650     660     670     680     690
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|141 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
700     710     720     730     740     750
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
gi|141 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
760     770     780     790     800     810
Cry1Ac NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|141 NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
820     830     840     850     860     870
Cry1Ac EKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|141 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880     890     900     910     920     930
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
940     950     960     970     980     990
Cry1Ac SCWNVKGHVDEEQNNQRSVLPVPEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|141 LCWNVKGHVDEEQNNHRSVLPVPEWAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
1000    1010    1020    1030    1040    1050
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|141 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNQGYDEAYGNNSVSP
1060    1070    1080    1090    1100    1110
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYYVTKLELYFPETDKVWIEIGETEG
gi|141 ADYASVYEEKSYTDGRRENPCESNRGYGDTPLPAGYVTKLELYFPETDKVWIEIGETEG
1120    1130    1140    1150    1160    1170
Cry1Ac TFIVDSVELLLMEE
gi|141 TFIVDSVELLLMEE
1170    1180

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>>gi|23325082|gb|AAN23782.1| Sequence 8 from patent US 6 (1189 aa)  
initn: 4540 init1: 3093 opt: 4994 Z-score: 5879.5 bits: 1099.9 E(): 0

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Smith-Waterman score: 5265; 68.099% identity (83.058% similar) in 1210 aa overlap (5-1182:1-1189)

Sequence alignment for Cry1Ac vs gi|233. Includes residue numbers (10-60, 70-120, 130-180, 190-240, 250-290, 300-350, 360-400, 410-460, 470-520, 530-580) and amino acid sequences for both proteins.

Sequence alignment for Cry1Ac vs gi|233. Includes residue numbers (520-570, 590-630, 640-690, 700-750, 760-810, 820-870, 880-930, 940-990, 1000-1050, 1060-1100, 1110-1160) and amino acid sequences for both proteins.

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Cry1Ac ADYASVYEEKSYTDGRENPCFNRYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|233 ADYASVYEEKSYTDGRENPCFNRYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|233 TFIVDSVELLLMEE
      1180

>>gi|56664636|gb|AAW18061.1| Sequence 6 from patent US 6 (1189 aa)
      initn: 4539 initl: 3093 opt: 4993 Z-score: 5878.4 bits: 1099.7 E(): 0
Smith-Waterman score: 5264; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|566 MEEN-NQNCQIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIIFGSPQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWGIIVGSPQWDAFLVQIEQLINERIAEFARNAATAANLEGLGNPNFYVEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|566 WEEDPNNPATRTRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566 IFGEAWGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQG----IEGS-
gi|566 TLTVLDIAAFFPNYDNRYPYIQQVGLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac IRSPHLMIDILNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQ
gi|566 IRNPHLFDILNNTLIFTDFWFSVGRNFYWGHRVSSLIG--GNGNITSPIYGREANQEPFR
      300     310     320     330     340     350

      360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|566 SFT--FNGPVFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVVFS--TPTN--SFTYRGRG
      360     370     380     390     400

      410     420     430     440     450     460

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Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSLTELPEDNSVPPREGYSHRLCHATFVQRSQVLTGTVV---FSWTHRSATLNTN
      410      420      430      440      450      460

      470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPS
gi|566 TIDPERINQIPLVKGFVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMLPKQTMIEIGENLTSRTFRYTDFS
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSPFRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFCDECYPTYLYQKIDESKLAFT
gi|566 NFRGINRQDRGWGGSTDTITIQGGDDVFKENYVTLTSGTFCDECYPTYLYQKIDESKLAFT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
gi|566 NPDLDSCSRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|566 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|566 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

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1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDVEEQNNQRSVLVVPWEAEVVSQEVRCVCPGRGYILRVYTAYKEGYGEGCVTI
gi|566 LCWNVKGHVDVEEQNNHRSVLVVIPEWEAEVVSQEVRCVCPGRGYILRVYTAYKEGYGEGCVTI
1000      1010      1020      1030      1040      1050

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1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|566 HEIEDNTDELKFSNCVVEEIVPNNTVTCCNYTGTQEEYEGTYTSRNRQGYDEAYGNPNVSP
1060      1070      1080      1090      1100      1110

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1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|566 ADYASVYEEKSYTDGRRENPCESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEG
1120      1130      1140      1150      1160      1170

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1170      1180
Cry1Ac TFIVDSVELLMEE
gi|566 TFIVDSVELLMEE
1180

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>>gi|56642269|gb|AAW11987.1| Sequence 6 from patent US 6 (1189 aa)  
 in1tn: 4539 in1t1: 3093 opt: 4993 Z-score: 5878.4 bits: 1099.7 E(): 0  
 Smith-Waterman score: 5264; 68.099% identity (83.058% similar) in 1210 aa overlap  
 (5-1182:1-1189)

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|566 MEEN-NQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

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70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|566 LVGLIDFVWGIWGFQPSQWDAFLVQIEQLINERIAEFARNAATANLEGLGNPNFIYVEAFKE
60      70      80      90      100      110

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130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|566 WEEDPNNPATRTRVDRFRILDGLLERDIPSFRIISGFVPLLSVYQAANLHLAILRDSV
120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|566 IFGEAWGLTTINVENYNRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180      190      200      210      220      230

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250      260      270      280      290
Cry1Ac TLTVLVDIVSLFPNYSRTPYRTVSQTLREIYTNVPLENFDGSRFGSAQ-----IEGS-
gi|566 TLTVLVDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
240      250      260      270      280      290

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300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|566 IRNPHLFDILNNTIFTDFWFSVGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

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360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSNLPMSAVYRKSG
gi|566 SFT--FNGPVFRTLSNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

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410      420      430      440      450      460
Cry1Ac TVDSLDEIIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|566 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
410      420      430      440      450      460

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470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|566 TIDPERINQIPLVKGFVWGGTSSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIT
470      480      490      500      510

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530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPPIHLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|566 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTDPS
520      530      540      550      560      570

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590      600      610      620      630
Cry1Ac NAFTASSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|566 NPFSTRANPDIIGISEQPLFAGSISGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

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640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|566 FTSSNIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

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```

700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|566 NFRGINRQPDGRWGGSTDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

```

```

760      770      780      790      800      810
Cry1Ac RYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
gi|566 RYELRGIYEDSQDLEIYLIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

```

```

820      830      840      850      860      870
Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
gi|566 NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLE
820      830      840      850      860      870

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700      710      720      730      740      750
Cry1Ac  760      770      780      790      800      810
RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|158  760      770      780      790      800      810
RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW

820      830      840      850      860      870
Cry1Ac  NPDLDCSCRDKGEKCAHSHSHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|158  NPDLDCSCRDKGEKCAHSHSHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE

880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIA
gi|158  EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA

940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|158  MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL

1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHVDFVEEQNNQSVLVVPEWAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI
gi|158  LCWNVKGHVDFVEEQNNHRSVLVPEWAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI

1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVVEEIIYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|158  HEIEDNTDELKFSNCVVEEIVPNNVTTCNNYTGTEYEGTYTSRNRQYDEAYGNPNPSVP

1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPEYDQKLVWIEIGETEG
gi|158  ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKDLEYFPEYDQKLVWIEIGETEG

1170     1180
Cry1Ac  TFIVDVSELLLMEE
gi|158  TFIVDVSELLLMEE
1180

>>gi|23325081|gb|AAN23781.1| Sequence 6 from patent US 6 (1189 aa)
  initn: 4539  initl: 3093  opt: 4993  Z-score: 5878.4  bits: 1099.7  E(): 0
Smith-Waterman score: 5264; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|233  MEEN-NQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF

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10      20      30      40      50
Cry1Ac  70      80      90      100     110     120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISREGLSNLYQIYAESFRE
gi|233  LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNFNFIYVEAFKE

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|233  WEEDPNNPATRTRVIDRFRILDGLLERDIPSPFRISGFVEVPLLSVYVQAANLHLAIRDVS

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|233  IPGEAWGLTTINWENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQG----IEGS-
gi|233  TLTVLDIAAFFPNYDNRRYPIQVPGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMESSA

300     310     320     330     340     350
Cry1Ac  IRSPHLMIDLNSITIIYTDADR-GE-YWWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQ
gi|233  IRNPHLFDILNNTLIFTDFWFSVGRNRYWGGHRVVISLIG--GGNITSPIYGREANQEPFR

360     370     380     390     400
Cry1Ac  RIVAQLGQGVYRTLSSLTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPYSAVYRKSG
gi|233  SFT--FNGVPVFRTLNPTLRLQLQPPWAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG

410     420     430     440     450     460
Cry1Ac  TVDSLDEIPQNNVPPRQGFSHRSLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|233  TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV----FSWTHRSATLTN

470     480     490     500     510     520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPST
gi|233  TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS----LQVNIINSPIT

530     540     550     560     570     580
Cry1Ac  STRYRVRVRYASVTPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|233  Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMLQKTMIEIGENLTSRTFRYTDPS

590     600     610     620     630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL

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gi|233 NPFSFRANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDS
.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|233 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRSLDERNLLQDP
640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITTIQGGDDVFKENYVTLSGTFDECYPTLYQKIDESKPKAFT
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 NFRGINRQPDGRWGSTDTITIQGGDDVFKENYVTLPGTVEDECYPTLYQKIDESKPKAYT
700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYLSIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEGKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKITQDGHARLGNLEFLE
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 NPDLDCSCRDEGKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKITQDGHARLGNLEFLE
820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 MIHAADKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGL
940      950      960      970      980      990

      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVEEQNNQRSVLLVPEWEAEVVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTI
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 LCWNVKGVHDVEEQNNHRSVLLVPEWEAEVVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTI
1000     1010     1020     1030     1040     1050

      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 HEIEDNTDELKFSNCVVEEVYNNVTVCNNYTGTEYEGYTSRNRQYDEAYGNPSPV
1060     1070     1080     1090     1100     1110

      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 ADYASVYEEKSYTDGRRENPCESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170

      1170     1180
Cry1Ac TFIVDSVELLLMEE

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.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|233 TFIVDSVELLLMEE
1180

>>gi|17920872|gb|AAE86492.1| Sequence 6 from patent US 6 (1189 aa)
initn: 4539 initl: 3093 opt: 4993 Z-score: 5878.4 bits: 1099.7 E(): 0
Smith-Waterman score: 5264; 68.099% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIQFSPQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 LVGLIDFVWGIQFSPQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 WEEDNNPATRTRVIDRFRILDGLLERDIPSPRISGFVPLLSVYAQAANLHLAALRDSV
120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 IPGEANGLTTINNVENYRNLIRHIDEYADHCANTYNRGLNNLPKSTYQDWIYTNRLRRDL
180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDDGSGFRGSAQG----IEGS-
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVTYDPLI-NFNPQLQSVLQPTFNVMESSA
240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac IRSPHLMIDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 IRNPHLFDILNLLTIFTDWFSVGRNRYWGGHRVISSLIG--GGNITSPIYGREANQEPFR
300     310     320     330     340     350

      360     370     380     390     400
Cry1Ac RIVAQLGGVYRTLSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSG
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 SPT--FNGVVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
360     370     380     390     400

      410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.: :.:
gi|179 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPTFLTGVV---FSWTHRSATLTN
410     420     430     440     450     460

      470     480     490     500     510     520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST

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      . . . . .
gi|179 TIDPERINQIPLVKGRVWGGSVTITGPGFTGGDILRRNTFGDFVS---LQVNIINSPI
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPPIHLNVNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      . . . . .
gi|179 Q-RYRLRFRYASSRDRARVIVLTGAASTGVGGQVSVNMPQLQKTMEIGENLTSRTFRYTFDS
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVTTATLEAEYNLERAQKAVNAL
      . . . . .
gi|179 NPFSFRANPDIIGISEQPLFGAGSISSEGLYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
      . . . . .
gi|179 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGSGTITIQGGDDVFKENYVTLSTGTFDECPYTYLYQKIDESKPKAFT
      . . . . .
gi|179 NFRGINRQPDGRWGSTDTITIQGGDDVFKENYVTLPGTVDCEPTYTYLYQKIDESKPKAYT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYLSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      . . . . .
gi|179 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDCSRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      . . . . .
gi|179 NPDLDCSRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      . . . . .
gi|179 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPESVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      . . . . .
gi|179 MIHAADKRVHRIREAYLPESVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHV DVEEQNNQSVLVPPEWAEVVSQEVVRVCPGRGYILRVTA YKEGYEGGCVTI
      . . . . .
gi|179 LCWNVKGHV DVEEQNNHRSVLVIPPEWAEVVSQEVVRVCPGRGYILRVTA YKEGYEGGCVTI
      1000      1010      1020      1030      1040      1050

      1060      1070      1080      1090      1100

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Cry1Ac HEIENNTDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP
      . . . . .
gi|179 HELEDNTDELKFSNCVEEEVYPNNTVTCNNYTGTEYEGTYTSRNGYDEAYGNPSPV
      1060      1070      1080      1090      1100      1110

      1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFENRGRDYTPPLVGVYTKLELYFPETDKVWIEIGETEG
      . . . . .
gi|179 ADYASVYEEKSYTDGRRENPCFENRGRDYTPPLVGVYTKLELYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIVDSVELLLMEE
      . . . . .
gi|179 TFIVDSVELLLMEE
      1180

>>gi|14112741|gb|AAE58156.1| Sequence 6 from patent US 6 (1189 aa)
      initn: 4539 init1: 3093 opt: 4993 Z-score: 5878.4 bits: 1099.7 E(): 0
      Smith-Waterman score: 5264; 68.099% identity (83.058% similar) in 1210 aa overlap
      (5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEPIYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      . . . . .
gi|141 MEEN-NQNCIPYCNLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi|141 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
      . . . . .
gi|141 WEEDPNPATRTRVIDRFRILDGLLERDIPSRISGFVPLLSVYAQAANLHLAILLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      . . . . .
gi|141 IFGEAWGLTTINVENYNNRIRHIDEYADHCANTYRNLGNLPLKSTYQDWITYNRLRDL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQG-----IEGS-
      . . . . .
gi|141 TLTVLDIAAFPNYDNRRIPIQFVGLTRVYTDPLI-NFNPQLQSVQALPTFNVMESSA
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE--YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQ
      . . . . .
gi|141 IRNPHLFDLNLITFTDWFVGRNRYWGGHRVIVSSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350

      360      370      380      390      400

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      250      260      270      280      290
Cry1Ac TLTVLDIIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENLFDGSRGSAQG-----IEGS-
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 TLTVLDAIAAFPNYNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQ
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 IRNPHLFDILNLLTIFTDWFVSVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350

      360      370      380      390      400
Cry1Ac RIVAQLGGQVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG
      .. . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400

      410      420      430      440      450      460
Cry1Ac TVDSLDEIPPNQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPPLTTGVV---FSWTHRSATLITN
      410      420      430      440      450      460

      470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRTFGDFVS---LQVNNISPIT
      470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac STRYRVRYASVTPIHNLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTIMEIGENLTSRTFRYTD
      520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
      : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 NPFSSFRANPDIIGISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLAFT
      : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 NFRGINRQPDGRGWRGSDTITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

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      820      830      840      850      860      870
Cry1Ac NPDLDSCSRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 NPDLDSCSRDGEKCAHSHHFTLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNG
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNG
      940      950      960      970      980      990

      1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDEVEEQNNQSVLVVPEWAEVSEVVRVCPGRGYILRVYAYKEGYGEGCVTI
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 LCWNVKGHVDEVEEQNNHRSVLVIPWAEVSEVVRVCPGRGYILRVYAYKEGYGEGCVTI
      1000      1010      1020      1030      1040      1050

      1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPV
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 HEIEDNTDELKFSNCVEEEVYPNNTVTCNNYTGTEQEEYEGYTSRNRQGYDEAYGNNPSPV
      1060      1070      1080      1090      1100      1110

      1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 ADYASVYEEKSYTDGRRENPCSNRQYGDYTPLPAGYVTKDLELYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIVDSVELLLMEE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 TFIVDSVELLLMEE
      1180

>>gi|14111121|gb|AAE57661.1| Sequence 8 from patent US 6 (1189 aa)
      initn: 4534 init1: 3093 opt: 4988 Z-score: 5872.5 bits: 1098.6 E(): 0
      Smith-Waterman score: 5259; 68.017% identity (82.893% similar) in 1210 aa overlap
      (5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 MEEN-NQNCQIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFMVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIWVGSQWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE
      .....: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 VLGLIDFVWGIWVGSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLNLLNIYVEAFKE
      60      70      80      90      100      110

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Smith-Waterman score: 5259; 68.017% identity (82.893% similar) in 1210 aa overlap (5-1182:1-1189)

Sequence alignment for Cry1Ac and gi|627. The alignment shows amino acid sequences with positions 10-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, 430-480, 490-540, 550-600. The sequences are highly conserved, with only a few substitutions noted.

Sequence alignment for Cry1Ac and gi|627. The alignment shows amino acid sequences with positions 520-570, 590-640, 650-700, 710-760, 770-820, 830-880, 890-940, 950-1000, 1010-1060, 1070-1120, 1130-1180. The sequences are highly conserved, with only a few substitutions noted.

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Cry1Ac ADYASVYEEKSYTDGRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|627 ADYASVYEEKSYTDGRENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120      1130      1140      1150      1160      1170

      1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|627 TFIVDSVELLLMEE
      1180

>>gi|27436034|gb|AAO13295.1|AF336114_1 crystal delta-end (1174 aa)
      initn: 4822 initl: 2872 opt: 4979 Z-score: 5861.9 bits: 1096.6 E(): 0
      Smith-Waterman score: 5103; 66.583% identity (83.627% similar) in 1191 aa overlap
      (5-1182:1-1174)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|274 MKNNIQ-NQCVPNCLSNPEVEILSEER-STGRPLDISLSLTRFLLSEFVPGVGV
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|274 AFGLFDLIWGFITPSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
gi|274 WEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLLRDAV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|274 SFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGTNTRQWSRFNQFRREL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLN--FDGSRFGSAQGIIEGSIKSP
gi|274 TLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRP
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac HLMIDLNSITIIYTDARHGEYVWGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQL
gi|274 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNPINFPIYGIF-NPGGAIWADED
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPASVYKSGTVDSLDEI
gi|274 PRPFYRTLSDPVVFVRG---GFGNPHYVLGLRGVAFQ-QTGTN-HTRTFRNSGTIDSLDEI
      360     370     380     390     400

      420     430     440     450     460     470

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Cry1Ac PPQNNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|274 PPQDNGAPWNYDYSVHLNHVTFVWRPGEIAGSDSWRAPMFSWTHRSADRTNIIINPNIITQ
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
gi|274 IPAVKAHNLHSGSTVVRGPGFTGGDLLRRINTGTAFDIRVNIITGPL----SQRYRVRIR
      470      480      490      500      510      520

      540      550      560      570      580      590
Cry1Ac YASVTPIHLNVNWGNSSIFSNVTPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGV
gi|274 YASTTDLQFFTRINGTISVNQGNFQRTMNRGGNLESGNFRTAGFSTPFSSNAQSTFTLTGT
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|274 QAFSNQE-VYIDRIEFVPAEVTFAESDLERAQKAVNALFTSTSQLGLKTNVTDYHIDQV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTIT
gi|274 SNLVALSDEFCLDEKRELSEKVKHAKRLSDKRNLLQDPNFRGINRQPDHGWGSGTDIT
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|274 QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
      710      720      730      740      750      760

      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|274 NSKHETVNVPGTGSWLVENQIGPCGEPNRCAPHLEWNPDLHCSRDGEKCVHSHSHF
      770      780      790      800      810      820

      840      850      860      870      880      890
Cry1Ac SLDIDVGCETDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEPLVGEALARVKRAEKKWRD
gi|274 SLDIDVGCETDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEPLVGEALARVKRAEKKWRD
      830      840      850      860      870      880

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|274 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHRIREAYLPELS
      890      900      910      920      930      940

      960      970      980      990     1000     1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSVL
gi|274 VIPGVNAAFEELEGRIFTAYSLSYDARNVIKNGDFNNGLLCWNVKGHVVDVEEQNNHRSVL
      950      960      970      980      990     1000

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1020      1030      1040      1050      1060      1070
Cry1Ac  VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFNCSNVEEIIY
gi|274  VIPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIEDNTDELKFNCSNVEEG-Y
1010      1020      1030      1040      1050

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```

1080      1090      1100      1110      1120
Cry1Ac  PNNTVTCNDYTVNQE--EYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|274  PNNTVTCNEYTMNQVGECTDACNVRNRGYEDAYGHPNTPVHYHTPYEETTYTDERREN
1060      1070      1080      1090      1100      1110

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```

1130      1140      1150      1160      1170      1180
Cry1Ac  PCEFNRGRYDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|274  PCEANKGYVNYTLPVGYVTKLEYFPETDTVWIEIGETEGTFIVDSVELLLMEE
1120      1130      1140      1150      1160      1170

```

```

>>gi|295866|emb|CAA80235.1| crystal protein [Bacillus th (1174 aa)
  in1tn: 4822 in1t1: 2872 opt: 4979 Z-score: 5861.9 bits: 1096.6 E(): 0
Smith-Waterman score: 5103; 66.583% identity (83.627% similar) in 1191 aa overlap
(5-1182:1-1174)

```

```

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF
gi|295  MKNNIQ-NQCVPYNCLSNPEVEILSEER-STGRLPLDISLSLTRFLLESEFVPGVGV
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGLESLNYQIYAESFRE
gi|295  AFGLFDLIWGFITPSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVS
gi|295  WEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAAHLHLSLLRDAV
120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|295  SFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLRGNTTRQWSRFNQGFRREL
180     190     200     210     220     230

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```

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVEN--FDGSRGSAQIEGSIIRSP
gi|295  TLTVLDIVALFPNYPARAYPIQTSSQLTREIYTSVIEDSPSANIPNGFNRAEFGVVRPP
240     250     260     270     280     290

```

```

300     310     320     330     340     350
Cry1Ac  HLMIDILNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|295  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNPINFPIYGIF-NPGGAIWAIED
300     310     320     330     340     350

```

```

360      370      380      390      400      410
Cry1Ac  GGGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTTEFAYGTSSNLPASVYRKSQSTVDSLDEI
gi|295  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360      370      380      390      400

```

```

420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|295  PPQDNGAPWNDYSHVLNHVTFVRWPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIIITQ
410      420      430      440      450      460

```

```

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFSTSTRYRVRV
gi|295  IPAVKAHLHSGSTVVRGPGFTGGDLLRRRTNTGTAFDIRVNIITGPL----SQRYRVRIR
470      480      490      500      510      520

```

```

540      550      560      570      580      590
Cry1Ac  YASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGV
gi|295  YASTTDLQFTRINGTSVNGQNFQRTMNRGGNLESGNFRTAGFSTPFPSNAQSTFTLTGT
530      540      550      560      570      580

```

```

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|295  QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTSQLGLKTNVTGYHIDQV
590      600      610      620      630      640

```

```

660      670      680      690      700      710
Cry1Ac  SNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|295  SNLVACLSDEFCLDEKRELSEKVKHAKRLSDKRNLLQDPNFRGINRQPDHGWGRSTDIIT
650      660      670      680      690      700

```

```

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|295  QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
710      720      730      740      750      760

```

```

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDEKCAHSHSHF
gi|295  NSKHEIVNVPGTGLWPLSVENQIGPCGEPNRCAPHEWNPDLHDCSCRDEKCVHSHSHF
770      780      790      800      810      820

```

```

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|295  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEEPLLGEALARVKRAEKKWRD
830      840      850      860      870      880

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900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|295  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHRIREAYLPELS
890      900      910      920      930      940

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      820      830      840      850      860      870
      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIA
gi|539 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVNTNIA
      880      890      900      910      920      930
      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|539 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990
      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQSRVSVLVPVEWAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI
gi|539 LCWNVKGVHDVVEEQNNHRSVSVLVIPEWAEVSVQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050
      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGAYTSRNRGYNEA---PSVP
gi|539 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNPNPSVP
      1060     1070     1080     1090     1100     1110
      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFENRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEG
gi|539 ADYASVYEEKSYTDGRRENPCESNRGYDGYTPLPAGYVTKLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170
      1170     1180
Cry1Ac TFIIVDSVELLLMEE
gi|539 TFIIVDSVELLLMEE
      1180
>>gi|142750|gb|AAA22343.1| cryIC(b) (1189 aa)
  in1n: 4530 in1l: 3075 opt: 4978 Z-score: 5860.7 bits: 1096.4 E(): 0
Smith-Waterman score: 5249; 67.851% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|142 MEEN-NQNCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|142 LVGLIDFVWIVGQPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|142 WEEDPNPATRTRVDRFRILDGLLERDIPFRISGFVPLLSVYAQAANLHLAALRDSV

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      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGPDSRSDWIRYNQFREL
gi|142 IPGERWGLTTINVENYRNRLIRHIDEYADHCANTYNRGLNNLPKSTYQDWIITYNRLRDL
      180      190      200      210      220      230
      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQG----IEGS-
gi|142 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQVAQLPTFNVMSSA
      240      250      260      270      280      290
      300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGSGPEFTFPYLYGTMGNAAPQQ
gi|142 IRNPHLFDILNNTLIFTDFWFSVGRNFYWGGRVVISLIG--GGNITSPIYGREANQEPFR
      300      310      320      330      340      350
      360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSG
gi|142 SFT--FNGPVFRTLNSPTLRLQLQWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360      370      380      390      400
      410      420      430      440      450      460
Cry1Ac TVDSLDEIIPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNN
gi|142 QVDSLTELPPEDNSVPPREGYSHRSLCHATFVQVRSRGTPTLTTGVV---FSWTHRSATLTN
      410      420      430      440      450      460
      470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|142 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNSPIT
      470      480      490      500      510
      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPPIHLNVNNGNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|142 Q-RYRLRFYASSRDARVILVTGAASTGVGGQVSVNMPKQKMEIGENLTSRTFRYTFDFS
      520      530      540      550      560      570
      590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|142 NPFSTRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
      580      590      600      610      620      630
      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|142 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690
      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGSGTGITIQGGDDVFKENYVTLTSGTFDECYPTLYQKIDESKLAFT

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gi|142 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECPYTYLQKIDESKCLKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

gi|142 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac NPDLDCSCRDEGKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

gi|142 NPDLDCSCRDEGKCAHSHHFTLDIDVGCTDLNEDLGLWVIFKIKTQDNHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

gi|142 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVNTNIA
880 890 900 910 920 930

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

gi|142 MIHAADKRVHRIREAYLPELSVIPGVNAAI FEELEGRIFTAYSLSYDARNVIKNGDFNNGL
940 950 960 970 980 990

Cry1Ac SCWNVKGHV DVEEQNNQRSVLVPWEAEVVSQEVVRVCPGRGYILRV TAYKEGYEGCVTI
1000 1010 1020 1030 1040 1050

gi|142 LCWNVKGHV DVEEQNNHRSVLVIPWEAEVVSQEVVRVCPGRGYILRV TAYKEGYEGCVTI
1000 1010 1020 1030 1040 1050

Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
1060 1070 1080 1090 1100

gi|142 HEIEDNTDELKFSNCVVEEVYPNNTVT CNNYTGQEEYEGTYTSRNQGYDEAYGNNSVP
1060 1070 1080 1090 1100 1110

Cry1Ac ADYASVYEEKSYTDGRENPC EFNRGYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEG
1110 1120 1130 1140 1150 1160

gi|142 ADYASVYEEKSYTDGRENPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEG
1120 1130 1140 1150 1160 1170

Cry1Ac TFIVDSVELLLMEE
1170 1180

gi|142 TFIVDSVELLLMEE
1180

>>gi|118907898|gb|ABL55896.1| Sequence 6 from patent US (1189 aa)
initn: 4530 initl: 3075 opt: 4978 Z-score: 5860.7 bits: 1096.4 E(): 0
Smith-Waterman score: 5249; 67.851% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFLLSEFVPGAGF
10 20 30 40 50 60

gi|118 MEEN-NQNQCIPYNCLSNPEEVL DGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|118 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|118 WEEDPNPATRTRVIDRFRILDGLLERDIPSRISGFVEVPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
190 200 210 220 230 240

gi|118 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNPLPKSTYQDWITYNRLRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQG----IEGS-
250 260 270 280 290

gi|118 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPLTFNVMSSA
240 250 260 270 280 290

Cry1Ac IRSPHLM DILNSITIYTD AHR-GE--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
300 310 320 330 340 350

gi|118 IRNPHLFDILNLTIFTDWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLQGQVYRTLSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSG
360 370 380 390 400

gi|118 SFT--FNGPVFRTL SNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLHVSMSF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
410 420 430 440 450 460

gi|118 QVDSLTELPEPNDSPREGYSHRLCHATFVQRSGTPFLTGTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPFST
470 480 490 500 510 520

gi|118 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDLLRRNTFGDFVS---LQVNNSPIT
470 480 490 500 510

Cry1Ac STRYRVRYASVTPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|118 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDPS
520 530 540 550 560 570

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
590 600 610 620 630

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      : . . . . . : : . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 NFFSFRANPDIIGISEQLFGAGSISSGELYIDKIEIILADATFAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDS
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRSLDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac NFKDINRQPERGGSTGITIQGGDDVFKENYVTLPGTVEDECPYTYLQKIDESLKAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 NFRGINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVEDECPYTYLQKIDESLKAFT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEW
      760      770      780      790      800      810

      820      830      840      850      860      870
Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLFE
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGLWVIFKIKTQDNHARLGNLFLFE
      820      830      840      850      860      870

      880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVNTNIA
      880      890      900      910      920      930

      940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFELEGRIFTAYSLYDARNVIKNGDFNNGL
      940      950      960      970      980      990

      1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGHVDVEEQNNQRSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 LCWNVKGHVDVEEQNNHRSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTI
      1000     1010     1020     1030     1040     1050

      1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 HEIEDNTDELKFSNCVEEIVPNNTVTCNNYTGQEEYEGYTSRNQGYDEAYGNPNSVP
      1060     1070     1080     1090     1100     1110

      1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEG
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118 ADYASVYEEKSYTDGRRNPCESNRYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
      1120     1130     1140     1150     1160     1170

      1170     1180

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Cry1Ac TFIVDSVELLLMEE
      : . . . . . :
gi|118 TFIVDSVELLLMEE
      1180

>>gi|12819675|gb|AAE47789.1| Sequence 6 from patent US 6 (1189 aa)
      initn: 4530 initl: 3075 opt: 4978 Z-score: 5860.7 bits: 1096.4 E(): 0
Smith-Waterman score: 5249; 67.851% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      : . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|128 MEEN-NQNCQIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIQVPSQWDAFLVQIEQLINORIEEFARNQAISRLEGLSNLYQIYAESFRE
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|128 LVGLIDFVWGIQVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 WEEDPNPATRTRVIDRFRILDLGLLERDIPSPRISGFVEPLLSVYAQAANLHLAILRDSV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 IFGERWGLTTINVENYENRIRHIDEYADHCANTYRGLNLLPKSTYQDWITYNRLRDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREYVTDPLI-NFNPQLQSVLQPLTFNVMESSA
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac IRSPHLMIDLNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAPQQ
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQEPFR
      300     310     320     330     340     350

      360     370     380     390     400
Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLSVAVYRKSG
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
      360     370     380     390     400

      410     420     430     440     450     460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLHVSMSF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
      : . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|128 QVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFPFLTTGVV---FSWTHRSATLTN
      410     420     430     440     450     460

      470     480     490     500     510     520

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360      370      380      390      400
Cry1Ac RIVAQLGGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQ
gi|301 SFT--FNGPVFRTLSTLNPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

410      420      430      440      450      460
Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|301 QVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTN
410      420      430      440      450      460

470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|301 TIDPERINQIPLVKGRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPIT
470      480      490      500      510

530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHNLNVNMGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|301 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTDIFS
520      530      540      550      560      570

590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|301 NPFSSFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFEAESDLERAQKAVNAL
580      590      600      610      620      630

640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|301 FTSSNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKPKAFT
gi|301 NFRGINRQPDGRWGRSTDITIQGGDDVFKENYVTLPGTVDCEPYTYLYQKIDESKPKAYT
700      710      720      730      740      750

760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSLSLWPLSAQSPIGKCGEPNRCAPHLEW
gi|301 RYELRGYIEDSQDLEIYLIRYNAKHEIVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEW
760      770      780      790      800      810

820      830      840      850      860      870
Cry1Ac NPDLDCSCRDEKCAHSHHSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
gi|301 NPDLDCSCRDEKCAHSHHFTLDIDVGCTDLNEDLGLWVIFKIKTQDNHARLGNLEFLE
820      830      840      850      860      870

880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|301 EKPLLGEALARVKRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVNTNIA
880      890      900      910      920      930

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940      950      960      970      980      990
Cry1Ac MIHAADKRVHSTREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|301 MIHAADKRVHSTREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGL
940      950      960      970      980      990

1000     1010     1020     1030     1040     1050
Cry1Ac SCWNVKGVHDVVEEQNNQSRVSVLVPWEAEVSEQEVRVCPGRGYLLRVTAKEGYGEGCVTI
gi|301 LCWNVKGVHDVVEEQNNHRSVSVLVPWEAEVSEQEVRVCPGRGYLLRVTAKEGYGEGCVTI
1000     1010     1020     1030     1040     1050

1060     1070     1080     1090     1100
Cry1Ac HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|301 HEIEDNTDELKFSNCVVEEIVPNNTVTCNNYTGTEEEYEGTYTSRNRQGYDEAYGNNPSPV
1060     1070     1080     1090     1100     1110

1110     1120     1130     1140     1150     1160
Cry1Ac ADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLELYFPETDKVWIEIGETEG
gi|301 ADYASVYEEKSYTDGRRENPCSNRYGDDYTPLPAGYVTKDLELYFPETDKVWIEIGETEG
1120     1130     1140     1150     1160     1170

1170     1180
Cry1Ac TFIIVDSVELLLMEE
gi|301 TFIIVDSVELLLMEE
1180

>>gi|33734264|gb|AAQ38645.1| Sequence 6 from patent US 6 (1189 aa)
initn: 4530 init1: 3075 opt: 4978 Z-score: 5860.7 bits: 1096.4 E(): 0
Smith-Waterman score: 5249; 67.851% identity (83.058% similar) in 1210 aa overlap
(5-1182:1-1189)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|337 MEEN-NQNQCIPYNCLSNPEEVLGGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIGWIFGSPQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLYQIYAESFRE
gi|337 VLGLIDFVWGVGSPQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|337 WEEDPNNPATRTVIDRFRILDGLLERDIPSPRISGFVPLLSVYAQAANLHLLAIRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|337 IPGERWGLTTINWVNNYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180     190     200     210     220     230

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                250      260      270      280      290
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVLENFDGSRFRGSAQG-----IEGS-
gi|337 TLTVLVDIAAAPPNYNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
                240      250      260      270      280      290

                300      310      320      330      340      350
Cry1Ac IRSPHMDILNSITITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|337 IRNPHLFDILNLLTIFTDFWFSVGRNFYWGGRVIVSSLIG--GGNITSPIYGREANQPEPPR
                300      310      320      330      340      350

                360      370      380      390      400
Cry1Ac RIVAQLGQGVYRTLSSTLYR--RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSAG
gi|337 SFT--FNGPVPFRTLNSPTLRLLQQPWPAPPFN--LRGVEGVFEFS--TPTN--SFTYRGRG
                360      370      380      390      400

                410      420      430      440      450      460
Cry1Ac TVDSDLDEIPQNNVPPRQGFSHRLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNN
gi|337 QVDSLTELPEPENSVPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTN
                410      420      430      440      450      460

                470      480      490      500      510      520
Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|337 TIDPERINQIPLVKGFRVWGGTSVITGPGFTGGDLRRTFGDFVS---LQVNNISPIIT
                470      480      490      500      510

                530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVTPIHLNVNWNSSII-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|337 Q-RYRLRFYRASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTFDFS
                520      530      540      550      560      570

                590      600      610      620      630
Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNAL
gi|337 NPFSSFRANPDIIGISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNAL
                580      590      600      610      620      630

                640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|337 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
                640      650      660      670      680      690

                700      710      720      730      740      750
Cry1Ac NFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTFDECPYTYLYQKIDESLKAFT
gi|337 NFRGINRQPRDGRWGSTDITIQGDDVFKENYVTLPGTVDECPYTYLYQKIDESLKAFT
                700      710      720      730      740      750

                760      770      780      790      800      810
Cry1Ac RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW
gi|337 RYELRGYIEDSQDLEIYLIRYNAKHIEIVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEW

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                760      770      780      790      800      810
Cry1Ac NPDLDSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLE
gi|337 NPDLDSCDRDGEKCAHSHHFLDIDVGCTDLNEDLGLVWVIFKIKTQDNHARLGNLEFLE
                820      830      840      850      860      870

                880      890      900      910      920      930
Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|337 EKPLLGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVNTNIA
                880      890      900      910      920      930

                940      950      960      970      980      990
Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|337 MIHAADKRVHRIREAYLPELSVIPGVNAAIFFEELEGRIFTAYSLYDARNVIKNGDFNNGL
                940      950      960      970      980      990

                1000      1010      1020      1030      1040      1050
Cry1Ac SCWNVKGHVDVEEQNNQRSVLVVPEWEAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
gi|337 LCWNVKGHVDVEEQNNHRSVLVPEWEAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTI
                1000      1010      1020      1030      1040      1050

                1060      1070      1080      1090      1100
Cry1Ac HEIENNTDELKFSNCVVEEIEYPNNTVTTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVP
gi|337 HEIEDNTDELKFSNCVVEEIEYPNNTVTTCNNYTGTEYEGYTSRNQGYDEAYGNPSPV
                1060      1070      1080      1090      1100      1110

                1110      1120      1130      1140      1150      1160
Cry1Ac ADYASVYEEKSYTDGRENPCFENRGRDYTPPLVGYVTKLELYFPETDKVWIEIGETEG
gi|337 ADYASVYEEKSYTDGRENPCESNRGYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEG
                1120      1130      1140      1150      1160      1170

                1170      1180
Cry1Ac TFIVDSVELLLMEE
gi|337 TFIVDSVELLLMEE
                1180

>>gi|3010036|gb|AAC10641.1|I73895 Sequence 4 from patent (1168 aa)
initn: 4729 init1: 2942 opt: 4970 Z-score: 5851.4 bits: 1094.7 E(): 0
Smith-Waterman score: 5094; 66.190% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1168)

                10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|301 MKNNIQ-NQCVPYNCLSNPEVEILSEER-STGRPLDISLSLTRFLLSEFVPGVGV
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISREGLSNLYQIYAESFRE
gi|301 AFGLFDLIWGFITPSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVYLEALRE

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60      70      80      90      100     110
Cry1Ac  130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|301  WEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVWGPDSRDWIRYNOFRREL
gi|301  SFGQWGLDIATVNNHYNRLINLIHRYTEHCLDLYNQLENLRGTNRQWSRFNOFRREL
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQGIIEGSIRSP
gi|301  TLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRPP
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac  HLMIDLINSITIYDHAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|301  HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNPINFPYGVF--NPGGAIWADED
300      310      320      330      340      350

360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPNAVYRKSQTVDSLDEI
gi|301  PRPFYRTLSDPVVFVRG---GFGDPHYVLGLRQVGFQQ--TGTN-HTRTFRNSGTIDSLDEI
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac  PFQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|301  PPDNSGAPWNDYSHVLNHTVFRVWPGEIAGSDSWRAPMFSWTHRSADRTNIINPNIITQ
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYLEVPIHFPSTSTRYRVRVR
gi|301  IPAVKAHNLHSGSTVVRGPGFTGGDLLRRTNTGTTFADIRVNIITGPL----SQRYRVRIR
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  YASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFSTSLGNI-VGV
gi|301  YASTTDLQFFTRINGTSMVQGNFQRTMNRGDNLESNGNFRTAGFSTPFSFSNAQSTFTLGT
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|301  QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI

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gi|301  SNLVACLSDEFCLDEKRELSKVKHAKRLSDKRNLLQDPNFRGINRQPDHGWGRGSTDITI
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLSGTFDECYPTLYYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|301  QGGDDVFKENYVTLPGTFDECYPTLYYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|301  NSKHEIVNVPGTGSWLPLSVENQIGPCGEPNRCAPHLEWNPDLHCSRCRDEKCVHSHSHF
770      780      790      800      810      820

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|301  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEEPLLEALGRVKRAEKKWRD
830      840      850      860      870      880

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|301  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHIREAYLPELS
890      900      910      920      930      940

960      970      980      990      1000     1010
Cry1Ac  VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVVDVEEQNNQRSVL
gi|301  VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVVDVEEQNNHRSVL
950      960      970      980      990      1000

1020     1030     1040     1050     1060     1070
Cry1Ac  VVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEII
gi|301  VVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEVDNNTDELKFSNCEKEQVY
1010     1020     1030     1040     1050     1060

1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|301  PGNTVACNDY--NKNHGANACSSRNRGYDESYESNSSIPADYAPVYEEEAAYTDGQRGNPC
1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac  EFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|301  EFNRGH---TPLPAGYVTALEYFPETDTVWVEIGETEGTFIVDSVELLLMEE
1120     1130     1140     1150     1160

>>gi|10059079|gb|AAE35985.1| Sequence 4 from patent US 5 (1168 aa)
initn: 4729 initl: 2942 opt: 4970 Z-score: 5851.4 bits: 1094.7 E(): 0
Smith-Waterman score: 5094; 66.190% identity (84.020% similar) in 1189 aa overlap
(5-1182:1-1168)

10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLEFVPGAGF

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gi|100      MKNNIQ-NQCVPNCLSNPEVEILSEER-STGRPLPLDISLSLTRFLLSEFVPGVGV
              10      20      30      40      50
              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 AFGLFDLIWGFITPSEWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEVVYLEALRE
              60      70      80      90      100     110
              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 WEENPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
              120     130     140     150     160     170
              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 SFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLLENLRCINTRQWSRFNQFRREL
              180     190     200     210     220     230
              250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPLEN--FDGSRFGSAQGIIEGSIKSP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 TLTVLDIVALFPNYDARAYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPP
              240     250     260     270     280     290
              300     310     320     330     340     350
Cry1Ac HLMIDLNSITIYTDHRGEYYSWGHQIMASPVGSGPEFTFPPLYGTMGNAAPQQRIVAQL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 HLMDFMNSLFTAETVRSQTVWGGH--LVSSRNTAGNPIFPYGVF--NPGGAIWIADDE
              300     310     320     330     340     350
              360     370     380     390     400     410
Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPASVYRKSQVDSLDEI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 PRPFYRTLSDPVFVRG---GFGDPHYVLGLRGVGFQQ-TGTN-HTRTFPNSGTIDSLDEI
              360     370     380     390     400
              420     430     440     450     460     470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 PPQDMSGAPWNDYSVHLNHVTFVRWPGELIAGSDSWRAPMFSWTHRSADRNTIINPNIITQ
              410     420     430     440     450     460
              480     490     500     510     520     530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 IPAVKAHLNHSGSTVVRGPGFTGGDLLRRTNTGTADIRVNTIGPL----SQRYRVRIR
              470     480     490     500     510     520
              540     550     560     570     580     590
Cry1Ac YASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 YASTFDLQFFTRINGTSVNQGNFQRTMNRGDNLESGNFRTAGFSTPFSFSNAQSTFTLGT
              530     540     550     560     570     580
              600     610     620     630     640     650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEBYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV

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      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 QAFSNQE-VYIDRIEVPVAEVTFAESDLERAQKAVNALFTSTSQLGLKTNVTDYHIDQV
              590     600     610     620     630     640
              660     670     680     690     700     710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 SNLVACLSDEFCLDEKRELSEKVKHAKRLSDKRNLLQDPNFRGINRQPDHGRGSDTITI
              650     660     670     680     690     700
              720     730     740     750     760     770
Cry1Ac QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
              710     720     730     740     750     760
              780     790     800     810     820     830
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 NSKHETVNVPGTGSWPLSVENQIGKCGEPNRCAPHLEWNPDLHDCSCRDEKCVHSHHF
              770     780     790     800     810     820
              840     850     860     870     880     890
Cry1Ac SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEPLVGEALARVKRAEKKWRD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEPLVGEALGRVKRAEKKWRD
              830     840     850     860     870     880
              900     910     920     930     940     950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHIREAYLPELS
              890     900     910     920     930     940
              960     970     980     990     1000    1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 VIPGVNAAFEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
              950     960     970     980     990     1000
              1020    1030    1040    1050    1060    1070
Cry1Ac VVPEWEAEVSQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 VVPEWEAEVSQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEVDNNTDELKFSNCEQVY
              1010    1020    1030    1040    1050    1060
              1080    1090    1100    1110    1120
Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 PGNTVACNDY--NKNHGANACSSRNRGYDESYESNSSIPADYAPVYEEEAAYTDGQRNCP
              1070    1080    1090    1100    1110
              1130    1140    1150    1160    1170    1180
Cry1Ac EFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|100 EFNRGH---TPLPAGYVTALEYFPETDTVWVEIGETEGTFIVDSVELLLMEE
              1120    1130    1140    1150    1160
>>gi|2982744|dbj|BAA25298.1| CryINA67-1 [Bacillus thuringiensis] (1168 aa)

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initn: 4721 init1: 2941 opt: 4966 Z-score: 5846.6 bits: 1093.8 E(): 0
Smith-Waterman score: 5090; 66.106% identity (83.852% similar) in 1189 aa overlap
(5-1182:1-1168)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|298 MKNNIQ-NQCVPYNCLSNPEVEILSEER-STGRPLDISLSLTRFLLSEFVPGVGV
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|298 AFGLFDLWGFITPSEWSLFLQIEQLIEQRLETLEARNRAITTLRGLADSYEVYLEALRE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|298 WEENPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|298 SFGQGWGLDIATVNNHYNRLINLIHRYTEHCLDTYNQGLENLGRNTNRQWSRFNQFRREL
Cry1Ac TLTVDLIVSLFPNYDSRTYPIRTVSQLTREIYTNPVEN--FDGSFRGSAQIEGSI RSP
gi|298 TLTVDLIVALFPNYDARAYPIQTSSQLTREIYTSVIEDSPSANIPNGFNRAEFGVRRP
Cry1Ac HLMIDLNSITITYTDAHRGEYVWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQL
gi|298 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNPINFPIYGIF-NPGGAIWADED
Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI
gi|298 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQ-QGTN-HTRTFRNSGTIDSLDEI
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|298 PPQDNSGAPWNDYSHVLNHVTFVRWPGEIAGSDSWRAPMFSWTHRSADR TNINPNIITQ
Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNGRYIEVPIHPFSTSTRYRVRVR
gi|298 IPAVKAHNLHSGSTVVRGPGFTGGDLLRRTNTGT FADIRVNTGPL----SQRYRVRIR
Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNGRYIEVPIHPFSTSTRYRVRVR
gi|298 IPAVKAHNLHSGSTVVRGPGFTGGDLLRRTNTGT FADIRVNTGPL----SQRYRVRIR

Cry1Ac YASVTPIHLNVNWGNSSIFSNTV PATATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGV
gi|298 YASTTDLQFFTRINGTSVNOGNFQRTMNRGGNLESGNFRTAGFSTPFSSNAQSTFTLGT
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|298 QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTSQLGLKTNVTGYHIDQV
Cry1Ac SNLVTYLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|298 SNLVACLSDDEFCLDEKRELSKVKHAKRLSDKRNLLQDPNFRGINRQPDHWRGSTDITI
Cry1Ac QGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|298 QGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLI RY
Cry1Ac NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF
gi|298 NSKHEVNVPGTGLWPLSVENQIGPCGEPNRCAPHLEWNPDLHCSCRDEKCVHSHSHF
Cry1Ac SLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|298 SLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEEPLLGEALARVKRAEKKWRD
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAYPELS
gi|298 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNAMIHAADKRVHIREAYPELS
Cry1Ac VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVL
gi|298 VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVL
Cry1Ac VVPEWAEVSVQVRRVCPGRGYILRV TAYKEGEGCVTIHEIENNTDELKFSNCEVEEIIY
gi|298 VVPEWAEVSVQVRRVCPGRGYILRV TAYKEGEGCVTIHEVDNNTDELKFSNCEQVY
Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYN EAAA--PSVPADYASVYEEKSYTDGRENPC
gi|298 PGNTVACNDY--NKNHGANACSSRNRG YDESYESNSSIPADYAPVYEEEA YTDGQRGNPC



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1080      1090      1100      1110      1120
Cry1Ac  YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|665  YPGNTVACNDY--NKNHGANACSSRRNGGYDESYESSNIPADYAPVYEEEAAYTDQGRGNP
      1070      1080      1090      1100      1110

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1130      1140      1150      1160      1170      1180
Cry1Ac  CEFNRRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|665  CEFNRGH---TLPAGYVTALEYFPETDTVWVEIGETEGTFIVDSVELLLMEE
      1120      1130      1140      1150      1160

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>>gi|1247709|emb|CAA01879.1| PS81A2 endotoxin [Bacillus (1174 aa)  
 initn: 4836 initl: 2899 opt: 4870 Z-score: 5733.4 bits: 1072.8 E(): 0  
 Smith-Waterman score: 5202; 67.393% identity (83.990% similar) in 1193 aa overlap  
 (5-1182:1-1174)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|124  MENNIE-NQCIPYNCLNPEVEILGIERSNSN-VAEIGLGLTRLLVSR-IPLGDF
      10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLLEGLSNLYQIYAESFRE
gi|124  ILGLFDVIWGAIGPSQWDFLEQIEQLINQRIEEFARNQAI SRLQGLSNLYRIYTNAFKN
      60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|124  WEVDPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

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190     200     210     220     230
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSD-RDWIRYNQFRRE
gi|124  VFGQRWGFDAATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNFRFRE
      180     190     200     210     220     230

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240     250     260     270     280     290
Cry1Ac  LTLTVDLIVLFFPNYSRTPYPIRTVSQLTREIYTNPNVLENFDFGSRGSAQGI EGS-IRSP
gi|124  LTISVLDLILSFFQYNSRLYPIPTIYQLTREYVTDVINITDYRVTPSFESIENSAITSP
      240     250     260     270     280     290

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300     310     320     330     340     350
Cry1Ac  HLMIDLNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|124  HLMDFLNIIIDTDLIRGVHYWAGHRVTSHTG-SSQVLISSPYGITANAEPSTIAPST
      300     310     320     330     340     350

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360     370     380     390     400     410
Cry1Ac  GQGV---YRTLSTLYRRPFNIGINNQQLSVLDGTFEYAGTSSNLPASAVYRKSGTVDSLD
gi|124  FPGLNLFYRTLSDPFRRSDNI-MPTLGINVVQGVGFI---QPNNGEVLYRRRRTGTVDSLD
      360     370     380     390     400

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420      430      440      450      460      470
Cry1Ac  EIPPQNNVPPRQGFHSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSI
gi|124  ELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWVTHSATDRNIYYPDVI
      410      420      430      440      450      460

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480      490      500      510      520      530
Cry1Ac  TQIPAVKGNFLPFG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRV
gi|124  TQIPLVKSFLTSGTSSVVRGPGFTGGDIIRTNVNGN-----VLSMSLNFSTSLQRYRV
      470      480      490      500      510

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540      550      560      570      580      590
Cry1Ac  RVRYSVTPIHLLNVWGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFSTSLGNIVGV
gi|124  RVRYAASQTMVMRVNVGGSTTFDQGFPSSTMSANGSLTSQSFRAEFPVGIISTSGSQTAGI
      520      530      540      550      560      570

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600      610      620      630      640      650
Cry1Ac  R--NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
gi|124  SISNPNPGRQTFHLDRIFIPVDATFEAEYDLERAQKAVNSLFTSSNQIELKTDVTDYHID
      580      590      600      610      620      630

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660      670      680      690      700      710
Cry1Ac  QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|124  QVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPRGWRGSTDII
      640      650      660      670      680      690

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720      730      740      750      760      770
Cry1Ac  TIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
gi|124  TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYNRYQLRGYIEDSQDLEIYLI
      700      710      720      730      740      750

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780      790      800      810      820      830
Cry1Ac  RYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSH
gi|124  RYNAKHETVNVPGTGLWPLSVESPIGRCEPNRCVPHLEWNPDLDCSRDGEKCAHSH
      760      770      780      790      800      810

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840      850      860      870      880      890
Cry1Ac  HFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFIEEKPLVGEALARKRAEKKW
gi|124  HFSLDIDLGCTDLQEDLGVWVIFKIKTQEGYARLGNLEFIEEKPLIGEALSRVKRAEKKW
      820      830      840      850      860      870

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900      910      920      930      940      950
Cry1Ac  RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPE
gi|124  RDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIIHAADRLVHQIHEAYLPE
      880      890      900      910      920      930

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960      970      980      990     1000     1010
Cry1Ac  LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRS
gi|124  LPIPIGINVVIFFEELENRISTALSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRS

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940      950      960      970      980      990
Cry1Ac  1020  1030  1040  1050  1060  1070
VLVVPWEAEVQSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEE
gi|124  VLVVPWEAEVQSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEE
1000    1010    1020    1030    1040    1050

1080  1090  1100  1110  1120
Cry1Ac  IYPNNTVTCNDYTVNQEEYGGAYT--SRNRGYNEA---PSPVADYASVYEEKSYTDGRR
gi|124  VYPTDTGTCNDYTAHQGTAGSTDSNSRNIRYEDAYEMNTTASVNYKPTYEERYTDVQG
1060    1070    1080    1090    1100    1110

1130  1140  1150  1160  1170  1180
Cry1Ac  ENPCEFNRYRDTYPLVGVYTKLEYFPETDKVWIEIGETEGTIVDSVELLLMEE
gi|124  DNHCYDRGVNRYRVPVAGYVTKLEYFPETDKVWIEIGETEGKFIVDNVELLLMEE
1120    1130    1140    1150    1160    1170

>>gi|911030|gb|AAA70484.1| Sequence 3 from Patent US 540 (1174 aa)
initn: 4840 initl: 2903 opt: 4868 Z-score: 5731.0 bits: 1072.4 E(): 0
Smith-Waterman score: 5211; 67.477% identity (84.074% similar) in 1193 aa overlap
(5-1182:1-1174)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|911  MENNIE-NQCIPYNCLNPEVEILGIERSNSN-VAAEIGLGLSRLVSR-IPLGDF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIWIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLLEGLSNLYQIYAESFRE
gi|911  ILGLFDVIWGAIGPSQWDFLEQIELLIGQRIEEFARNQAI SRLQGLSNLYRIYTNAFKN
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|911  WEVDPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS-RDWIRYQFRRE
gi|911  VFGQRWGFDAATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNRFRE
180     190     200     210     220     230

240     250     260     270     280     290
Cry1Ac  LTLTVDLIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDPGSRGSAQGIIEGS-IRSP
gi|911  LTISVLDIISFFQNYDSRLYPIPTIYQLTREYVYTDYVINITDYRVTSPFESIENSAIRSP
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  HLMIDLNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQL
gi|911  HLMDFLNIIIDTDLIRGVVHYWAGHRVTSHTG-SSQVISSPOYGITANAEPRTIAPST

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300      310      320      330      340      350
Cry1Ac  360  370  380  390  400  410
GQGV--YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQGVDSLD
gi|911  FPGLNLFYRTLSDPFFRRSDNI-MPTLGINVQGVGFI--QPNNGEVLYRRRGTVDSDL
360      370      380      390      400

420     430     440     450     460     470
Cry1Ac  EIPPQNNVPPRQGFVSHRSLVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
gi|911  ELPIDGEN--SLVGYSHRSLVTLTRSLYNTNITSL---PTFVWTHHSATDRNIYDPVVI
410     420     430     440     450     460

480     490     500     510     520     530
Cry1Ac  TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTST-RYRV
gi|911  TQIPLVKFSLSLTSVVRGPGFTGGDIIRTNVNGN-----VLSMSLNFSTSLQRYRV
470     480     490     500     510

540     550     560     570     580     590
Cry1Ac  RVRVYASVTPIHLNVNWNSSIFSNVTPATATSLDNLQSSDFGFYFESANAFTSSLGNIVGV
gi|911  RVRVYASQTMVMVRVNVGGSTTFDQGFPSMANGSLTSQSFRAEFPVGISSGSGTAGI
520     530     540     550     560     570

600     610     620     630     640     650
Cry1Ac  R--NFSGTAGVVIDRFEFIPVTATLEAEYNLEAQAVALNSTSTNQLGLKTNVTDYHID
gi|911  SISNPNRQTFHLDRIEIPVDATFEAEYDLERAQKAVNSLFTSSNQLKTDVTDYHID
580     590     600     610     620     630

660     670     680     690     700     710
Cry1Ac  QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|911  QVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPERGWRGSDTI
640     650     660     670     680     690

720     730     740     750     760     770
Cry1Ac  TIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
gi|911  TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYNRYQLRGYIEDSQDLEIYLI
700     710     720     730     740     750

780     790     800     810     820     830
Cry1Ac  RYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHHS
gi|911  RYNAKHETVNVPGTGLWPLSVESPIGRCEPNCVPHLEWNPDLDCSRDGEKCAHHS
760     770     780     790     800     810

840     850     860     870     880     890
Cry1Ac  HFSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|911  HFSLDIDVGTDLQEDLGVWVIFKIKTQEGYARLGNLEFIEEKPLIGEALSrvkRAEKKW
820     830     840     850     860     870

900     910     920     930     940     950
Cry1Ac  RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPE

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gi|911 RDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADRLVHQIHEAYLPE
880 890 900 910 920 930

Cry1Ac LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRS
960 970 980 990 1000 1010

gi|911 LPFIPGINVWIFELENRISTALSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNHRS
940 950 960 970 980 990

Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEE
1020 1030 1040 1050 1060 1070

gi|911 VLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFKNCEEEE
1000 1010 1020 1030 1040 1050

Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYT--SRNRYNEA----PSVPADYASVYEKSYTDGRR
1080 1090 1100 1110 1120

gi|911 VYPTDTGTCNDYTAHQGTAGTSDSCNSRNIRYEDAYEMNTTASVNYKPTYEERYTVDVQG
1060 1070 1080 1090 1100 1110

Cry1Ac ENPCEFNRGRYDPTPLVGVYTKLEYPFETDKVWIEIGETEGTFIVDSVELLMEE
1130 1140 1150 1160 1170 1180

gi|911 DNHCYEYDRGVNYPVPAGYVTKLEYPFETDKVWIEIGETEGTFIVDNVELLMEE
1120 1130 1140 1150 1160 1170

>>gi|3010035|gb|AAC10640.1|I73894 Sequence 2 from patent (1174 aa)
initn: 4840 initl: 2903 opt: 4868 Z-score: 5731.0 bits: 1072.4 E(): 0
Smith-Waterman score: 5211; 67.477% identity (84.074% similar) in 1193 aa overlap
(5-1182:1-1174)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF
10 20 30 40 50 60

gi|301 MENNIE-NQCIPYNCLNPEVEIILGIERSNSN-VAAEIGLGLSRLLSR- IPLGDF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|301 ILGLFDVIWGAIGPSQWDIFLEQIELLIGQRIEEFARNQAI SRLQGLSNLYRIYTNAPKN
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
130 140 150 160 170 180

gi|301 WEVDPPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPPLLSVYQAAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS-RDWIRYNQFRRE
190 200 210 220 230

gi|301 VFGQRWGFDAATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNFRRE
180 190 200 210 220 230

Cry1Ac LTLTVDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDPGSRGSAQGLEGS- IRSP
240 250 260 270 280 290

Cry1Ac LTLTVDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDPGSRGSAQGLEGS- IRSP
240 250 260 270 280 290

gi|301 LTVSVDLIISFFQNYDSRLYPIPTIYQLTREVYTDVFINITDYRVTPSFESIENSAIRSP
240 250 260 270 280 290

Cry1Ac HLMDILNSITIIYTDHARGEYIWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
300 310 320 330 340 350

gi|301 HLMDFLNNIIIDTDLIRGVHYWAGHRVTSHTFTG-SSQVISSPQYGITANAEPSTIAPST
300 310 320 330 340 350

Cry1Ac GQGV---YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLD
360 370 380 390 400 410

gi|301 FPGNLFLYRTLSDDPFRSNDNI-MPTLGINVVGQVGFV---QPNNGEVLYRRRGTVDSLD
360 370 380 390 400

Cry1Ac EIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSI
420 430 440 450 460 470

gi|301 ELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWVTHSATDRNIIYPDVI
410 420 430 440 450 460

Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTST-RYRV
480 490 500 510 520 530

gi|301 TQIPLVKFSPLTSGTSSVVRGPGFTGGDIIRTNVNGN-----VLSMSLNFSTSLQRYRV
470 480 490 500 510

Cry1Ac RVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGV
540 550 560 570 580 590

gi|301 RVRYAASQTMVMRNVVGGSTTFDQGFPSMTSANGSLTSQSFRFAEFPVGISSGSGQTAGI
520 530 540 550 560 570

Cry1Ac R--NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
600 610 620 630 640 650

gi|301 SISNNPGRQTFHLDRIEFIPVDATFEAEYDLERAQKAVNSLFTSSNQIELKTDVTDYHID
580 590 600 610 620 630

Cry1Ac QVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
660 670 680 690 700 710

gi|301 QVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWGSTDI
640 650 660 670 680 690

Cry1Ac TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
720 730 740 750 760 770

gi|301 TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYNRYQLRGYIEDSQDLEIYLI
700 710 720 730 740 750

Cry1Ac RYNAKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDDLDCSCRDGEKCAHSH
780 790 800 810 820 830

gi|301 RYNAKHETVNVPGTGSGLWPLSVESPIGRCGEPNRCVPHLEWNPDDLDCSCRDGEKCAHSH
760 770 780 790 800 810

Cry1Ac HFSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKW
840 850 860 870 880 890

Cry1Ac HFSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKW
840 850 860 870 880 890

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gi | 301 820 830 840 850 860 870
      900 910 920 930 940 950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPE
      880 890 900 910 920 930
gi | 301 RDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIAADRLVHQIHEAYLPE
      960 970 980 990 1000 1010
Cry1Ac LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRS
      940 950 960 970 980 990
gi | 301 LPPFIPGINVVFEELENRISTALSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRS
      1020 1030 1040 1050 1060 1070
Cry1Ac VLVVPEWEAEVVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEE
      1000 1010 1020 1030 1040 1050
gi | 301 VLVVPEWEAEVVSQTRVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFKNCEEEE
      1080 1090 1100 1110 1120
Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYT--SRNRYNEA---PSVPADYASVYEKSYTDGRR
      1060 1070 1080 1090 1100 1110
gi | 301 VYPTDTGTCNDYTAHQGTAGSTDCNSNRNIRYEDAYEMNTTASVNYKPTYEERYTDVQG
      1130 1140 1150 1160 1170 1180
Cry1Ac ENPCFENRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120 1130 1140 1150 1160 1170
gi | 301 DNHCYEYDRGVYVYRVPVAGYVTKLEYFPETDKVWIEIGETEGKFIVDNVVELLLMEE
      1120 1130 1140 1150 1160 1170

>>gi|142754|gb|AAA22346.1| cryIE(b) (1174 aa)
  initn: 4840 initl: 2903 opt: 4868 Z-score: 5731.0 bits: 1072.4 E(): 0
Smith-Waterman score: 5211; 67.477% identity (84.074% similar) in 1193 aa overlap
(5-1182:1-1174)

      10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      70 80 90 100 110 120
gi | 142 MENNIE-NQICIPYNCLNNEPEVEILGIERSNSN-VAAEIIGLGLSRLVSR-IPLGDF
      10 20 30 40 50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLLEGLSNLYQIYAESFRE
      60 70 80 90 100 110
gi | 142 ILGLFDVWGAIGPSQWDIFLEQIPELLIGQRIEEFARNQAI SRLQGLSNLYRIYTNAPFN
      130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120 130 140 150 160 170
gi | 142 WEVDPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYVQAANLHLSVLRDVS
      190 200 210 220 230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS-RDWIRYNQFRRE

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gi | 142 180 190 200 210 220 230
      240 250 260 270 280 290
Cry1Ac LTLTVLTDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGFSFRGSAQGLIEGS-IRSP
      240 250 260 270 280 290
gi | 142 LTISVLDDIISFFQNYDSRLYPIPTIYQLTREVYTDVFINITIDYRVTPSFESIENSAIRSP
      300 310 320 330 340 350
Cry1Ac HLMDDLNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQL
      300 310 320 330 340 350
gi | 142 HLMDFLNNIIIDTDLIRGVHYWAGHRVTSHTFG-SSQVISSPQYGITANAEPSTIAPST
      360 370 380 390 400 410
Cry1Ac GQGV---YRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSL
      360 370 380 390 400
gi | 142 FPGLNLFYRTLSDPPFRSDNI-MPTLGINVVQGVGFI---QPNNGEVLYRRRGTVDLSD
      420 430 440 450 460 470
Cry1Ac EIPPQNNVPRQGFVSHRSLSHVSMFRSFGFSNSVSIIRAPMFSWIHRSAEFNIIASDSI
      410 420 430 440 450 460
gi | 142 ELPIDGEN--SLVGYSHRSLSHVTLRSLYNTNITSL---PTFWTHHSATDRNIIYPDVI
      480 490 500 510 520 530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTST-RYRV
      470 480 490 500 510
gi | 142 TQIPLVKFSFLTSGTSVVRGPGFTGGDIIRTNVNGN-----VLMSLNFNSNTSLQRVYR
      540 550 560 570 580 590
Cry1Ac RVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGV
      520 530 540 550 560 570
gi | 142 RVRYAASQTMVMRVNVGGSTTFDQGFPTMSANGSLTSQSFRFAEFPVGI STSGSQTAGI
      600 610 620 630 640 650
Cry1Ac R--NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
      580 590 600 610 620 630
gi | 142 SISNPNPGRQTFHLDRIEFIPVDATFEAEYDLERAQKAVNSLFTSSNQIELKTDVTDYHID
      660 670 680 690 700 710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGSTGI
      640 650 660 670 680 690
gi | 142 QVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGSGTDI
      720 730 740 750 760 770
Cry1Ac TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLI
      700 710 720 730 740 750
gi | 142 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYNRYQLRGYIEDSQDLEIYLI
      780 790 800 810 820 830

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Cry1Ac RYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHH
gi|142 RYNAKHETVNVPGTGSWLPLSVESPIGRCEPNRCVPHLEWNPDLDCSCRDGEKCAHSHH
760 770 780 790 800 810

Cry1Ac HPSLDDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|142 HPSLDDIDVGCTDLQEDLGWVWVFKIKTQEGYARLGNLEFIEEKPLIGEALSrvkRAEKKW
820 830 840 850 860 870

Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRvHSIREAYLPE
gi|142 RDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAADRLVHQIHEAYLPE
880 890 900 910 920 930

Cry1Ac LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVVEEQNNQRS
gi|142 LFPFIPGINVVIFEELNRISTALSlyDARNVIKNGDFNNGLSCWNVKGHVDVVEEQNNHRS
940 950 960 970 980 990

Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAyKEGYGEGCVTIHEIENNTDELKFSNcVEEE
gi|142 VLVVPEWEAEVSEQTIRVCPGRGYILRVTAyKEGYGEGCVTIHEIENNTDELKFKNcEEEE
1000 1010 1020 1030 1040 1050

Cry1Ac IYPNNTVTCNDYTVNQEYGGAYT--SRNrgYNEA----PSVPADYASVYEEKSYTDGRR
gi|142 VYPTDTGTCNDYTAHQGTAGSTDCNSRNIRYEDAYEMNTTASVNYKPTYEERYTDVQG
1060 1070 1080 1090 1100 1110

Cry1Ac ENPCEFNRGYRDYTPLPVGYVTKELEYFPETDKVWIEIETEGTFIVDSVellLMEE
gi|142 DNHCEYDRGYVNYRVPAGYVTKELEYFPETDKVWIEIETEGTFIVDNVellLMEE
1120 1130 1140 1150 1160 1170

>>gi|10059078|gb|AAE35984.1| Sequence 2 from patent US 5 (1174 aa)
inith: 4840 initl: 2903 opt: 4868 Z-score: 5731.0 bits: 1072.4 E(): 0
Smith-Waterman score: 5211; 67.477% identity (84.074% similar) in 1193 aa overlap
(5-1182:1-1174)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|100 MENNIE-NQCIPYNCLNPEVEILGIERSNSN-VAEIEGLGLSRLVSR-IPLGDF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLGLSNLYQIYAESFRE
gi|100 ILGLFDVWGAIGPSQWDFLEQIEQLINQRIEEFARNQAI SRLGLSNLYRIYTNAFKN
60 70 80 90 100 110

130 140 150 160 170 180

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|100 WEVDPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS-RDWIRYNQFRRE
gi|100 VFGQRWGFDAATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNFRRE
180 190 200 210 220 230

Cry1Ac LTLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIEGS-IRSP
gi|100 LTIISVLDIISFQNYDSRLYPIPTIYQLTREVYTDVINITDYRVVTPSFESIENSAIRSP
240 250 260 270 280 290

Cry1Ac HLMDDILNSITITDAHRGEYYSWGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQL
gi|100 HLMDFLNNIIIDTLIRGVHYWAGHRVTSHTG--SSQVLISSPQYGITANAEPSTIAPST
300 310 320 330 340 350

Cry1Ac GQGV---YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDSLd
gi|100 FPLGNLFYRTLSDPPFRSDNI-MPTLGINVVQGVGFI--QPNNGEVLYRRRGTVDSLD
360 370 380 390 400 410

Cry1Ac EIPPQNNVPPRQGFSHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNIIASDSI
gi|100 ELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWTHSATDRNIYDPDVI
420 430 440 450 460 470

Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQNRGYIEVPIHFPSTST-RYRV
gi|100 TQIPLVKSFSLTSGETSVVRGPGFTGGDIIRTNVNGN-----VLSMSLNFsNTSLQRYRV
480 490 500 510 520 530

Cry1Ac RVRYASVTPPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGV
gi|100 RVRYAASQTMVMRVNvGGSTTFDQGFpSTMSANGSLTSQsFRFAEFPVGIStSGSQTAGI
540 550 560 570 580 590

Cry1Ac R--NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
gi|100 SISNPNGRQTFHLDRIEFIPVDATFEAEYDLERAQKAVNSLFTSSNQIELKTDVTDYHID
600 610 620 630 640 650

Cry1Ac QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|100 QVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPRDGRWGSTDI
660 670 680 690 700 710

640 650 660 670 680 690

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          720      730      740      750      760      770
Cry1Ac TIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGVIEDSQDLEIYISI
gi|100 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYNRYQLRGVIEDSQDLEIYILI
          700      710      720      730      740      750

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          780      790      800      810      820      830
Cry1Ac RYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSH
gi|100 RYNAKHETVNVPGTGLWPLSVESPIGRGCEPNRCVPHLEWNPDLDCSCRDGKCAHSH
          760      770      780      790      800      810

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          840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|100 HFSLDIDVGCTDLQEDLGVVWVFKIKTQEGYARLGNLEFIEEKPLIGEALSrvkRAEKKW
          820      830      840      850      860      870

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          900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
gi|100 RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIGMIHAADRLVHQIHEAYLPE
          880      890      900      910      920      930

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          960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAIIFELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRS
gi|100 LFPFIPGINVVIPEELENRISTALSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNHRS
          940      950      960      970      980      990

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          1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAKEGEGCVTIHEIENNTDELKFSNCVEE
gi|100 VLVVPEWEAEVSEQEVRVCPGRGYILRVTAKEGEGCVTIHEIENNTDELKFKNCEEE
          1000      1010      1020      1030      1040      1050

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          1080      1090      1100      1110      1120
Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYT--SRNRGYNEA---PSVPADYASVYEEKSYTDGRR
gi|100 VYPTDTGTCDYTAHQGTAGSTDCNSRNIRYEDAYEMNTTASVNYKPTYEERETDVGQ
          1060      1070      1080      1090      1100      1110

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          1130      1140      1150      1160      1170      1180
Cry1Ac ENPCEFNRGRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|100 DNHCHEYDRGYVNYRVPVAGYVTKELEYFPETDKVWIEIGETEGTFIVDNVELLMEE
          1120      1130      1140      1150      1160      1170

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>>gi|34422133|gb|AAQ68244.1| Sequence 4 from patent US 5 (1174 aa)
  initn: 4840 init1: 2903 opt: 4868 Z-score: 5731.0 bits: 1072.4 E(): 0
  Smith-Waterman score: 5211; 67.477% identity (84.074% similar) in 1193 aa overlap
  (5-1182:1-1174)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|344  MENNIE-NQCIPYNCLNNPEVEILGIERSNSN-VAEEIGLGLSRLLVSR-IPLGDF
          10      20      30      40      50

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          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFRE
gi|344 ILGLFDVIWGAIGPSQWDFLEQIELLIGQRIEEFARNQAIISRLQGLSNLYRIYTNAFKN
          60      70      80      90      100      110

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          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|344 WEVDPTNPALREEMRIQFNDMNSALTTAIPLFSVQGYEIPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

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          190      200      210      220      230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS-RDWIRYNQFRRE
gi|344 VFGQRWGFDAATINSRYNDLTRLIGEYTDYAVRWYNTGLNRLPRNEGVRGWARFNRFRRE
          180      190      200      210      220      230

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          240      250      260      270      280      290
Cry1Ac LTLTVDLIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGS-IRSP
gi|344 LTLTVDLIVSLFPNYSRTPYIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGS-IRSP
          240      250      260      270      280      290

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          300      310      320      330      340      350
Cry1Ac HLMDFLNNSITTYDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|344 HLMDFLNNSITTYDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
          300      310      320      330      340      350

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          360      370      380      390      400      410
Cry1Ac GQGV---YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLD
gi|344 GQGV---YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLD
          360      370      380      390      400

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          420      430      440      450      460      470
Cry1Ac EIPPQNNVPPRQGFVSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
gi|344 EIPPQNNVPPRQGFVSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
          410      420      430      440      450      460

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          480      490      500      510      520      530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRV
gi|344 TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRV
          470      480      490      500      510

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          540      550      560      570      580      590
Cry1Ac RVRYASVTPIHLNVNWNSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVG
gi|344 RVRYASVTPIHLNVNWNSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVG
          520      530      540      550      560      570

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          600      610      620      630      640      650
Cry1Ac R--NFGSTAGVIIDRFEFIPVTATLEAEYNLEAQAVALFTSTNQLGLKTNVTDYHID
gi|344 R--NFGSTAGVIIDRFEFIPVTATLEAEYNLEAQAVALFTSTNQLGLKTNVTDYHID
          580      590      600      610      620      630

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Cry1Ac 660 670 680 690 700 710
QVSNLVVTLSDVEFCLDEKRELSKVKHAKRLSDERNLQDSNFKDINRQPERGWGSGTGI
gi|344 QVSNLVVTLSDVEFCLDEKRELSKVKHAKRLSDERNLQDPNFRGINRQPRGWRGSDTI
640 650 660 670 680 690

Cry1Ac 720 730 740 750 760 770
TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYYSI
gi|344 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKAYNRYQLRGYIEDSQDLEIYLI
700 710 720 730 740 750

Cry1Ac 780 790 800 810 820 830
RYNAKHETVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHS
gi|344 RYNAKHETVNVVPGTGLWPLSVESPIGRGEPNRCVPHLEWNPDLDCSCRDGKCAHSHS
760 770 780 790 800 810

Cry1Ac 840 850 860 870 880 890
HFSLDIDVGCTDLNEDLGWVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|344 HFSLDIDVGCTDLQEDLGWVWVFKIKTQEGYARLGNLEFIEEKPLIGEALSRVKRAEKKW
820 830 840 850 860 870

Cry1Ac 900 910 920 930 940 950
RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPE
gi|344 RDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIGMIAHADRLVHQIHEAYLPE
880 890 900 910 920 930

Cry1Ac 960 970 980 990 1000 1010
LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRS
gi|344 LRFIPGINVWIFELENRISTALSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRS
940 950 960 970 980 990

Cry1Ac 1020 1030 1040 1050 1060 1070
VLVPEWEAEVVSQEVVPCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEE
gi|344 VLVPEWEAEVVSQEVVPCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEE
1000 1010 1020 1030 1040 1050

Cry1Ac 1080 1090 1100 1110 1120
IYPNNTVTCNDYTVNQEYGGAYT--SRNRYNEA---PSVPADYASVYEKSYTDGRR
gi|344 VYPTDTGTCNDYTAHQGTAGSTDSNRSNIRYEDAYEMNTTASVNYKPTYEERYTQVQ
1060 1070 1080 1090 1100 1110

Cry1Ac 1130 1140 1150 1160 1170 1180
ENPCEFNRGYRDYTPPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|344 DNHCYDRGVNRYRVPVAGYVTKELEYFPETDKVWIEIGETEGKFIVDNVELELLMEE
1120 1130 1140 1150 1160 1170

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>>gi|82468528|gb|ABB76664.1| Cry1A-type pesticidal cryst (850 aa)
  initn: 4768  initl: 2410  opt: 4786  Z-score: 5636.4  bits: 1054.4  E(): 0
Smith-Waterman score: 5030; 86.552% identity (93.103% similar) in 870 aa overlap
(5-874:1-849)

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Cry1Ac 10 20 30 40 50 60
CMQAMNPNNEPINEPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|824 MEIVNNQNCQVFPYNCLNPEIEILEGGRIISVGNTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFPGSOWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|824 VLGLVDIIWGFPGSOWDAFLVQIEQLINQRIEAEAVRNTAIQIELEGMARVYRTYATAFAE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|824 WEKAPDDPELREALRTQFTATETYSGRISVLKIQTTFEVQLLSVFAQAANLHLSLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRREL
gi|824 VFGQRWGFSTTTVNNYYNDLTEGISTYTDYAVRWYNTGLERWVGPDSRDWIRYQFRREL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|824 TLTVLDIVSLFPNYSRRYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|824 MDILNSITTYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|824 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
gi|824 NNVVPPRQGFSHRLSHVSMFRSG--SSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530 540
VKNFNLVNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVYASV
gi|824 VKNFNLVNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVYASV
480 490 500 510 520 530

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|824 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

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540      550      560      570      580      590
Cry1Ac  GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
610      620      630      640      650      660
gi|824  GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTCL
600      610      620      630      640      650

670      680      690      700      710      720
Cry1Ac  SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
670      680      690      700      710      720
gi|824  SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF
660      670      680      690      700      710

730      740      750      760      770      780
Cry1Ac  KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV
730      740      750      760      770      780
gi|824  KENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETL
720      730      740      750      760      770

790      800      810      820      830      840
Cry1Ac  NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHHSHHSLDIDVDF
790      800      810      820      830      840
gi|824  NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHHSHHSLDIDVDF
780      790      800      810      820      830

850      860      870      880      890      900
Cry1Ac  CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDKREKLEW
850      860      870      880      890      900
gi|824  CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVVKRAEKKWRDKREKLEW
820      830      840      850      860      870

910      920      930      940      950      960
Cry1Ac  ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNA
910      920      930      940      950      960

>>gi|46409857|gb|AAS93796.1| cry1A type crystal protein (793 aa)
  inith: 4665 inilt: 2272 opt: 4762 Z-score: 5608.5 bits: 1049.2 E(): 0
Smith-Waterman score: 4762; 90.314% identity (95.597% similar) in 795 aa overlap
(13-805:2-793)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50      60
gi|464  MQCVPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50      60

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
70      80      90      100     110     120
gi|464  VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
50      60      70      80      90      100

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130     140     150     160     170     180
gi|464  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
110     120     130     140     150     160

190     200     210     220     230     240

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Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFREL
170     180     190     200     210     220
gi|464  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFREL
170     180     190     200     210     220

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHPL
250     260     270     280     290     300
gi|464  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHPL
230     240     250     260     270     280

310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310     320     330     340     350     360
gi|464  MDILNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
290     300     310     320     330     340

370     380     390     400     410
Cry1Ac  GVYRTLSSITLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPFAVYRKSQGVSDSLDEIP
370     380     390     400     410
gi|464  GVYRTLSSITLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPFAVYRKSQGVSDSLDEIP
350     360     370     380     390     400

420     430     440     450     460     470
Cry1Ac  PQNNVPPRQGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
420     430     440     450     460     470
gi|464  PQNNVPPRQGFVSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
410     420     430     440     450     460

480     490     500     510     520     530
Cry1Ac  PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYA
480     490     500     510     520     530
gi|464  PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYA
470     480     490     500     510     520

540     550     560     570     580     590
Cry1Ac  SVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGNIVGVRNFGS
540     550     560     570     580     590
gi|464  SVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGNIVGVRNFGS
530     540     550     560     570     580

600     610     620     630     640     650
Cry1Ac  TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
600     610     620     630     640     650
gi|464  TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
590     600     610     620     630     640

660     670     680     690     700     710
Cry1Ac  YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD
660     670     680     690     700     710
gi|464  YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD
650     660     670     680     690     700

720     730     740     750     760     770
Cry1Ac  VFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
720     730     740     750     760     770
gi|464  VFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
710     720     730     740     750     760

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780 790 800 810 820 830  
 Cry1Ac TVNVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDID  
 :.....  
 gi|464 TLNVPGTGSLWPLAVKSPIGRCGEPNR  
 770 780 790

>>gi|5052774|gb|AAD38701.1|AF148644\_1 insecticidal prote (723 aa)  
 initn: 2933 initl: 2906 opt: 4715 Z-score: 5553.7 bits: 1038.9 E(): 0  
 Smith-Waterman score: 4715; 98.619% identity (99.448% similar) in 724 aa overlap  
 (5-728:1-723)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 :.....  
 gi|505 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
 :.....  
 gi|505 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 :.....  
 gi|505 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL  
 :.....  
 gi|505 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRDWIRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYSRRTYPIRTVSQTLREIYTNPNVLENFDGSGFRGSAQGIERSIRSPHL  
 :.....  
 gi|505 TLTVLDIVSLFPNYSRRTYPIRTVSQTLREIYTNPNVLENFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 :.....  
 gi|505 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLSAVYRKSQTVDLSDEIPPQ  
 :.....  
 gi|505 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLSAVYRKSQTVDLSDEIPPQ  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 :.....  
 gi|505 NNNVPPRQGFSHRLSHVSMFRSG-SSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 420 430 440 450 460 470

490 500 510 520 530 540  
 Cry1Ac VKGNFLFNQSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 :.....  
 gi|505 VKGNFLFNQSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

550 560 570 580 590 600  
 Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 :.....  
 gi|505 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 540 550 560 570 580 590

610 620 630 640 650 660  
 Cry1Ac GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 :.....  
 gi|505 GVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 600 610 620 630 640 650

670 680 690 700 710 720  
 Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF  
 :.....  
 gi|505 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVDF  
 660 670 680 690 700 710

730 740 750 760 770 780  
 Cry1Ac KENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV  
 :.....  
 gi|505 KENYVTLSTL  
 720

>>gi|546641|gb|AAB30710.1| insecticidal protein Cry I A (723 aa)  
 initn: 2921 initl: 2894 opt: 4677 Z-score: 5508.8 bits: 1030.6 E(): 0  
 Smith-Waterman score: 4677; 97.928% identity (98.757% similar) in 724 aa overlap  
 (5-728:1-723)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 :.....  
 gi|546 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
 :.....  
 gi|546 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 :.....  
 gi|546 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL  
 :.....  
 gi|546 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRDWIRYNQFRREL  
 180 190 200 210 220 230

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                250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL
gi|546 TLTVLDIVALFPNYSRRYPIRTVSQLPREIYTNPVLENFDGSRGSAQGIERSIRSPHL
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|546 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac GvyrtlsstlyrrpfniginnqqlsvldgTEfayGTSSNlPSAVYRkSGTVDslDEIppQ
gi|546 GvyrtlsstlyrrpfniginnqqlsvldgTEfayGTSSNlPSAVYRkSGTVDslDEIppQ
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac NNNVpPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIASDSITQIPA
gi|546 NNNVpPRQGFShRLSHVSMFRSG-SSSSVSIIRAPMfSWIHRSAEFNNIIASDSITQIPA
                420      430      440      450      460      470

                490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHfPSTSTRYRVRVRYASV
gi|546 VKGNFLFNGSVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHfPSTSTRYRVRVRYASV
                480      490      500      510      520      530

                550      560      570      580      590      600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANaFTSSlGNIVGVRNfSGTA
gi|546 TPIHLNVNWGNSSIFSNTPATATSCDNLQSSDFGYFESANaFTSSlGNIVGVRNfSGTA
                540      550      560      570      580      590

                610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYnLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|546 GVIIDRFEFIPVTATLEAEYnLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
                600      610      620      630      640      650

                670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
gi|546 SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVF
                660      670      680      690      700      710

                730      740      750      760      770      780
Cry1Ac KENyVtLSGTFDEcYPTyLYQIDESklKafTRyQLRgyIEDSODLEIYSIRYNAKHETV
gi|546 KENyVtLS
                720

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>>gi|112088055|gb|ABI06962.1| Sequence 40 from patent US (1167 aa)  
 initn: 5078 initl: 3808 opt: 4592 Z-score: 5405.5 bits: 1012.2 E(): 0  
 Smith-Waterman score: 5346; 69.412% identity (84.034% similar) in 1190 aa overlap  
 (5-1182:1-1167)

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                10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLESEFVPGAGF
gi|112 MERN-NQDQCIPYnCLNnPEIEILDVENFNLELVS-QVSVGLTRFLLESAPVPGAGF
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIpGpSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
gi|112 ALGLFDIIWALGVDQWLSFLAQIEQLINERITTVERNRAIQTLGSLSSSYEVYIEALRE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTtAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WENPNPNPASQERVRTRFRRTDDALITAIPLNLAIPDFEATLSVYVQAANLHLSLRDAV
                120      130      140      150      160      170

                190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAvRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112 YFGERWGLTQVNIEdLYTRLTRNIHIYSDHcARWYNQGLNnIGATNTR---YLEFQREL
                180      190      200      210      220      230

                250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHL
gi|112 TSLVLDIVALFPNYDIRTYSIPTQSQLTREIYTD-IAAPNAS--NLIVGTQGLVRAPHL
                240      250      260      270      280

                310      320      330      340      350
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTF---PLYGTMGNAAPQQRIV--
gi|112 MDFLVRLNIYTLGARNIRHWAGHEVISRRTG--GVDLNTIQSPLYGTAATTESPRLLIIPF
                290      300      310      320      330      340

                360      370      380      390      400      410
Cry1Ac ---AQLGQGVYRTLSSTLYRRPfniginnqqlsvldgTEfayGTSSNlPSAVYRkSGTVD
gi|112 NEDSYLGGFIYRTLSSPIYVPPS--GISSQRTSLVEGVGFQTPNNSILQ---YRQRGLTD
                350      360      370      380      390      400

                420      430      440      450      460      470
Cry1Ac SLDEIPPQNNVpPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIAS
gi|112 SLEQVPLQEEGRPGGFgASHRLCHATFAQSPiGTNY--IRAPLFSWTHLSATLTNEVRV
                410      420      430      440      450

                480      490      500      510      520      530
Cry1Ac DSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHfPSTSTRY
gi|112 SRITQLPMVKAHTLHAGATVVRGPGFTGGDILRRITSGS---FGDMRIT-NFSSSSSRY
                460      470      480      490      500      510

                540      550      560      570      580
Cry1Ac RVRVRyASVTPiHLNVNWGNSSIFSNTPATATSLDNLQSSDF--GYFESANaFTSSlGN
gi|112 RVRIRYASTTDLQFFLNVGGTPVNVADFPKTI DRGENLEyGSRfTAGTTPPFVfVSSSTNN
                520      530      540      550      560      570

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460      470      480      490      500      510
Cry1Ac 540      550      560      570      580
RVRVRYASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANAFSTSSLGN
gi|135 RVRIRYASTTDLQFFLNVGSTPVPVADFPKTIIDRGENLEYGSRFTAGFTTTPFSVSSSTNN
520      530      540      550      560      570

590      600      610      620      630      640
Cry1Ac I-VGVNRFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDY
gi|135 FTLGVQSVSSGNEIFVDRIEFVPADATFEAEYDLERAQEAVALFTSTNQRLKTDVTDY
580      590      600      610      620      630

650      660      670      680      690      700
Cry1Ac HIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGS
gi|135 HIDQVSNLVDCLSDDEFCLDEKRELSKIKHAKRLSDERNLLQDSNFRGINRQPDGRWGRS
640      650      660      670      680      690

710      720      730      740      750      760
Cry1Ac TGITIQQGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
gi|135 TDITIQGNDVFKENYVTLPGTDFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
700      710      720      730      740      750

770      780      790      800      810      820
Cry1Ac YSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
gi|135 YLIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
760      770      780      790      800      810

830      840      850      860      870      880
Cry1Ac HSHHFLSDIDVGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
gi|135 HSHHFLSDIDVGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
820      830      840      850      860      870

890      900      910      920      930      940
Cry1Ac KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAY
gi|135 KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSIREAY
880      890      900      910      920      930

950      960      970      980      990      1000
Cry1Ac LPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVKNKGNDFNGLSCWNVKGVHDVVEEQNN
gi|135 LPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVKNKGNDFNGLSCWNVKGVHDVVEEQNN
940      950      960      970      980      990

1010     1020     1030     1040     1050     1060
Cry1Ac QRSVLVVPWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCV
gi|135 QRSVLVVPWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCV
1000     1010     1020     1030     1040     1050

1070     1080     1090     1100     1110     1120
Cry1Ac EEEIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNP

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gi|135 EEEIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRNP
1060     1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac CEFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|135 CEFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120     1130     1140     1150     1160

>>gi|33765730|gb|AAQ52381.1| Sequence 40 from patent US (1167 aa)
initn: 5078 init1: 3808 opt: 4592 Z-score: 5405.5 bits: 1012.2 E(): 0
Smith-Waterman score: 5346; 69.412% identity (84.034% similar) in 1190 aa overlap
(5-1182:1-1167)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFPVPGAGF
gi|337 MERN-NQDQCIPYNCLNPEIEILDVENFNLELVS-QVSVGLTRFLESVAVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEFARNQAIISREGLSNLYQIYAESFRE
gi|337 ALGLFDIIWALGVDQWLSFLAQIEQLINERITTVERNRAIQITLSGLSSSEYEVYIALRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS
gi|337 WENPNPNPASQERVRTRFRRTDDALITAIPLNLAIPDFEATLTSVYVQAAANLHLSLRDAV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFRREL
gi|337 YFGERWGLTQVNIEDLYTRLTRNIHIYSDHRCARWYNQGLNNGATNTR----YLEFQREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL
gi|337 TLSVLDIVALFPNYDIRTYSIPTQSLTREIYTD-IAAPNAS--NLIVGTQGLVRAPHL
240     250     260     270     280

310     320     330     340     350
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASVPGFSGPEFTF---PLYGTMGNAAPQQRIV--
gi|337 MDFLVRNLNITGLARNIRHWAGHEVISRRTG--GVDLNTIQSPLYGTAATTESPLRIIPF
290     300     310     320     330     340

360     370     380     390     400     410
Cry1Ac ---AQLGQGVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVD
gi|337 NEDSYLGGFIYRTLSSPIYVPPS--GISSQRTSLVEGVGFQTPNNSILQ---YRQRGTLD
350     360     370     380     390     400

420     430     440     450     460     470
Cry1Ac SLDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIAS

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gi|337 SLEQVPLQEGRPGGFAGSHRLCHATFAQSPIGTNY--IRAPLFSWTHLSATLTNEVRV
      410      420      430      440      450
Cry1Ac      480      490      500      510      520      530
DSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRY
gi|337 SRITQLPMVKAHTLHAGATVVRGPGFTGGDILRRITSGS---FGDMRIT-NFSSSSSRY
      460      470      480      490      500      510
Cry1Ac      540      550      560      570      580
RVRVRYASVTPPIHLNVNNGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFSSSLGN
gi|337 RVRIRYASTTDLQFFLNVGGTPVNVADFPKTTIDRGENLEYGFRTAGFTTFFSFSVSTNN
      520      530      540      550      560      570
Cry1Ac      590      600      610      620      630      640
I-VGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDY
gi|337 FTLGVQSVSSGNEIFVDRIEFVPADATFEAEYDLERAQEAVALFTSTNQRGLKTDVTDY
      580      590      600      610      620      630
Cry1Ac      650      660      670      680      690      700
HIDQVSNLVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGS
gi|337 HIDQVSNLVDCLSDEFCLDEKRELESEKIKHAKRLSDERNLLQDSNFRGINRQDRGRWGS
      640      650      660      670      680      690
Cry1Ac      710      720      730      740      750      760
TGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEI
gi|337 TDITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEI
      700      710      720      730      740      750
Cry1Ac      770      780      790      800      810      820
YSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
gi|337 YLIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
      760      770      780      790      800      810
Cry1Ac      830      840      850      860      870      880
HSHHFLSDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
gi|337 HSHHFLSDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
      820      830      840      850      860      870
Cry1Ac      890      900      910      920      930      940
KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAY
gi|337 KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAY
      880      890      900      910      920      930
Cry1Ac      950      960      970      980      990      1000
LPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNN
gi|337 LPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNN
      940      950      960      970      980      990
Cry1Ac     1010     1020     1030     1040     1050     1060
QRSVLVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCV

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gi|337 QRSVLVPEWEAEVSEVVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCV
      1000     1010     1020     1030     1040     1050
Cry1Ac     1070     1080     1090     1100     1110     1120
EEEIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNP
gi|337 EEEIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRNP
      1060     1070     1080     1090     1100     1110
Cry1Ac     1130     1140     1150     1160     1170     1180
CEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|337 CEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120     1130     1140     1150     1160
>>gi|3010046|gb|AAC10651.1|I73905 Sequence 27 from paten (1174 aa)
initn: 4031 init1: 2603 opt: 4562 Z-score: 5370.0 bits: 1005.6 E(): 0
Smith-Waterman score: 4562; 61.261% identity (74.034% similar) in 1190 aa overlap
(5-1182:1-1174)
Cry1Ac     10      20      30      40      50      60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|301     MXNNIQ-NQCVPYNCLXNPEVEILXEER-STGRLEPLDISLSLTRFLLSEFVPGVGV
      10      20      30      40      50
Cry1Ac     70      80      90      100     110     120
VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISREGLSNLYQIYAESFRE
gi|301     AFLGLFDLIWGFITPSXWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEXYXALRE
      60      70      80      90      100     110
Cry1Ac     130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|301     WEXNPNNAQLREEDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
      120     130     140     150     160     170
Cry1Ac     190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRIRYNQFRREL
gi|301     SFGQGWGLDIATVNNHYNRLINLIHRYTXHCLDTYNQGLLENLRTNTRQWXRFRNFRRXL
      180     190     200     210     220     230
Cry1Ac     250     260     270     280     290
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRFGSAQGIEGSIRSP
gi|301     TLTVLDIVALFPNYDXRXYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFVGRVP
      240     250     260     270     280     290
Cry1Ac     300     310     320     330     340     350
HLMIDLNSITTYTDAHRGEYYSWGHQIMASPVGFGPEFTFPPLYGTMGNAAPQQRIVAQL
gi|301     HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNXINFPXYGVF-NPGGAIWIADBD
      300     310     320     330     340     350
Cry1Ac     360     370     380     390     400     410
GQGVYRTLSSSTLYRPFNIGINNQLSVLDGTEFAYGTSSNLSFSAVYRKSGETVDSLDEIP

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Cry1Ac HLMIDLNSITIIYTDahrgeyywSGHQIMASpVgFSGPEFTFFLYGTMGNAAPQQRIVAQL
gi|100 HLMDFMNSLFVTAETVRSQTvWGGH--LVSSRNTAGNINFPXYGVF--NPGGAIWIADSD
300 310 320 330 340 350

360 370 380 390 400 410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEfAYGTSNLSAVYRKSGVTDSLDEIP
gi|100 PRPFYRTLSDPVfVRG-GFGXPHYVLG-LRGVXFQQ-TGTN-HTRTFRNSGTTIDSLDEIP
360 370 380 390 400

420 430 440 450 460 470
Cry1Ac PQNNNVPPRQGFShRLSHVSMFR-SGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|100 PQDnSGAPWnDYSHVLNHVTFVRWPGEIXGSDSW-RAPMFSWThRSAXXTNXIXPXXITQ
410 420 430 440 450 460

480 490 500 510 520 530
Cry1Ac IPAVKGnFLFNG-SVIsGPGFTGGDLVRLNssGNNIQNRGyIEVPiHPFST-STRYRVRV
gi|100 IPXVxAHLXSGXTVVRGPGFTGGDXLRRTXXGX-----FAXXXVNIxGLXQRyRXRI
470 480 490 500 510 520

540 550 560 570 580 590
Cry1Ac RYASVTPiHLNVNWGNSSIFsNTVPATATSLDNLQSSDFGyFESANaFTSSLGN---IVG
gi|100 RYASTTLXlXXXXXXXXGXXXXGXFXXTMXGDxLXXXXFXAXXXTPFXXXXQsXFTXG
530 540 550 560 570 580

600 610 620 630 640 650
Cry1Ac VRNfSGTAGViiDRFEFiPVTATLEAEYnLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
gi|100 XXXfSXsXxEVYIDXXEEXFPXXTFEAEKDXERAQXAVNALFTSXXQXGXXTXVTYHIDQ
590 600 610 620 630 640

660 670 680 690 700 710
Cry1Ac VSNLVTyLSDEFCLDEKRELSekVKHAKRLSDERNLLQDSnFKDINRQPERGWGGSTGIT
gi|100 VSNLVXCLSDDEFCLDEXRELSExVHXAXRLSDxRNLQDPNFxGINRQXDXGWRGSTDIT
650 660 670 680 690 700

720 730 740 750 760 770
Cry1Ac IQGGDDVfKEnyVTLsGTFDEcYPTyLYQKIDESKLKAFTRYQLRGyIEDSDLEIYSIR
gi|100 IQXGDDVfXEnyVTLPGTFDEcYPTyLYQXIDESKLXXYTRYQLRGyIEDSDLEIYILIR
710 720 730 740 750 760

780 790 800 810 820 830
Cry1Ac YNAKHETVnVPGTgSLWPLsAQSPiGKCGEPnRCAPhLEWnPDLCsCRDgEKCAHSHH
gi|100 YNXXHEPvNVXGTgSLWPLsVXXXIXXCGEpNRCAPhLEWnPDLCsCRDgEXCXHSHH
770 780 790 800 810 820

840 850 860 870 880 890
Cry1Ac FSLDIDVgCTDLNEDLgVwVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKkWR
gi|100 FSLDIDVgCTDLNEDLXVwVIFXIXTQDGHARLGNLFLEEXPLXGEALXRVXRAEXkWR
830 840 850 860 870 880

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900 910 920 930 940 950
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMiHAADKRVHSIREAYLPEL
gi|100 DXREXLXLETNIVYXEAXESVDALFVNSQYDXLQADTNIAMiHAADKRVHRIREAYLPEL
890 900 910 920 930 940

960 970 980 990 1000 1010
Cry1Ac SVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVdVEEQNNQRsv
gi|100 SVIPGVNXXIFEEELXGRIFTAXXLYDARNVIXNGXFNNGLXCWNVXGHVDVEEQNNHRSV
950 960 970 980 990 1000

1020 1030 1040 1050 1060 1070
Cry1Ac LVVPEWAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEII
gi|100 LVVPEWAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEXNNNTDELXFSNCXXEXV
1010 1020 1030 1040 1050 1060

1080 1090 1100 1110 1120
Cry1Ac YPNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRRENp
gi|100 YPXNTVXCNDYXXNXXXXXXXXXSRNRGYDEXYXSNSSXPADYAXVYEEKSYTDGGRXNP
1070 1080 1090 1100 1110 1120

1130 1140 1150 1160 1170 1180
Cry1Ac CEFNRGYRDYTPLVGYVTKELEYPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|100 CEXNRGXXXXTPLPAGYVTKELEYPETDXVWKEIGETEGTFIVDSVELLLMEE
1130 1140 1150 1160 1170

>>gi|37524001|gb|AAQ92302.1| truncated CRYIA(b) [synthet (818 aa)
initn: 4653 initl: 3174 opt: 4503 Z-score: 5302.8 bits: 992.7 E(): 0
Smith-Waterman score: 4582; 83.726% identity (89.976% similar) in 848 aa overlap
(5-848:1-817)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|375 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|375 VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTtAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|375 WEADPTNPALREEMRIQFNDMNSALTtAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGRQWGFDAATINSRYNDLTRLIGNyTdhAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|375 VFGRQWGFDAATINSRYNDLTRLIGNyTdhAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

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      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKRSPLH
gi|375 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKRSPLH
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|375 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
gi|375 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIppQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIASDSITQIPa
gi|375 NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIqNRgyIEVPIHfPSTSTRYrVRVRYAS
gi|375 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQLSTLRVNITAPL-----SQRYRVRIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNtVpATATSLDNLQSSDFGyFESANAFtSSLGNIV---GVRNF
gi|375 TTNLQFHTSIDGRPIQGNFSATMSSGSNLQSGSFRTVGFTTFPFNFSGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYnLERAQKAVNALFTSTnQLGLKtNVtDYHIDQVSNL
gi|375 NSGNEVYIDRIEFVPAEVTfEAeyDLERAQKAVNELFTSSnQIGLKTdVtDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTyLsDEfCLDEKRElSEKvKHAKRLSDERNLLQDSNFKDINRQpERGwGGSgtGITIQGG
gi|375 VECLsDEfCLDEKRElSEKvKHAKRLSDERNLLQDPNFRGINRQLDRGWRGStDITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVfKENyVtLsGtPDECyPTyLYQKIDESKlKAYTRyQLRgyIEDsQDLeySIRyNAK
gi|375 DDVfKENyVtLLGtPDECyPTyLYQKIDESKlKAYTRyQLRgyIEDsQDLeyLIRyNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVnVpGTGSLWPLsAQSPiGKCGEPNRCAPHLewNPDLDCSCRdGECaHSHHfSLD
gi|375 HETVnVpGTGSLWPLsAPSPiGK-----AHSHHfSLD
      780      790      800

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      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVfIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
gi|375 IDVGCTDLNEDFR
      810

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>>gi|1610957|gb|AAB13936.1| Sequence 33 from patent US 5 (1165 aa)
  initn: 6348 initl: 3175 opt: 4504 Z-score: 5301.7 bits: 993.0 E(): 0
Smith-Waterman score: 6698; 86.616% identity (92.003% similar) in 1188 aa overlap
(3-1182:9-1165)

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      10      20      30      40      50
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEF
gi|161 CRYIABMPePMDNNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEF
      10      20      30      40      50      60

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      60      70      80      90      100      110
Cry1Ac VPGAGfVLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIY
gi|161 VPGAGfVLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIY
      70      80      90      100      110      120

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      120      130      140      150      160      170
Cry1Ac AESfREWEADPTNPALREEMRIQFNdMNSALtTAIPLFAVQNYQVPLlSVYVQAANLHLs
gi|161 AESfREWEADPTNPALREEMRIQFNdMNSALtTAIPLFAVQNYQVPLlSVYVQAANLHLs
      130      140      150      160      170      180

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      180      190      200      210      220      230
Cry1Ac VLrDVsVfGQRWGFDAATINSRYNDLTRLIGNyTDHAvRWYNTGLERVWGPDSRDWIRYn
gi|161 VLrDVsVfGQRWGFDAATINSRYNDLTRLIGNyTDHAvRWYNTGLERVWGPDSRDWIRYn
      190      200      210      220      230      240

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      240      250      260      270      280      290
Cry1Ac QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGS
gi|161 QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGS
      250      260      270      280      290      300

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      300      310      320      330      340      350
Cry1Ac IRSPHLMdILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRi
gi|161 IRSPHLMdILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRi
      310      320      330      340      350      360

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      360      370      380      390      400      410
Cry1Ac VAQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsL
gi|161 VAQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsL
      370      380      390      400      410      420

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      420      430      440      450      460      470
Cry1Ac DEIPPNnNVPPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIASDS
gi|161 DEIPPNnNVPPRQGFShRLSHVSMFRSGFSNSsvSIIrAPMfSWIHRSAEFNNIIPSSQ
      430      440      450      460      470      480

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480      490      500      510      520      530
Cry1Ac ITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGIEVPIHFPSTSTRYRV
gi|161 ITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRV
490      500      510      520      530

540      550      560      570      580      590
Cry1Ac RVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFSTSSLGNIV--
gi|161 RIRYASTTNLQPHFTSIDGRPINQGNFSATMSSGSLNLSGSGFRVTGFTTFFNFNSGSSVFT
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac -GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|161 LSAHFVNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYDIHI
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|161 DQVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTD
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYS
gi|161 ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYL
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac IRYNAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRGEKCAHHS
gi|161 IRYNAKHETVNVPGTGLSLWPLSAPSIGK-----AHHS
780      790      800

840      850      860      870      880      890
Cry1Ac HHFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKK
gi|161 HHFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKK
810      820      830      840      850      860

900      910      920      930      940      950
Cry1Ac WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLP
gi|161 WRDKREKLEWETNIVYKEAKESVDALFVNSQYDRIQADTNIAMIHAADKRVHSIREAYLP
870      880      890      900      910      920

960      970      980      990      1000     1010
Cry1Ac ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQR
gi|161 ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHR
930      940      950      960      970      980

1020     1030     1040     1050     1060     1070
Cry1Ac SVLVVPEWEAEVSEQEVRVCPGRGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEE
gi|161 SVLVVPEWEAEVSEQEVRVCPGRGYILRVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEE

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990      1000     1010     1020     1030     1040
Cry1Ac EIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRE
gi|161 EVYPNNTVTCNDYATQEEYEGYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRD
1050     1060     1070     1080     1090     1100

1130     1140     1150     1160     1170     1180
Cry1Ac NPCEFNRGRYDYTPLPVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|161 NPCESNRGYDYPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1110     1120     1130     1140     1150     1160

>>gi|5987869|gb|AAE17034.1| Sequence 33 from patent US 5 (1165 aa)
initn: 6348 init1: 3175 opt: 4504 Z-score: 5301.7 bits: 993.0 E(): 0
Smith-Waterman score: 6698; 86.616% identity (92.003% similar) in 1188 aa overlap
(3-1182:9-1165)

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEF
gi|598 CRYIABMPEPMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEF
10      20      30      40      50      60

60      70      80      90      100     110
Cry1Ac VPGAGFVLGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIY
gi|598 VPGAGFVLGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIY
70      80      90      100     110     120

120     130     140     150     160     170
Cry1Ac AESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
gi|598 AESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
130     140     150     160     170     180

180     190     200     210     220     230
Cry1Ac VLRDVSVFQQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYN
gi|598 VLRDVSVFQQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYN
190     200     210     220     230     240

240     250     260     270     280     290
Cry1Ac QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGS
gi|598 QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGS
250     260     270     280     290     300

300     310     320     330     340     350
Cry1Ac IRSPHLMIDLNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQR
gi|598 IRSPHLMIDLNSITIIYTDHARGEYYSWGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQR
310     320     330     340     350     360

360     370     380     390     400     410
Cry1Ac VAQLQGQVYRVLSTSLYRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGTVDLSL
gi|598 VAQLQGQVYRVLSTSLYRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGTVDLSL

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370      380      390      400      410      420
Cry1Ac  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDS
gi|598  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQ
      420      430      440      450      460      470
Cry1Ac  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQ
gi|598  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQ
      430      440      450      460      470      480
Cry1Ac  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQ
gi|598  DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQ
      480      490      500      510      520      530
Cry1Ac  ITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRV
gi|598  ITQIPLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRV
      490      500      510      520      530
Cry1Ac  ITQIPLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRV
gi|598  ITQIPLTKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRV
      540      550      560      570      580      590
Cry1Ac  RVRVYASVTPIHLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV--
gi|598  RIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGSLNQLQSGSFRVTGFTTFFNFSNGSSVFT
      540      550      560      570      580      590
Cry1Ac  RVRVYASVTPIHLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV--
gi|598  RIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGSLNQLQSGSFRVTGFTTFFNFSNGSSVFT
      600      610      620      630      640      650
Cry1Ac  -GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|598  LSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQLGLKTDVTDYHI
      600      610      620      630      640      650
Cry1Ac  -GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|598  LSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQLGLKTDVTDYHI
      660      670      680      690      700      710
Cry1Ac  DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|598  DQVSNLVTECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTD
      660      670      680      690      700      710
Cry1Ac  DQVSNLVTECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTD
gi|598  DQVSNLVTECLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTD
      720      730      740      750      760      770
Cry1Ac  ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYS
gi|598  ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYL
      720      730      740      750      760      770
Cry1Ac  ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYS
gi|598  ITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYL
      780      790      800      810      820      830
Cry1Ac  IRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHHS
gi|598  IRYNAKHETVNVPGTGSWPLSAPSPIGK-----AHHS
      780      790      800
Cry1Ac  IRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHHS
gi|598  IRYNAKHETVNVPGTGSWPLSAPSPIGK-----AHHS
      840      850      860      870      880      890
Cry1Ac  HHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKK
gi|598  HHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKK
      810      820      830      840      850      860
Cry1Ac  HHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKK
gi|598  HHFSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKK
      900      910      920      930      940      950
Cry1Ac  WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVSIREAYLP
gi|598  WRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVSIREAYLP
      870      880      890      900      910      920
Cry1Ac  WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVSIREAYLP
gi|598  WRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVSIREAYLP
      960      970      980      990      1000      1010
Cry1Ac  ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQR
gi|598  ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQR

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gi|598  ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHR
      930      940      950      960      970      980
Cry1Ac  ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHR
gi|598  ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHR
      1020      1030      1040      1050      1060      1070
Cry1Ac  SVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEE
gi|598  SVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEE
      990      1000      1010      1020      1030      1040
Cry1Ac  SVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEE
gi|598  SVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIENNTDELKFSNCVVEE
      1080      1090      1100      1110      1120
Cry1Ac  EIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRE
gi|598  EVYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRE
      1050      1060      1070      1080      1090      1100
Cry1Ac  EIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRE
gi|598  EVYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRE
      1130      1140      1150      1160      1170      1180
Cry1Ac  NPCEFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|598  NPCEFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110      1120      1130      1140      1150      1160
Cry1Ac  NPCEFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|598  NPCEFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
>>gi|594314|gb|AAA5921.1| Sequence 3 from Patent EP 029 (1154 aa)
      initn: 5193 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6679; 86.678% identity (91.990% similar) in 1186 aa overlap
(5-1182:1-1154)
      10      20      30      40      50      60
Cry1Ac  CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
Cry1Ac  CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      70      80      90      100      110      120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
gi|594  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
gi|594  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
      130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNFRREL
gi|594  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNFRREL
      180      190      200      210      220      230
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNFRREL
gi|594  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNFRREL
      250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
gi|594  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
      240      250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
gi|594  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
      310      320      330      340      350      360
Cry1Ac  MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|594  MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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gi|594 MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
gi|594 GYVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIPPQ
      360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|594 NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
gi|594 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNFNSGSSVFTLSAHVF
      540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|594 VECLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLTSGTFDECYPTLYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
gi|594 DDVFKENYVTLTSGTFDECYPTLYLYQKIDESKLFKAYTRYQLRGYIEDSDLEIYLIRYNAK
      720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHHSFLD
gi|594 HETVNVPGTGSWPLSAPSPIGKC-----AHSHHHSFLD
      780      790      800
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
gi|594 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP

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gi|594 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920
Cry1Ac 960      970      980      990      1000      1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQSRVSLVVP
gi|594 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVSLVVP
      930      940      950      960      970      980
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYIPNN
gi|594 EWEAEVSQ-VRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYVYVNN
      990      1000      1010      1020      1030      1040
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSPADYASVYEEKSYTDGRRENPECFN
gi|594 TVTCNDYATQEEYEGTYTSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050      1060      1070      1080      1090      1100
Cry1Ac 1140      1150      1160      1170      1180
RGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE
gi|594 RGYDGYTLPAGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE
      1110      1120      1130      1140      1150
>>gi|21713536|emb|CAD38221.1| unnamed protein product [s (1155 aa)
      initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|217 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100      110      120
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|217 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|217 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|217 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHL

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gi|217 240 250 260 270 280 290
Cry1Ac 310 320 330 340 350 360
gi|217 300 310 320 330 340 350
Cry1Ac 370 380 390 400 410 420
gi|217 360 370 380 390 400 410
Cry1Ac 430 440 450 460 470 480
gi|217 420 430 440 450 460 470
Cry1Ac 490 500 510 520 530
gi|217 480 490 500 510 520 530
Cry1Ac 540 550 560 570 580 590
gi|217 540 550 560 570 580 590
Cry1Ac 600 610 620 630 640 650
gi|217 600 610 620 630 640 650
Cry1Ac 660 670 680 690 700 710
gi|217 660 670 680 690 700 710
Cry1Ac 720 730 740 750 760 770
gi|217 720 730 740 750 760 770
Cry1Ac 780 790 800 810 820 830
gi|217 780 790 800
Cry1Ac 840 850 860 870 880 890

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Cry1Ac IDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|217 IDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860
Cry1Ac 900 910 920 930 940 950
gi|217 KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920
Cry1Ac 960 970 980 990 1000 1010
gi|217 GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRSVLVVP
      930      940      950      960      970      980
Cry1Ac 1020 1030 1040 1050 1060 1070
gi|217 EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN
      990      1000      1010      1020      1030      1040
Cry1Ac 1080 1090 1100 1110 1120 1130
gi|217 TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPECFN
      1050      1060      1070      1080      1090      1100
Cry1Ac 1140 1150 1160 1170 1180
gi|217 RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETGTFIVDSVELLLMEE
      1110      1120      1130      1140      1150
>>gi|2095429|gb|AAB57611.1|I42024 Sequence 9 from patent (1155 aa)
  initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)
Cry1Ac 10 20 30 40 50 60
gi|209 CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10 20 30 40 50
Cry1Ac 70 80 90 100 110 120
gi|209 VLGLVDIINGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      60 70 80 90 100 110
Cry1Ac 130 140 150 160 170 180
gi|209 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120 130 140 150 160 170
Cry1Ac 190 200 210 220 230 240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|209 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKRSRPHL
gi|209 TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKRSRPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|209 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
gi|209 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|209 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|209 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVINITAPL----SQRYRVIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|209 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSPRTVGFTTPPFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|209 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNIGLKTVDVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|209 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQDRGWRGSTDITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYLRINAK
gi|209 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLRINAK
      720      730      740      750      760      770

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      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHHSHFLSD
gi|209 HETVNVPGTGSWPLSAPSPIGK-----AHSHHSHFLSD
      780      790      800

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFIKIQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|209 IDVGCTDLNEDLGVWVIFIKIQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860

      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|209 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNRQSVLVVP
gi|209 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNRHSVLVVP
      930      940      950      960      970      980

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVPCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
gi|209 EWEAEVSQEVVPCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
      990      1000      1010      1020      1030      1040

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPECFN
gi|209 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050      1060      1070      1080      1090      1100

      1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|209 RGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110      1120      1130      1140      1150

>>gi|117553202|gb|ABK35130.1| Cry1Ab [Bacillus thuringie (1155 aa)
initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

      10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|117 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIWIFGSPQWDAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFRE
gi|117 VLGLVDIIWGIWIFGSPQWDAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFRE
      60      70      80      90      100      110

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130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|117 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|117 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQTLREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL
gi|117 TLTVLDIVSLFPNYSRTPYPIRTVSQTLREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQGLGQ
gi|117 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQGLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDLDEIPPQ
gi|117 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDLDEIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|117 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|117 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|117 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTGFTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|117 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|117 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAK
gi|117 DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYLRINA
720      730      740      750      760      770

780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRGKCAHSHHSHFLSD
gi|117 HETVNVPGTGSWPLSAPSPIGK-----AHSHHSHFLSD
780      790      800

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|117 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810      820      830      840      850      860

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIP
gi|117 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPELSVIP
870      880      890      900      910      920

960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNQRSVLPV
gi|117 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNNHRSVLPV
930      940      950      960      970      980

1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
gi|117 EWEAEVSQEVVRCPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
990      1000      1010      1020      1030      1040

1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEN
gi|117 TVTCNDYATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1050      1060      1070      1080      1090      1100

1140      1150      1160      1170      1180
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|117 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110      1120      1130      1140      1150

>>gi|47270462|gb|AAT27226.1| Sequence 9 from patent US 6 (1155 aa)
initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E( ) 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
gi|472 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
10      20      30      40      50

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              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLRGLSNLYQIYAESFRE
gi|472 VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLRGLSNLYQIYAESFRE
              60      70      80      90      100     110

              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170

              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              180     190     200     210     220     230

              250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIEGSIRSPHL
gi|472 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIEGSIRSPHL
              240     250     260     270     280     290

              310     320     330     340     350     360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
              300     310     320     330     340     350

              370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
gi|472 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQ
              360     370     380     390     400     410

              430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNNI IPSSQITQIPL
              420     430     440     450     460     470

              490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|472 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
              480     490     500     510     520     530

              540     550     560     570     580     590
Cry1Ac VTIHLNVNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVRNF
gi|472 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRFTVGFPTTFNFNSGSSVFTLSAHVF
              540     550     560     570     580     590

              600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|472 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYTDYHIDQVSNL

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              600     610     620     630     640     650
Cry1Ac VTYLSEDFCLDEKREKLESEKVKHAKRSLDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|472 VECLSEDFCLDEKKEKLESEKVKHAKRSLDERNLLQDPNFRGINRQLDRGWRGSDTITIQGG
              660     670     680     690     700     710

              720     730     740     750     760     770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|472 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
              720     730     740     750     760     770

              780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|472 HETVNVPGTGSWLPLSAPSPIGK-----AHHSHHFSLD
              780     790     800

              840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|472 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
              810     820     830     840     850     860

              900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|472 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
              870     880     890     900     910     920

              960     970     980     990     1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNHRSVLPV
gi|472 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNHRSVLPV
              930     940     950     960     970     980

              1020    1030    1040    1050    1060    1070
Cry1Ac EWAEVSVQEVVRCVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYV
gi|472 EWAEVSVQEVVRCVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYV
              990     1000    1010    1020    1030    1040

              1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN
gi|472 TVTCNDYATQEEYEGTYTSRNRGYDGYESNSSVPADYASVYEEKAYTDGRRDNPCESN
              1050    1060    1070    1080    1090    1100

              1140    1150    1160    1170    1180
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|472 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
              1110    1120    1130    1140    1150

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>>gi|5973546|gb|AAE12826.1| Sequence 33 from patent US 5 (1155 aa)
initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0

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Regulatory Product Characterization Team

Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap (5-1182:1-1155)

Sequence alignment for Cry1Ac and gi|597. Includes residue numbers 10-60, 70-120, 130-180, 190-240, 250-300, 310-360, 370-420, 430-480, 490-530, 540-590.

Sequence alignment for Cry1Ac and gi|597. Includes residue numbers 540-590, 600-650, 660-710, 720-770, 780-830, 840-890, 900-950, 960-1010, 1020-1070, 1080-1130, 1140-1180.







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      870      880      890      900      910      920
Cry1Ac  960      970      980      990      1000     1010
        GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDEEQNNQRSVLVVP
        .....
gi|216  960      970      980      990      1000     1010
        GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDEEQNNQRSVLVVP
        .....
      930      940      950      960      970      980

      1020     1030     1040     1050     1060     1070
Cry1Ac  1020     1030     1040     1050     1060     1070
        EWEAEVSEQVRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCVEEEIYPNN
        .....
gi|216  1020     1030     1040     1050     1060     1070
        EWEAEVSEQVRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCVEEEIYPNN
        .....
      990      1000     1010     1020     1030     1040

      1080     1090     1100     1110     1120     1130
Cry1Ac  1080     1090     1100     1110     1120     1130
        TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPVADYASVYEEKSYTDGRRNPECFN
        .....
gi|216  1080     1090     1100     1110     1120     1130
        TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPVADYASVYEEKSYTDGRRNPECFN
        .....
      1050     1060     1070     1080     1090     1100

      1140     1150     1160     1170     1180
Cry1Ac  1140     1150     1160     1170     1180
        RGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
        .....
gi|216  1140     1150     1160     1170     1180
        RGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
        .....
      1110     1120     1130     1140     1150

>>gi|143124|gb|AAA22561.1| crystal protein precursor (1155 aa)
  initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
        .....
gi|143  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
        .....
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESPFE
        .....
gi|143  VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESPFE
        .....
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        .....
gi|143  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
        .....
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
        .....
gi|143  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
        .....
      180     190     200     210     220     230

      250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGESIRSPHL
        .....
gi|143  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQIGESIRSPHL
        .....

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      240      250      260      270      280      290
Cry1Ac  310      320      330      340      350      360
        MDILNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
        .....
gi|143  310      320      330      340      350      360
        MDILNSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
        .....

      370      380      390      400      410      420
Cry1Ac  370      380      390      400      410      420
        GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
        .....
gi|143  370      380      390      400      410      420
        GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
        .....
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac  430      440      450      460      470      480
        NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
        .....
gi|143  430      440      450      460      470      480
        NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
        .....
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac  490      500      510      520      530
        VKGNFLFNG-SVIGSPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
        .....
gi|143  490      500      510      520      530
        VKGNFLFNG-SVIGSPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
        .....
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac  540      550      560      570      580      590
        VTIHNLNVNWNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
        .....
gi|143  540      550      560      570      580      590
        VTIHNLNVNWNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
        .....

      600      610      620      630      640      650
Cry1Ac  600      610      620      630      640      650
        SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
        .....
gi|143  600      610      620      630      640      650
        SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
        .....

      660      670      680      690      700      710
Cry1Ac  660      670      680      690      700      710
        VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGTIQQG
        .....
gi|143  660      670      680      690      700      710
        VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGTIQQG
        .....

      720      730      740      750      760      770
Cry1Ac  720      730      740      750      760      770
        DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAK
        .....
gi|143  720      730      740      750      760      770
        DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYIRYNAK
        .....

      780      790      800      810      820      830
Cry1Ac  780      790      800      810      820      830
        HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
        .....
gi|143  780      790      800      810      820      830
        HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
        .....

      840      850      860      870      880      890
Cry1Ac  840      850      860      870      880      890
        IDVGCTDLNEDLVGVVIFIKTKQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
        .....
gi|143  840      850      860      870      880      890
        IDVGCTDLNEDLVGVVIFIKTKQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
        .....

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gi|143 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860
      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPPELSVIP
      .....
gi|143 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPPELSVIP
      870      880      890      900      910      920
      960      970      980      990      1000      1010
Cry1Ac GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHV DVEEQNNQRSVLVVP
      .....
gi|143 GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHV DVEEQNNHRSVLVVP
      930      940      950      960      970      980
      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNN
      .....
gi|143 EWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIVPNN
      990      1000      1010      1020      1030      1040
      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRRENPCFN
      .....
gi|143 TVTCNDYTATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050      1060      1070      1080      1090      1100
      1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|143 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110      1120      1130      1140      1150

>>gi|21690365|emb|CAD37455.1| unnamed protein product [s (1155 aa)
      initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      .....
gi|216 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      .....
gi|216 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|216 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      .....

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gi|216 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
      .....
gi|216 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|216 MDILNSITIIYTDHAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      .....
gi|216 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360      370      380      390      400      410
      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|216 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470
      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
      .....
gi|216 TKSTNLGSGTSSVVKGPGFTGGDLRLRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
      .....
gi|216 TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRFTVGFPTPFNFNGSSVFTLSAHVF
      540      550      560      570      580      590
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|216 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650
      660      670      680      690      700      710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGG
      .....
gi|216 VECLSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGRWGSDTITIQGG
      660      670      680      690      700      710
      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYLSIRYNAK
      .....
gi|216 DDVFKENYVTLGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYLSIRYNAK
      720      730      740      750      760      770
      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHFLSLD

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gi|216 HETVNVPGTGLWPLSAPSPIGKC-----AHSHHFLSD
      780      790      800

Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|216 IDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860

Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|216 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920

Cry1Ac 960      970      980      990      1000     1010
GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDFVEEQNNRHSVLPVVP
gi|216 GVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDFVEEQNNRHSVLPVVP
      930      940      950      960      970      980

Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
gi|216 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
      990      1000     1010     1020     1030     1040

Cry1Ac 1080     1090     1100     1110     1120     1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRNPCEFN
gi|216 TVTCNDYTVNQEEYEGTYTSRNRGYDYGAYESSNSVPADYASAYEEKAYTDGRRDNPCESN
      1050     1060     1070     1080     1090     1100

Cry1Ac 1140     1150     1160     1170     1180
RGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|216 RGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110     1120     1130     1140     1150

>>gi|490188|emb|CAA00840.1| delta-endotoxin [Bacillus th (1155 aa)
  initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|490 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEERFARNAQAIISRLRGLSNLYQIYAESFRE
gi|490 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEERFARNAQAIISRLRGLSNLYQIYAESFRE
      60      70      80      90      100     110

Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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gi|490 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQFREL
gi|490 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYQFREL
      180      190      200      210      220      230

Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKSPHLL
gi|490 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKSPHLL
      240      250      260      270      280      290

Cry1Ac 310      320      330      340      350      360
MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVVAQLGQ
gi|490 MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVVAQLGQ
      300      310      320      330      340      350

Cry1Ac 370      380      390      400      410      420
GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|490 GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410

Cry1Ac 430      440      450      460      470      480
NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|490 NNVVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470

Cry1Ac 490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|490 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

Cry1Ac 540      550      560      570      580      590
VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|490 TTNLQFHTSIDGRPINQGNFSAATMSSGNSLNQSGSFRFTVGFSTPFNFNSGSSVFTLSAHVF
      540      550      560      570      580      590

Cry1Ac 600      610      620      630      640      650
SGTAGVVIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|490 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
      600      610      620      630      640      650

Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|490 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSDTITIQGG
      660      670      680      690      700      710

Cry1Ac 720      730      740      750      760      770

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Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|490 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK

Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|490 HETVNVPGTGSWPLSAPSPIGKC-----AHSHHFFSLD

Cry1Ac IDVGCTDLNEDLGVVWVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|490 IDVGCTDLNEDLGVVWVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|490 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP

Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLVVP
gi|490 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNHRSVLVVP

Cry1Ac EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCEEIYPNN
gi|490 EWEAEVSEQEVRVCPGRGYILLRVTAKEGYGEGCVTIHEIENNTDELKFSNCEEIYPNN

Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
gi|490 TVTCNDYATQEEYEGTYTSRNRGYDYGAYESNNSVPADYASAYEEKAYTDGRRNDPCESN

Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|490 RGYGDTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

>>gi|58759040|gb|AAW81956.1| Cry1Ab [Chloroplast transfo (1155 aa)
initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|587 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|587 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|587 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|587 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH
gi|587 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|587 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRSLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIIPPQ
gi|587 GVYRSLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIIPPQ

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|587 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL

Cry1Ac VKNFNLFG-SVLSGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|587 TKSTNLGSGTSVWKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRVRYAS

Cry1Ac VTIPIHLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|587 TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRVTGFTTFFNFNSGNSVFTLSAHVF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|587 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL





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480      490      500      510      520      530
540      550      560      570      580      590
Cry1Ac  VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
.: . . . . . : . . . : . : . . . . . : . . . : . : . . . : . . . : . . . :
gi|402  TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRFTVGFPTTFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590
600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650
660      670      680      690      700      710
Cry1Ac  VTLYSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  VECLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710
720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAFTRYQLRGIYEDSQDLEIYSIRYNK
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAYTRYQLRGIYEDSQDLEIYLIRYNK
      720      730      740      750      760      770
780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  HETVNVPGTGSWPLSAPSPIGK-----AHSHHFFSLD
      780      790      800
840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVVWVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  IDVGCTDLNEDLGVVWVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860
900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920
960      970      980      990      1000     1010
Cry1Ac  GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQNNQRSVLVVP
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  GVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQNNHRSVLVVP
      930      940      950      960      970      980
1020     1030     1040     1050     1060     1070
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIEIENNTDELKFSNCVVEEIIYPNN
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIEIENNTDELKFSNCVVEEIVYPNN
      990     1000     1010     1020     1030     1040
1080     1090     1100     1110     1120     1130
Cry1Ac  TVTCNDYTVNQBEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRRENPCFEFN
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

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gi|402  TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVVPADYASAYEEKAYTDGRRDNPCESN
      1050     1060     1070     1080     1090     1100
      1140     1150     1160     1170     1180
Cry1Ac  RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402  RGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110     1120     1130     1140     1150
>>gi|27436100|gb|AA013302.1|AF358861_2 crystal endotoxin (1155 aa)
  initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E( ): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)
      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLQG
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLQG
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|274  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac  NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
.: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

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gi|412 GYRFLSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP SAVA RYKSGTVDLSDEIIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480
gi|412 NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530
gi|412 TKSTNLGSGT SVVKGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
480 490 500 510 520 530

Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
540 550 560 570 580 590
gi|412 TTNLQFHTSIDGRPINQGNFSAATMSSGNSLQSGSFRTVGFPTTFFNFNSGSSVFTLSAHVF
540 550 560 570 580 590

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650
gi|412 NSGNEVYIDRIEFVPAEVTFFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600 610 620 630 640 650

Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKIDINRQPERGWGGSTGITIQGG
660 670 680 690 700 710
gi|412 VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWGGSTDITIQGG
660 670 680 690 700 710

Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNK
720 730 740 750 760 770
gi|412 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNK
720 730 740 750 760 770

Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
780 790 800 810 820 830
gi|412 HETVNVPGTGSWPLSAQSPIGK-----AHSHHFFSLD
780 790 800

Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840 850 860 870 880 890
gi|412 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810 820 830 840 850 860

Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
900 910 920 930 940 950
gi|412 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
870 880 890 900 910 920

Cry1Ac
960 970 980 990 1000 1010

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Cry1Ac GVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVP
gi|412 GVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVLVVP
930 940 950 960 970 980

Cry1Ac EWEAEVSQEVVRCVPCGRGYILRVYAYKEGYEGECVTTIHEIENNTDELKFSNCVVEEYIPNN
1020 1030 1040 1050 1060 1070
gi|412 EWEAEVSQEVVRCVPCGRGYILRVYAYKEGYEGECVTTIHEIENNTDELKFSNCVVEEYIPNN
990 1000 1010 1020 1030 1040

Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
1080 1090 1100 1110 1120 1130
gi|412 TVTCNDYTVNQEEYGGAYTSRNRGYDYGAYESNSVVPADYASAYEEKAYTDGRRNPCEFN
1050 1060 1070 1080 1090 1100

Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180
gi|412 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1110 1120 1130 1140 1150

>>gi|12808282|gb|AAE43502.1| Sequence 9 from patent US 6 (1155 aa)
initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50 60
gi|128 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120
gi|128 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
190 200 210 220 230 240
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQIEGSIKSPHL
250 260 270 280 290 300
gi|128 TLTVLDIVSLFPNYDSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQIEGSIKSPHL
240 250 260 270 280 290

Cry1Ac
310 320 330 340 350 360

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Cry1Ac MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|128 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS
gi|128 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|128 TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSGSGFRTVGFSTPPFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 NSGNEVYIDRIEFVPAEVTFAEAYDLERAQKAVNELFTSSNQLGLKTNVTDYHIDQVSNL
      600      610      620      630      640      650

      660      670      680      690      700      710
Cry1Ac VTYLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|128 VECLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

      720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|128 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYFLIRYNAK
      720      730      740      750      760      770

      780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIKGCGEPNRCAPHLEWNPDLDCSCDRGKCAHSHHFFSLD
gi|128 HETVNVPGTGSWPLSAPSPIKGC-----AHSHHFFSLD
      780      790      800

      840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|128 IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860

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      900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|128 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920

      960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQQNQRSLVLPV
gi|128 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDEEQQNHRSLVLPV
      930      940      950      960      970      980

      1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
gi|128 EWEAEVSQEVVRCVGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEYVPPN
      990      1000      1010      1020      1030      1040

      1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN
gi|128 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050      1060      1070      1080      1090      1100

      1140      1150      1160      1170      1180
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
gi|128 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETGTFIVDSVELLMEE
      1110      1120      1130      1140      1150

>>gi|594204|gb|AAA55811.1| Sequence 4 from Patent EP 031 (1155 aa)
      initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
gi|594 VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      180      190      200      210      220      230

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                250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKRSPLH
gi|594 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKRSPLH
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVaQLGQ
gi|594 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVaQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSnLPSAVYrKSGTVdSLDEIPpQ
gi|594 GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSnLPSAVYrKSGTVdSLDEIPpQ
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac NNNVpPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNNIIASDSITQIPa
gi|594 NNNVpPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNNIIpSSQITQIPL
                420      430      440      450      460      470

                490      500      510      520      530
Cry1Ac VKGNfLfnG-SVIsGPGfTGGDLVrLNsSGnNIQNRgYIEVPIHfPSTSTRYrVRVrYAS
gi|594 TKSTNLGSGTSVvKGPgFTGGDILRrTSPGQLSTLrVNITAPL-----SQRYrVRIRYAS
                480      490      500      510      520      530

                540      550      560      570      580      590
Cry1Ac VPIHLNvNwGnSSIFsNTVpATATSLDNLQSSDFGfYFESANaFTSSLGNIV---GVRNF
gi|594 TTNLQfHTsIDGRpINQGNfSATMSSGSNLQSGSFRTVgFTTFPFNFsNGSSVfTTLsAHfF
                540      550      560      570      580      590

                600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFfIPVTATLEAEYnLERAQKAVNALfTSTnQLGLKtNVtDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAeyDLERAQKAVNELfTSSnQIGLKTdVtDYHIDQVSNL
                600      610      620      630      640      650

                660      670      680      690      700      710
Cry1Ac VTyLsDEfCLDEKRElSEKvKHAKRlSDERNLLQDSNFKDINRQPERGWGGSgtGITIQGG
gi|594 VECLsDEfCLDEKRElSEKvKHAKRlSDERNLLQDPNfRGINRQLDRGWRGStDITIQGG
                660      670      680      690      700      710

                720      730      740      750      760      770
Cry1Ac DDVfKENyVTLsGTFDEcYPTyLYQKIDESKlKAFTRyQLRgYIEDsQDLeyISIRYNAK
gi|594 DDVfKENyVTLlLGTfDEcYPTyLYQKIDESKlKAYTRyQLRgYIEDsQDLeyILIRYNAK
                720      730      740      750      760      770

                780      790      800      810      820      830
Cry1Ac HETVnVpGTGSWPLsAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGECaHhSHHfSLD
gi|594 HETVnVpGTGSWPLsAPSPiGK-----AHhSHHfSLD
                780      790      800

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                840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
gi|594 IDVGCTDLNEDLGVWVIFIKtQDGHARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
                810      820      830      840      850      860

                900      910      920      930      940      950
Cry1Ac KLEWETnIVYKEAKESVDALfVNSQYDQLQADtNIAMIHAADKRVHSIREAYLPELSVIP
gi|594 KLEWETnIVYKEAKESVDALfVNSQYDRlQADtNIAMIHAADKRVHSIREAYLPELSVIP
                870      880      890      900      910      920

                960      970      980      990      1000      1010
Cry1Ac GvNAaIFEELEGRIFtAFSLYDARNVIKNGDFnNGLSCWNVKghVDVEEQNNQRsVLVVP
gi|594 GvNAaIFEELEGRIFtAFSLYDARNVIKNGDFnNGLSCWNVKghVDVEEQNNHRSVLVVP
                930      940      950      960      970      980

                1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVsqEVRVCPGRGyILrVTAYKEGyGEGCVtIHEIENntDELKfSNcVEEeyPnN
gi|594 EWEAEVsqEVRVCPGRGyILrVTAYKEGyGEGCVtIHEIENntDELKfSNcVEEeyVpN
                990      1000      1010      1020      1030      1040

                1080      1090      1100      1110      1120      1130
Cry1Ac TVtCNdYtVnQEEYGGAYtSRNRgYNEA----PsvPAdYASvYEEKsYtDGRRENpCEFN
gi|594 TVtCNdYtAtQEEYEGYtSRNRgYDgAYESnSSVPAdYASAYEEKAYtDGRRDnPCESN
                1050      1060      1070      1080      1090      1100

                1140      1150      1160      1170      1180
Cry1Ac RgYrDYtPLPVgYVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
gi|594 RgYGDYtPLPAGYVtKELEyFPETDKVWIEIGETEGTFIVDSVellLMEE
                1110      1120      1130      1140      1150

>>gi|1608063|gb|AAB11018.1| Sequence 33 from patent US 5 (1155 aa)
  initn: 6347 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

                10      20      30      40      50      60
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGf
gi|160 MDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAGf
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGfGPsQWDAFLVQIEQLINQRIEEFARNQAIrSRLegLSNLYQIYAESfRE
gi|160 VLGLVDIIWIGfGPsQWDAFLVQIEQLINQRIEEFARNQAIrSRLegLSNLYQIYAESfRE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLlSVVYQAAANLHLSVLrDVS
gi|160 WEADPTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLlSVVYQAAANLHLSVLrDVS
                120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGDSDRDWIRYNQFRREL
gi|160 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGDSDRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQIEGSIIRSPHL
gi|160 TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVLENFDGSGFRGSAQIEGSIIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|160 MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
gi|160 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|160 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
420      430      440      450      460      470

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
gi|160 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
480      490      500      510      520      530

540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|160 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|160 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650

660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|160 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK
gi|160 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKATRYQLRGIYEDSQDLEIYLIRYNAK

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720      730      740      750      760      770
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLD
gi|160 HETVNVPGTGSWLPLSAPSPIGK-----AHSHHFFSLD
780      790      800      810      820      830

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|160 IDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810      820      830      840      850      860

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
gi|160 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
870      880      890      900      910      920

960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP
gi|160 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNHRSVLVVP
930      940      950      960      970      980

1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYYPNN
gi|160 EWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEYYPNN
990      1000      1010      1020      1030      1040

1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTYNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPECFN
gi|160 TVTCNDYTYNQEEYEGTYTSRNRGYDGAYESNSSVPADYASVYEEKAYTDGRRDNPESN
1050      1060      1070      1080      1090      1100

1140      1150      1160      1170      1180
Cry1Ac RGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|160 RGYRDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110      1120      1130      1140      1150

>>gi|25990352|gb|AAN76494.1|AF254640_1 insecticidal prot (1155 aa)
initn: 6347 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6697; 86.762% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|259 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|259 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE

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60      70      80      90      100     110
Cry1Ac 130      140      150      160      170      180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|259 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRREL
gi|259 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRREL
180      190      200      210      220      230
Cry1Ac 250      260      270      280      290      300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|259 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290
Cry1Ac 310      320      330      340      350      360
MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|259 MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSTLYRRPFIINNGQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIIPPQ
gi|259 GVYRTLSTLYRRPFIINNGQLSVLDGTEFAYGTSSNLPsAVYRKSgTVDsLDEIIPPQ
360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFsHRLSHVSMFRSGFSNSsVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|259 NNVVPPRQGFsHRLSHVSMFRSGFSNSsVSIIRAPMFSWIHRSAEFNIIIPSQITQIPL
420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGnFLFNG-SVISGPGFTGGDLVRLNssGNNIqNRgyIEVPIHFPSTSTRYRVRVRYAS
gi|259 TKSTNLGSGTSVVKGPgFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTPIHLNVNwGNSsIFsNTVPATATSLDNLQSSDFgyFESANAFTSSsLGNIV--GVRNF
gi|259 TTNLQFHTSIDGRPINQGNFSATMSSGSNlQSGSFRtVGFTPPFNFSSVFTLSAHVF
540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|259 NSGNEVYIDRIEFVPAEVTFFAEYDLERAQKAVNELFTSSNQIGLKTdVTDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSKVHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

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gi|259 VECLsDEFCLDEKkELSEKvKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLsGTFDECYPTLYLQKIDESKLKAFTRYQLRGYIEDSODLEIYSIRYNAK
gi|259 DDVFKENYVTLlGTFDECYPTLYLQKIDESKLKAYTRYQLRGYIEDSODLEIYLIRYNAK
720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGKCAHSHHFSLD
gi|259 HETVNVPGTGSWPLSAPSPiGK-----AHSHHFSLD
780      790      800
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|259 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810      820      830      840      850      860
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|259 KLEWETNIVYKEAKESVDALFVNSQYDRlQADTNIAMIHAADKRVHSIREAYLPELSVIP
870      880      890      900      910      920
Cry1Ac 960      970      980      990      1000     1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRsVLVVP
gi|259 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVLVVP
930      940      950      960      970      980
Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSQEVrVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIEYPNN
gi|259 EWEAEVSQEVrVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIVPNN
990      1000     1010     1020     1030     1040
Cry1Ac 1080     1090     1100     1110     1120     1130
TVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCEFN
gi|259 TVTCNDYtATQEEYEGTYTSRNRGYDGAYESNSsVPADYASAYEEKAYTDGRRDNPCEsN
1050     1060     1070     1080     1090     1100
Cry1Ac 1140     1150     1160     1170     1180
RGYRDYtPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|259 RGYGDYtPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1110     1120     1130     1140     1150
>>gi|594472|gb|AAA56079.1| Sequence 6 from Patent EP 026 (1156 aa)
initn: 5994 initl: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6667; 86.436% identity (91.828% similar) in 1187 aa overlap
(5-1182:1-1156)
Cry1Ac 10      20      30      40      50      60
CMQAMDNPNINECIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLEFVPGAGF

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gi|594 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|594 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIIEGSIIRSPHL
gi|594 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGIIEGSIIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|594 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPQ
gi|594 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|594 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL-----SQRYRVRIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594 TTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFTTPFNFSGNGSVFTLSAHVF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL

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gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQILGKTDVTDYHIDQVSNL
      600     610     620     630     640     650
      660     670     680     690     700     710
Cry1Ac VTYLSEDFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGSGTGTITIQGG
gi|594 VECLSEDFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|594 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSHHFSLD
gi|594 HETVNVPGTGSWPLSAPSPIGK-----AHSHHFSLD
      780     790
      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEK-PLVGEALARVKRAEKKWRDRK
gi|594 IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEGRAPLVGEALARVKRAEKKWRDRK
      810     820     830     840     850     860
      900     910     920     930     940     950
Cry1Ac EKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVI
gi|594 EKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVI
      870     880     890     900     910     920
      960     970     980     990     1000    1010
Cry1Ac PGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDVEEQNNRHSVLV
gi|594 PGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDVEEQNNRHSVLV
      930     940     950     960     970     980
      1020    1030    1040    1050    1060    1070
Cry1Ac PEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPN
gi|594 PEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIVYPN
      990     1000    1010    1020    1030    1040
      1080    1090    1100    1110    1120    1130
Cry1Ac NTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEKSYTDGRRRNPCEF
gi|594 NTVTCNDYATQEEYEGTYTSRNRGYDGAYESSNSVVPADYASAYEEKAYTDGRRRNPCE
      1050    1060    1070    1080    1090    1100
      1140    1150    1160    1170    1180
Cry1Ac NRGYRDYTPPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|594 NRGYGDYTPPLAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110    1120    1130    1140    1150
>>gi|594020|gb|AAA5627.1| Sequence 6 from Patent EP 034 (1156 aa)

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initn: 5994 init1: 3174 opt: 4503 Z-score: 5300.6 bits: 992.7 E(): 0
Smith-Waterman score: 6667; 86.436% identity (91.828% similar) in 1187 aa overlap
(5-1182:1-1156)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|594 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|594 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|594 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|594 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGSAQGIIEGSI RSPHL
gi|594 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDFGSRGSAQGIIEGSI RSPHL
Cry1Ac MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIV AQLGQ
gi|594 MDILNSITIYTDHRGEYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIV AQLGQ
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
gi|594 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
Cry1Ac NNNVPPRQGFSHR LSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|594 NNNVPPRQGFSHR LSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRG YIEVP IHPFSTSTRYRVRVRYAS
gi|594 TKSTNLGSGTSVVKGPGFTGGDLRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|594 TTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRFTVGF TPFNFNSNGSSVFTLSAHVF
Cry1Ac SGTAGVIIDRFEFIPV TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|594 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKT DVTDYHIDQVSNL
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|594 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|594 DDVFKENYVTLGTFDECYPTYLYQKIDESK LKAYTRYQLRGYIEDSQDLEIYLIRYNAK
Cry1Ac HETVNVPGTGS L WPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFLSD
gi|594 HETVNVPGTGS L WPLSAPSPIGK-----AHSHHFLSD
Cry1Ac IDVGCTDLNEDLGVWVIFIKITQDGHARLGNLEFLEEK-PLVGEALARVKRAEKKWRDKR
gi|594 IDVGCTDLNEDLGVWVIFIKITQDGHARLGNLEFLEGRAPLVGEALARVKRAEKKWRDKR
Cry1Ac EKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVI
gi|594 EKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVI
Cry1Ac PGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNR SVLVV
gi|594 PGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNR SVLVV
Cry1Ac PEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSN CVEEVIYPN
gi|594 PEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSN CVEEVIYPN
Cry1Ac NTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC EF
gi|594 NTVTCNDY TATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCE S



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1080      1090      1100      1110      1120      1130
Cry1Ac  TVTTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEKSYTDGRRNPCEF
gi|104   TVTTCNDYTATQEEYEGTYTSRNRGYDGDAYESNSSVPADYASAYEEKAYTDGRRNDPCE
1050      1060      1070      1080      1090      1100

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1140      1150      1160      1170      1180
Cry1Ac  RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|104   RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110      1120      1130      1140      1150

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>>gi|151655610|gb|ABS18384.1| delta-endotoxin Cry1Ab [Ba (1155 aa)  
 initn: 6339 initl: 3166 opt: 4495 Z-score: 5291.1 bits: 991.0 E(): 0  
 Smith-Waterman score: 6689; 86.678% identity (91.990% similar) in 1186 aa overlap  
 (5-1182:1-1155)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|151   MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|151   VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151   WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|151   VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQIEGSI RSPHL
gi|151   TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRFGSAQIEGSI RSPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|151   MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac  GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEI P P Q
gi|151   GVYRTLSSSTLYRRPFIINQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEI P P Q
360     370     380     390     400     410

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430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|151   NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420      430      440      450      460      470

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490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVLSGPGFTGGDLVRLNNSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|151   TKSTNLGSGT SVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
480      490      500      510      520      530

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540      550      560      570      580      590
Cry1Ac  VTPIHNLVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|151   TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590

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600      610      620      630      640      650
Cry1Ac  SGTAGVIIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151   NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
600      610      620      630      640      650

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660      670      680      690      700      710
Cry1Ac  VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|151   VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710

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720      730      740      750      760      770
Cry1Ac  DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRIRYNAK
gi|151   DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRIRYNAK
720      730      740      750      760      770

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780      790      800      810      820      830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|151   HETVNVPGTGSWPLSAPSPIGK-----AHSHHFSLD
780      790

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840      850      860      870      880      890
Cry1Ac  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|151   IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810      820      830      840      850      860

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900      910      920      930      940      950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|151   KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
870      880      890      900      910      920

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960      970      980      990     1000     1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQSRVSLVVP
gi|151   GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSVSLVVP
960      970      980      990     1000     1010

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          930      940      950      960      970      980
Cry1Ac 1020      1030      1040      1050      1060      1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYEGECVTIHEIENNTDELKFSNCVEEEIYPNN
gi|151 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYEGECVTIHEIENNTDELKFSNCVEEEIYPNN
          990      1000      1010      1020      1030      1040
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPCEF
gi|151 TVTTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPCEF
          1050      1060      1070      1080      1090      1100
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPCEF
gi|151 TVTTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNCPCEF
          1050      1060      1070      1080      1090      1100
Cry1Ac 1140      1150      1160      1170      1180
RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|151 RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1110      1120      1130      1140      1150
Cry1Ac 1140      1150      1160      1170      1180
RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|151 RGYRDYTPPLVPGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
>>gi|48734426|gb|AAT46415.1| parasporal crystal protein (1156 aa)
  initn: 6311 initl: 3158 opt: 4495 Z-score: 5291.1 bits: 991.0 E(): 0
Smith-Waterman score: 6682; 86.594% identity (91.906% similar) in 1186 aa overlap
(5-1182:1-1156)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|487 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|487 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|487 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|487 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          180     190     200     210     220     230
Cry1Ac 250     260     270     280     290     300
TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSI RSPHL
gi|487 TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSI RSPHL
          240     250     260     270     280     290
Cry1Ac 310     320     330     340     350     360
MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|487 MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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          300      310      320      330      340      350
Cry1Ac 370      380      390      400      410      420
GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
gi|487 GVYRTLSSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
          360      370      380      390      400      410
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|487 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
          420      430      440      450      460      470
Cry1Ac 490      500      510      520      530
VKGNFLENG-SVIGSGPFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|487 TKSTNLGSGTSVVKPGFTGGDILRRTSPGQISTLRVNIITAPL-----SQRYRVRIRYAS
          480      490      500      510      520      530
Cry1Ac 540      550      560      570      580      590
VTFIHLNVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|487 TTNLQFHTSIDGRPINQGNFSATMSSGSLNLSQSGSFRFTVGFSTPFNFSNGSSVFTLSAHVF
          540      550      560      570      580      590
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL
gi|487 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
          600      610      620      630      640      650
Cry1Ac 660      670      680      690      700      710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGGSGTITIQGG
gi|487 VECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSDTITIQGG
          660      670      680      690      700      710
Cry1Ac 720      730      740      750      760      770
DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|487 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRIRYNAK
          720      730      740      750      760      770
Cry1Ac 780      790      800      810      820      830
HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLD
gi|487 HETVNVPGTGSWLPLSAPSPIGKCG-----AHSHHFSLD
          780      790
Cry1Ac 840      850      860      870      880      890
IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|487 IDVGCTDLNEDLGVVWVIFIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRGKRE
          810      820      830      840      850      860
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELSVIP
gi|487 KLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELSVIP

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gi|487 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIMIHAADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920
      960      970      980      990      1000     1010
Cry1Ac GVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVVP
      .....
gi|487 GVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSVLVVP
      930      940      950      960      970      980
      1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEIYPNN
      .....
gi|487 EWEAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVYPNN
      990      1000     1010     1020     1030     1040
      1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFEN
      .....
gi|487 TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFEN
      1050     1060     1070     1080     1090     1100
      1140     1150     1160     1170     1180
Cry1Ac RGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|487 RGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110     1120     1130     1140     1150
>>gi|159024156|gb|ABW87320.1| endotoxin [Bacillus thurin (1155 aa)
      initn: 6729 initl: 3166 opt: 4489 Z-score: 5284.0 bits: 989.7 E(): 0
Smith-Waterman score: 6651; 86.341% identity (91.737% similar) in 1186 aa overlap
(5-1182:1-1155)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|159 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      .....
gi|159 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|159 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVL
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      .....
gi|159 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
      .....

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gi|159 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      .....
gi|159 MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
      .....
gi|159 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
      .....
gi|159 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
      .....
gi|159 TKSTNLGSGTSSVVKGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VTPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
      .....
gi|159 TTNLQFHTSIDGRPINQGNFSATMSSGSLNQLSGSFRVTGFTTFFNFSNGSSVFTLSAHVF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|159 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600     610     620     630     640     650
      660     670     680     690     700     710
Cry1Ac VTYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      .....
gi|159 VECLSDEFCLDEKRELSEKVKHAKRLSDERSLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
      .....
gi|159 DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLRINA
      720     730     740     750     760     770
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGKCAHSHHFSLD
      .....
gi|159 HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGKCAHSHHFSLD
      780     790
      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

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gi|159 IDVGTDLNEDLGVWEIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860
Cry1Ac 900      910      920      930      940      950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSTREAYLPELSVIP
gi|159 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSTREAYLPELSVIP
      870      880      890      900      910      920
Cry1Ac 960      970      980      990      1000     1010
GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVP
gi|159 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVLVVP
      930      940      950      960      970      980
Cry1Ac 1020     1030     1040     1050     1060     1070
EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
gi|159 EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
      990     1000     1010     1020     1030     1040
Cry1Ac 1080     1090     1100     1110     1120     1130
TVTTCNDYTVNQEEYGGAYTSRNRGYNEAP---SVPADYASVYEEKSYTDGRRENPCFEN
gi|159 TVTTCNDYTATQEEYEGTYTSRNRRYDYGAYESNFSVPADYASAYEEKAYTDGRRDNPCESN
      1050     1060     1070     1080     1090     1100
Cry1Ac 1140     1150     1160     1170     1180
RGYRDYTPPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|159 RGYGDYTPPLPAGYVTKLECFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100     1120     1130     1140     1150
>>gi|56900936|gb|AAW31761.1| Cry1Ab [Bacillus thuringien (1155 aa)
  initn: 6786 initl: 3163 opt: 4488 Z-score: 5282.9 bits: 989.5 E(): 0
Smith-Waterman score: 6671; 86.509% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)
Cry1Ac 10      20      30      40      50      60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|569 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|569 VLGLVDIIWGFPGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|569 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNQFREL

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gi|569 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQNQFREL
      180      190      200      210      220      230
Cry1Ac 250     260     270     280     290     300
TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH
gi|569 TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLH
      240     250     260     270     280     290
Cry1Ac 310     320     330     340     350     360
MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
gi|569 MDILNSITIIYTDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
      300     310     320     330     340     350
Cry1Ac 370     380     390     400     410     420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPO
gi|569 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPO
      360     370     380     390     400     410
Cry1Ac 430     440     450     460     470     480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|569 NNVVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470
Cry1Ac 490     500     510     520     530
VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFSTSTRYRVRVRYAS
gi|569 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac 540     550     560     570     580     590
VTPIHLLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|569 TTNLQFHTSIDGRPINQGNFSATMSSGNSLNQSGSFRFTVGFPTTFNPFNSGSSVFTLSAHVF
      540     550     560     570     580     590
Cry1Ac 600     610     620     630     640     650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|569 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSFNQIGLKTVDYHIDQVSNL
      600     610     620     630     640     650
Cry1Ac 660     670     680     690     700     710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|569 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
Cry1Ac 720     730     740     750     760     770
DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|569 DDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770
Cry1Ac 780     790     800     810     820     830

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Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|569 HETVNVPGTGSWPLSAPSPIGK-----AHHSHHFFSLD

780 790 800

Cry1Ac 840 850 860 870 880 890
IDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

gi|569 IDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE

810 820 830 840 850 860

Cry1Ac 900 910 920 930 940 950
KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP

gi|569 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAPADKRVHSIREAYLPELSVIP

870 880 890 900 910 920

Cry1Ac 960 970 980 990 1000 1010
GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSWCWNVKGHV DVEEQNNQRSVLVVP

gi|569 GVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSWCWNVKGHV DVEEQNNHRSVLVVP

930 940 950 960 970 980

Cry1Ac 1020 1030 1040 1050 1060 1070
EWEAEVSEQEVRVCPGRGYLLRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNN

gi|569 EWEAEVSEQEVRVCPGRGYLLRV TAYKEGYGEGCVTIHEIENNTDELKFSNCV EEEVYPNN

990 1000 1010 1020 1030 1040

Cry1Ac 1080 1090 1100 1110 1120 1130
TVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPCFEN

gi|569 TVTTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN

1050 1060 1070 1080 1090 1100

Cry1Ac 1140 1150 1160 1170 1180
RGYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMKE

gi|569 RGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSV ELLLMKE

1110 1120 1130 1140 1150

>>gi|143099|gb|AAA22551.1| insecticidal protein (1155 aa)
inith: 6322 initl: 3158 opt: 4487 Z-score: 5281.7 bits: 989.2 E(): 0
Smith-Waterman score: 6672; 86.594% identity (91.906% similar) in 1186 aa overlap
(5-1182:1-1155)

Cry1Ac 10 20 30 40 50 60
CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFPVPGAGF

gi|143 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFPVPGAGF

10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE

gi|143 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE

60 70 80 90 100 110

130 140 150 160 170 180

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|143 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPD SRDWIRYNQFRREL

gi|143 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPD SRDWIRYNQFRREL

180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENF DGSFRGSAQIEGSIRSPHL

gi|143 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENF DGSFRALAQIEGSIRSPHL

240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360
MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIVAQLGQ

gi|143 MDILNSITIIYTD AHRGEYYWSGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIVAQLGQ

300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYR KSGTVDSLDEIPPO

gi|143 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYR KSGTVDSLDEIPPO

360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NIIASDSITQIPLA

gi|143 NNVVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFN NIIIPSSQITQIPL

420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLENG-SVLSGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP STSTRYRVRVRYAS

gi|143 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNI TAPL----SQRYRVRIRYAS

480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VTPIHNLVNWGNSSIFSNVVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF

gi|143 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGF TTPFNFSNAGSSVFTLSAHVF

540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNV TDYHIDQVSNL

gi|143 NSGNEVYIDRIEFVFAEYVTLERAQKAVNELFTSSNQIGLKT DVTDYHIDQVSNL

600 610 620 630 640 650

Cry1Ac 660 670 680 690 700 710
VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG

gi|143 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG

660 670 680 690 700 710

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```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|143 DDVFKENYVTLTSGTDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
gi|143 HETVNVPGTGLWPLSAPSPIGK-----AHSHHFFSLD
780      790      800

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|143 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810      820      830      840      850      860

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKKAESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|143 KLEWETNIVYKKAESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
870      880      890      900      910      920

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWVKGHVDEEQQNRQSVLVVP
gi|143 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWVKGHVDEEQQNRQSVLVVP
930      940      950      960      970      980

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCFVEEIIYPNN
gi|143 EWEAEVSEQEVRVCPGRGYLLRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCFVEEIIYPNN
990      1000     1010     1020     1030     1040

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
gi|143 TVTCNDYATQEEYEGTYTSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1050     1060     1070     1080     1090     1100

```

```

1140     1150     1160     1170     1180
Cry1Ac RGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|143 RGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110     1120     1130     1140     1150

```

```

>>gi|14190061|gb|AAK55546.1|AF375608_1 Cry1Ab16 [Bacillus (1155 aa)
  initn: 6303 initl: 3155 opt: 4484 Z-score: 5278.1 bits: 988.6 E(): 0
  Smith-Waterman score: 6650; 86.172% identity (91.821% similar) in 1186 aa overlap
  (5-1182:1-1155)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|141 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFRE
gi|141 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYRVPLLSVYVQAVNLHLSVLRDVL
120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|141 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIIRSPHL
gi|141 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIIRSPHL
240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|141 MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
gi|141 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|141 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRYAS
gi|141 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRYAS
480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHNLVNWGNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|141 TTNLQPHTSIDGRPINQGNFSATMSSGSLNLSGSGFRFTVGFPTFPNFSNGSSVFTLSAHVF
540     550     560     570     580     590

```

```

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|141 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600     610     620     630     640     650

```

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```

660      670      680      690      700      710
Cry1Ac VTYLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: .....: .....: .....: .....: .....: .....:
gi|141 VECLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAK
: .....: .....: .....: .....: .....: .....:
gi|141 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSDLEIYLIRYNAK
      720      730      740      750      760      770

```

```

780      790      800      810      820      830
Cry1Ac HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
: .....: .....: .....: .....: .....: .....:
gi|141 HETVNVPGTGLWPLSAPSPIGKC-----AHHSHHFSLD
      780      790      800

```

```

840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
: .....: .....: .....: .....: .....: .....:
gi|141 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810      820      830      840      850      860

```

```

900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
: .....: .....: .....: .....: .....: .....:
gi|141 KLEWETNIVYKEAKESVDAVFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
      870      880      890      900      910      920

```

```

960      970      980      990      1000     1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVP
: .....: .....: .....: .....: .....: .....:
gi|141 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVLVVP
      930      940      950      960      970      980

```

```

1020     1030     1040     1050     1060     1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNN
: .....: .....: .....: .....: .....: .....:
gi|141 EWEAEVSEQEVRVCPGRGYILRV TAYKEEYEGECVTIHEIENNTAELKFSNCVEEIVPNN
      990      1000     1010     1020     1030     1040

```

```

1080     1090     1100     1110     1120     1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFEFN
: .....: .....: .....: .....: .....: .....:
gi|141 TVTCNDYTATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050     1060     1070     1080     1090     1100

```

```

1140     1150     1160     1170     1180
Cry1Ac RGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
: .....: .....: .....: .....: .....: .....:
gi|141 RGYGDTPLPAGYVTRLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110     1120     1130     1140     1150

```

```

>>gi|142886|gb|AAA22420.1| 5.3 class delta endotoxin (1155 aa)
  initn: 6321 initl: 3168 opt: 4483 Z-score: 5277.0 bits: 988.4 E(): 0
Smith-Waterman score: 6671; 86.425% identity (92.074% similar) in 1186 aa overlap
(5-1182:1-1155)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
: .....: .....: .....: .....: .....: .....:
gi|142 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
: .....: .....: .....: .....: .....: .....:
gi|142 VLGGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
: .....: .....: .....: .....: .....: .....:
gi|142 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
: .....: .....: .....: .....: .....: .....:
gi|142 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHLL
: .....: .....: .....: .....: .....: .....:
gi|142 TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHLL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
: .....: .....: .....: .....: .....: .....:
gi|142 MDILNSITIIYTDHARGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
: .....: .....: .....: .....: .....: .....:
gi|142 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
      360     370     380     390     400     410

```

```

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNFIASDSITQIIPA
: .....: .....: .....: .....: .....: .....:
gi|142 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNFIIPSSQITQIPL
      420     430     440     450     460     470

```

```

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHPSTSTRYRVRVRYAS
: .....: .....: .....: .....: .....: .....:
gi|142 TKSTNLGSGTSSVVKPGFTGGDILLRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

```

```

540     550     560     570     580     590
Cry1Ac VTPIHLLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
: .....: .....: .....: .....: .....: .....:
gi|142 TTNLQFHTSIHGRPINQGNFSATMSSGNSLQSGSFRHLGFTTFFNFSNGSSVFTLSAHVF

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540      550      560      570      580      590
Cry1Ac  SGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . .
gi|142  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
600      610      620      630      640      650
Cry1Ac  VTYLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
. . . . .
gi|142  VECLSDDEFCLDEKRELSKVKHANGLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660      670      680      690      700      710
Cry1Ac  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK
. . . . .
gi|142  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLIRYNAK
720      730      740      750      760      770
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLD
. . . . .
gi|142  HETVNVPGTGSWPLSAPSPIGK-----AHSHHFFSLD
780      790      800      810      820      830
Cry1Ac  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
. . . . .
gi|142  IDVGCTDLNEDLGVWVIFKIKTQDGHARLGLLEFLLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELSVIP
. . . . .
gi|142  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDVEEQNNQRSVLPV
. . . . .
gi|142  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVDVEEQNNHRSVLPV
960      970      980      990      1000     1010
Cry1Ac  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGECVTIHEIENNTDELKFSNCEEIYPNN
. . . . .
gi|142  EWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGTGCVTIHEIENNTDELKFSNCEEVYPNN
1020     1030     1040     1050     1060     1070
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEN
. . . . .
gi|142  TVTCNDYTATQEEYGGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCEEN
1080     1090     1100     1110     1120     1130
Cry1Ac  RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
. . . . .

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gi|142  RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1110     1120     1130     1140     1150
>>gi|40255|emb|CAA28405.1| unnamed protein product [Baci (1155 aa)
initn: 6320 init1: 3174 opt: 4476 Z-score: 5268.7 bits: 986.8 E(): 0
Smith-Waterman score: 6670; 86.594% identity (91.906% similar) in 1186 aa overlap
(5-1182:1-1155)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
. . . . .
gi|402  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
. . . . .
gi|402  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
. . . . .
gi|402  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
. . . . .
gi|402  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
180     190     200     210     220     230
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSRSPHL
. . . . .
gi|402  TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSRSPHL
240     250     260     270     280     290
Cry1Ac  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
. . . . .
gi|402  MDILNSITITYTDAHRGEYYWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
300     310     320     330     340     350
Cry1Ac  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPO
. . . . .
gi|402  GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPO
360     370     380     390     400     410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
. . . . .
gi|402  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL
420     430     440     450     460     470
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS
. . . . .

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Cry1Ac  GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPQ
gi|402  GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPQ
          360          370          380          390          400          410

          430          440          450          460          470          480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|402  NNNVPPRQGFSHRLSHVSMFRSGFNSVSIIRPPMFSWIHRSAEFNNIIPSSQITQIPL
          420          430          440          450          460          470

          490          500          510          520          530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|402  TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
          480          490          500          510          520          530

          540          550          560          570          580          590
Cry1Ac  VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|402  TTNLQLHTSIDGRIINQGNFSATMSSGNSLQSGSFRIVGFTTPFNFSNGSSVFTLSAHVF
          540          550          560          570          580          590

          600          610          620          630          640          650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNL
gi|402  NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
          600          610          620          630          640          650

          660          670          680          690          700          710
Cry1Ac  VTYLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|402  VECLSDPEFLDDEKRELSKVKHAKRLSDERNLLQDPNFRGILNRQLDRGWRGSTDITIQGG
          660          670          680          690          700          710

          720          730          740          750          760          770
Cry1Ac  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYSIRYNK
gi|402  DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSDLEIYLIRYNK
          720          730          740          750          760          770

          780          790          800          810          820          830
Cry1Ac  HETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRDGEKCAHSHHFLSLD
gi|402  HETVNVPGTGLWRLSAPSIGK-----AHSHHFLSLD
          780          790          800

          840          850          860          870          880          890
Cry1Ac  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRDKRE
gi|402  IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRDKRE
          810          820          830          840          850          860

          900          910          920          930          940          950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPPELSVIP
gi|402  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPPELSVIP
          870          880          890          900          910          920

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          960          970          980          990          1000          1010
Cry1Ac  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVP
gi|402  GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNHRSVLVVP
          930          940          950          960          970          980

          1020          1030          1040          1050          1060          1070
Cry1Ac  EWEAEVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
gi|402  EWEAEVSQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNN
          990          1000          1010          1020          1030          1040

          1080          1090          1100          1110          1120          1130
Cry1Ac  TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPCFEN
gi|402  TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSVVPADYASAYEEKAYTDGRRDNPESN
          1050          1060          1070          1080          1090          1100

          1140          1150          1160          1170          1180
Cry1Ac  RGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|402  RGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1110          1120          1130          1140          1150

>>gi|34426441|gb|AAQ70694.1| Sequence 4 from patent US 5 (1155 aa)
initn: 6311 initl: 3174 opt: 4467 Z-score: 5258.1 bits: 984.9 E(): 0
Smith-Waterman score: 6661; 86.509% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)

          10          20          30          40          50          60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|344  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10          20          30          40          50

          70          80          90          100          110          120
Cry1Ac  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|344  VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
          60          70          80          90          100          110

          130          140          150          160          170          180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|344  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120          130          140          150          160          170

          190          200          210          220          230          240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGGPDSRDWIRYNQFREL
gi|344  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGGPDSRDWIRYNQFREL
          180          190          200          210          220          230

          250          260          270          280          290          300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
gi|344  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHL
          240          250          260          270          280          290

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          310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|344 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPPQ
gi|344 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPPQ
          360      370      380      390      400      410

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|344 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
          420      430      440      450      460      470

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|344 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
          480      490      500      510      520      530

          540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSSLGNIV--GVRNF
gi|344 TTNLQFHTSIDGRPIQGNFSATMSSGNSLQSGSFRTVGFPTTFNFNSGSSVFTLSAHVF
          540      550      560      570      580      590

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|344 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
          600      610      620      630      640      650

          660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
gi|344 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPMFRGINRQLDRGWRGSTDITIQGG
          660      670      680      690      700      710

          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|344 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
          720      730      740      750      760      770

          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHHSFLD
gi|344 HETVNVPGTGSWPLSAPSPIGK-----AHHSHHHSFLD
          780      790      800

          840      850      860      870      880      890
Cry1Ac IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
gi|344 IDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRE
          810      820      830      840      850      860

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          900      910      920      930      940      950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
gi|344 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELSVIP
          870      880      890      900      910      920

          960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSVLVVP
gi|344 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNHRSVLVVP
          930      940      950      960      970      980

          1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSQEVVPCPRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN
gi|344 EWEAEVSQEVVPCPRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN
          990      1000      1010      1020      1030      1040

          1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPCFN
gi|344 TVTCNDYATQEEYEGTYTSRNRGYDGYESNSSVPADYASAYEEKAYTDGRRDNPESN
          1050      1060      1070      1080      1090      1100

          1140      1150      1160      1170      1180
Cry1Ac RGYRDYTPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|344 RGYDYPPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
          1110      1120      1130      1140      1150

>>gi|593702|gb|AAA55309.1| Sequence 1 from Patent EP 033 (1155 aa)
initn: 6309 init1: 3136 opt: 4465 Z-score: 5255.7 bits: 984.4 E(): 0
Smith-Waterman score: 6659; 86.256% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|593 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|593 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|593 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|593 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
          180      190      200      210      220      230

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                250      260      270      280      290      300
Cry1Ac  TLTVLDIIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGFSFRGSAQGIIEGSIIRSPHL
gi|593  TLTVLDIIVALFPNYSRRYPPIRTVSQLTREIYTNVLENFDGFSFRGSAQGIERSIRSPHL
                240      250      260      270      280      290

                310      320      330      340      350      360
Cry1Ac  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQRIVAQLGQ
gi|593  MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQRIVAQLGQ
                300      310      320      330      340      350

                370      380      390      400      410      420
Cry1Ac  GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIIPPQ
gi|593  GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIIPPQ
                360      370      380      390      400      410

                430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|593  NNNVPPRQGFShRLSHVSMFRSGFSNSsvSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL
                420      430      440      450      460      470

                490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYrvrvRYAS
gi|593  TKSTNLGSGTsvvKGPgFTGGDILRRTSPGQISTLrVNITAPL----SQRYrvRIRYAS
                480      490      500      510      520      530

                540      550      560      570      580      590
Cry1Ac  VTIHLNVNWGNSSIFSNtVpATATSLDNLQSSDFgyFESANAFtSSLGNIV---GVRNF
gi|593  TTNLQFHtSIDGRPinQGNfSATmSSGNLQSGSFrtVgFTTPFNfNSGNSSVfTLsAHVf
                540      550      560      570      580      590

                600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYnLERAQKAVNALFTSTnQLGLKtNVTDYHIDQVSNL
gi|593  NSGNEVYIDRIEFVPAEVTfEAeYDLERAQKAVNELFTSSnQIGLkTDVTDYHIDQVSNL
                600      610      620      630      640      650

                660      670      680      690      700      710
Cry1Ac  VTyLsDEfCLDEKkRElSEKvKHAKRLSDERNLLQDSnFKDInRQPERGwGGSgtITIQGG
gi|593  VECLsDEfCLDEKkRElSEKvKHAKRLSDERNLLQDPnFRGINRQLDRGWRGStDITIQGG
                660      670      680      690      700      710

                720      730      740      750      760      770
Cry1Ac  DDVfKEnYvTLlSGTfDECyPTyLYQKIDESklKAFtRYQLRgyIEDsQDLeySIRYNAK
gi|593  DDVfKEnYvTLlSGTfDECyPTyLYQKIDESklKAYtRYQLRgyIEDsQDLeyLIRYNAK
                720      730      740      750      760      770

                780      790      800      810      820      830
Cry1Ac  HETVnVpGTGSLwPLsAQSPiGKCGEPnRCAPhLEWnPDLCsCRDgEKCAHSHHfSLD
gi|593  HETVnVpGTGSLwPLsAPSPiGK-----AHSHHfSLD

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                780      790      800
Cry1Ac  IDVGCTDLNEDLGVVWIFKIKTQDGhARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
gi|593  IDVGCTDLNEDLGVVWIFKIKTQDGhARLGNLEfLEEKPLVGEALARVKRAEKkWRDKRE
                810      820      830      840      850      860

                900      910      920      930      940      950
Cry1Ac  KLEWETnIVyKEAKESVDALfVNSQYDQLQADtNIAMIHAADKRVHSIREAYLPELSVIP
gi|593  KLEWETnIVyKEAKESVDALfVNSQYDRLQADtNIAMIHAADKRVHSIREAYLPELSVIP
                870      880      890      900      910      920

                960      970      980      990      1000      1010
Cry1Ac  GVNAAIfEELEGRIFtAFSLYDARNVIKNGDFnNGLsCWnVKGHVDVEEQNNQRsvLVVp
gi|593  GVNAAIfEELEGRIFtAFSLYDARNVIKNGDFnNGLsCWnVKGHVDVEEQNNHRSvLVVp
                930      940      950      960      970      980

                1020      1030      1040      1050      1060      1070
Cry1Ac  EWEAEVsqEVRvCPGRgyILRvtAYKEgyGEGCVtIHEIENntDELKfSNcVVEEIPYnN
gi|593  EWEAEVsqEVRvCPGRgyILRvtAYKEgyGEGCVtIHEIENntDELKfSNcVVEEIPYnN
                990      1000      1010      1020      1030      1040

                1080      1090      1100      1110      1120      1130
Cry1Ac  TVTCNDYtVnQEEYGGAYtSRnRGYNEA----PSVPADYASVYEEKSYtDGRRENpCEFN
gi|593  TVTCNDYtATQEEYEGTYtSRnRGYDGAYESnSSVPADYASAYEEKAYtDGRRDnPCESN
                1050      1060      1070      1080      1090      1100

                1140      1150      1160      1170      1180
Cry1Ac  RgyRdytPLpVgyVtKEleyfPpETDKVWIEIGETEGtFIVDSVellLMEE
gi|593  RgyRdytPLpAGyVtKEleyfPpETDKVWIEIGETEGtFIVDSVellLMEE
                1110      1120      1130      1140      1150

>>gi|1608054|gb|AAB11009.1| Sequence 19 from patent US 5 (1155 aa)
  initn: 6303 init1: 3136 opt: 4459 Z-score: 5248.7 bits: 983.1 E(): 0
Smith-Waterman score: 6653; 86.172% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)

                10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|160  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
                10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|160  VLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
                60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLlSVYVQAANLHLSVLRDVS
gi|160  WEADPTNPALREEMRIQfNDMNSALtTAIPLFAVQNYQVPLlSVYVQAANLHLSVLRDVS

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120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|160 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180      190      200      210      220      230
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL
gi|160 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290      300
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|160 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310      320      330      340      350      360
Cry1Ac GVYRTLSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
gi|160 GVYRTLSTLYRRPFPNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
370      380      390      400      410      420
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|160 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
430      440      450      460      470      480
Cry1Ac VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|160 TKSTNLGSGTSVVKPGPFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVIRYAS
490      500      510      520      530
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
gi|160 TTNLQFHTSIDGRPINQGNFASATMSSGSNLQSGSPRTVGFTTTPFNFSNGSSVFTLSAHVF
540      550      560      570      580      590
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|160 NSGNEVYIDRIEFVPAEVTFFAEYDLERAQKAVNELFTSSNIIGLKTVDVTDYHIDRVSNL
600      610      620      630      640      650
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDQSNFKDINRQPERGWGGSTGITIQGG
gi|160 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDQPNFRGINRQDRGWRGSTDITIQGG
660      670      680      690      700      710
Cry1Ac DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
gi|160 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK

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gi|160 DDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720      730      740      750      760      770
Cry1Ac HETVNVPGTGSWLPESAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
gi|160 HETVNVPGTGSWLPESAPSPIGK-----AHSHHFFSLD
780      790      800      810      820      830
Cry1Ac IDVGCTDLNEDLGVWVIFIKIQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|160 IDVGCTDLNEDLGVWVIFIKIQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
840      850      860      870      880      890
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
gi|160 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYLPELSVIP
900      910      920      930      940      950
Cry1Ac GVNAAIFEELEGRIFTFASLYDARNVIKNGDFNNGLSWVKGHVDEEQQNQRSVLVVP
gi|160 GVNAAIFEELEGRIFTFASLYDARNVIKNGDFNNGLSWVKGHVDEEQQNHRSVLVVP
960      970      980      990      1000      1010
Cry1Ac EWEAEVSVQEVVPCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
gi|160 EWEAEVSVQEVVPCPRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEYIPNN
1020      1030      1040      1050      1060      1070
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPCEFN
gi|160 TVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRNDPCESN
1080      1090      1100      1110      1120      1130
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|160 RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1140      1150      1160      1170      1180
>>gi|5973537|gb|AAE12817.1| Sequence 19 from patent US 5 (1155 aa)
initn: 6303 init1: 3136 opt: 4459 Z-score: 5248.7 bits: 983.1 E(): 0
Smith-Waterman score: 6653; 86.172% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)
10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|597 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50
Cry1Ac VLGLVDIIWGIQFSPQWDAFLVQIEQLINQRIEAFARNQAIISRLGSLNLYQIYAESFRE

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gi|161 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      70      80      90      100     110     120
gi|161 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|161 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
      190     200     210     220     230     240
gi|161 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
      250     260     270     280     290     300
gi|161 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      310     320     330     340     350     360
gi|161 MDILNSITTYTDAHRGYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEIP PQ
      370     380     390     400     410     420
gi|161 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLP SAVA YRKS GTVDSLDEIP PQ
      360     370     380     390     400     410
Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IASDSITQIPA
      430     440     450     460     470     480
gi|161 NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNI IPSSQITQIPL
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490     500     510     520     530
gi|161 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVRNF
      540     550     560     570     580     590
gi|161 TTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTTFFNFSSGSSVFTLSAHVF
      540     550     560     570     580     590
Cry1Ac
      600     610     620     630     640     650

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Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .. : ..... : ..... : ..... : ..... : ..... : ..... : .....
gi|161 NSGNEVYIDRIEFVPAEVTFEAYDLERAQKAVNELFTSSNQIGLKTVDYHIDRVSNL
      600     610     620     630     640     650
Cry1Ac
      660     670     680     690     700     710
Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      : ..... : ..... : ..... : ..... : ..... : .....
gi|161 VECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660     670     680     690     700     710
Cry1Ac
      720     730     740     750     760     770
Cry1Ac DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK
      : ..... : ..... : ..... : ..... : ..... : .....
gi|161 DDVFKENYVTLTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYNAK
      720     730     740     750     760     770
Cry1Ac
      780     790     800     810     820     830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHSHFLSD
      : ..... : ..... : ..... : ..... : .....
gi|161 HETVNVPGTGSWLPLSAPSPIGK-----AHSHHSHFLSD
      780     790     800
Cry1Ac
      840     850     860     870     880     890
Cry1Ac IDVGCTDLNEDLGVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      : ..... : ..... : ..... : ..... : .....
gi|161 IDVGCTDLNEDLGVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
      810     820     830     840     850     860
Cry1Ac
      900     910     920     930     940     950
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADRKHVSIREAYLPELSVIP
      : ..... : ..... : ..... : ..... : .....
gi|161 KLEWETNIVYKEAKESVDALFVNSQYDRQLQADTNIAMIHAAADRKHVSIREAYLPELSVIP
      870     880     890     900     910     920
Cry1Ac
      960     970     980     990     1000    1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHVDVEEQNNQRSVLPVVP
      : ..... : ..... : ..... : ..... : .....
gi|161 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHVDVEEQNNHRSVLPVVP
      930     940     950     960     970     980
Cry1Ac
      1020    1030    1040    1050    1060    1070
Cry1Ac EWAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN
      : ..... : ..... : ..... : ..... : .....
gi|161 EWAEVSEQEVRVCPGRGYILRVITAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIPYNN
      990     1000    1010    1020    1030    1040
Cry1Ac
      1080    1090    1100    1110    1120    1130
Cry1Ac TVTCNDYTVNQEYEGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN
      : ..... : ..... : ..... : ..... : .....
gi|161 TVTCNDYATQEEYEGTYTSRNRGYD GAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
      1050    1060    1070    1080    1090    1100
Cry1Ac
      1140    1150    1160    1170    1180
Cry1Ac RGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      : ..... : ..... : ..... : ..... : .....
gi|161 RGYGDYTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1110    1120    1130    1140    1150

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>>gi|5987860|gb|AAE17025.1| Sequence 19 from patent US 5 (1155 aa)
initn: 6303 initl: 3136 opt: 4459 Z-score: 5248.7 bits: 983.1 E(): 0
Smith-Waterman score: 6653; 86.172% identity (91.821% similar) in 1186 aa overlap
(5-1182:1-1155)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|598 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|598 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110 120
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|598 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170 180
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|598 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230 240
Cry1Ac TLTVLDIVLSLFPNYDSRYPPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSIIRSPHL
gi|598 TLTVLDIVLSLFPNYDSRYPPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGSIIRSPHL
240 250 260 270 280 290 300
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|598 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350 360
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
gi|598 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQVDSLDEIIPPQ
360 370 380 390 400 410 420
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|598 NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
420 430 440 450 460 470 480
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|598 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL-----SQRYRVRIRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|598 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNPNFNGSSVFTLSAHVF
540 550 560 570 580 590
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|598 NSGNEVYIDRIEFVPAEVTFEAEYDLERAKAVNELFTSSNQIGLKTVDYDHYIDRVSNL
600 610 620 630 640 650
Cry1Ac VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG
gi|598 VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
660 670 680 690 700 710
Cry1Ac DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
gi|598 DDVFKENYVTLGTFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQDLEIYLIRYNAK
720 730 740 750 760 770
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSLD
gi|598 HETVNVPGTGSWLPLSAPSPIGK-----AHSHHFLSLD
780 790 800
Cry1Ac IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
gi|598 IDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
810 820 830 840 850 860
Cry1Ac KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
gi|598 KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHSIREAYLPELSVIP
870 880 890 900 910 920
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNHRSVVLVVP
gi|598 GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVVEEQNNHRSVVLVVP
930 940 950 960 970 980
Cry1Ac EWEAEVVSQEVVRCVGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIIYPNN
gi|598 EWEAEVVSQEVVRCVGRGYILRVTAKEGYGEGCVTTHEIENNTDELKFSNCVVEEIVPNN
990 1000 1010 1020 1030 1040
Cry1Ac TVTCNDYTVNQBEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPECFN
gi|598 TVTCNDYATQBEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPCESN
1050 1060 1070 1080 1090 1100



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          990      1000      1010      1020      1030      1040
Cry1Ac 1080      1090      1100      1110      1120      1130
TVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPVADYASVYEEKSYTDGRRENPECFNRGRY
gi|131 TVTCKIILRLKKNMRVRTLLVIEDMTEPMKAILLYQLIMHQPMKKKHIQMDDEETILVNLT
1050      1060      1070      1080      1090      1100

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>>gi|46409861|gb|AAS93798.1| cry1A type crystal protein (793 aa)
  initn: 4403 initl: 3041 opt: 4399 Z-score: 5180.3 bits: 969.9 E(): 0
Smith-Waterman score: 4399; 84.693% identity (92.221% similar) in 797 aa overlap
(13-805:2-793)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|464 MQCVPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40
Cry1Ac 70      80      90      100      110      120
VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|464 VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRA
50      60      70      80      90      100

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          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|464 WEADPTNPALRVEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
110      120      130      140      150      160
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|464 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
170      180      190      200      210      220

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          250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNPNVLEDFNGSFRGSAQGIQIRSPHL
gi|464 TLTVLDIVSLFPNYSRTPYPIRTVSQTLTREIYTNPNVLEDFNGSFRGSAQGIQIRSPHL
230      240      250      260      270      280

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          310      320      330      340      350      360
Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|464 MDILNSITTYTDAHRGYYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
290      300      310      320      330      340
Cry1Ac 370      380      390      400      410      420
GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPQ
gi|464 GVYRTLSSTFYRSPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPQ
350      360      370      380      390      400

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          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|464 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL

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          410      420      430      440      450      460
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|464 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVINITAPL-----SQRYRVRIRYAS
470      480      490      500      510      520

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          540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWGNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|464 TTNLQFHSTIDGRPINQGNFSATMSSGNSLQSGSFRTAGFTTFFNFNNGSSVFTLSAHVF
530      540      550      560      570      580

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          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|464 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNALFTSSNQIGLKTDTVTDYHIDQVSNL
590      600      610      620      630      640

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          660      670      680      690      700      710
Cry1Ac VTLYSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWSTGITIQQG
gi|464 VECLSDEFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRWINRQLDRGWRGSTDITIQQG
650      660      670      680      690      700

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          720      730      740      750      760      770
Cry1Ac DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLSIRYNAK
gi|464 DDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLSIRYNAK
710      720      730      740      750      760

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          780      790      800      810      820      830
Cry1Ac HETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLD
gi|464 HETVNVPGTGSWLPLSAQSPIGRCGEPNR
770      780      790

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>>gi|42717976|gb|AAS38435.1| cry1AcAT modified toxin [sy (675 aa)
  initn: 4379 initl: 4379 opt: 4379 Z-score: 5157.8 bits: 965.5 E(): 0
Smith-Waterman score: 4379; 98.370% identity (98.963% similar) in 675 aa overlap
(5-679:1-675)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|427 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50

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          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|427 VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
60      70      80      90      100      110

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          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|427 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|427 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|427 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|427 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRILSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKSGTVDLDEIIPPQ
gi|427 GVYRILSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKSETVDSLDEIIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|427 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420      430      440      450      460      470

490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|427 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480      490      500      510      520      530

550      560      570      580      590      600
Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|427 TPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|427 GVIIDRFEFIPVTATLEAEYNRERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
600      610      620      630      640      650

670      680      690      700      710      720
Cry1Ac SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTIQGGDDVF
gi|427 SDEFCLDEKRELSEKVKHA
660      670

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>>gi|27447986|gb|AAO13756.1|AF288683_1 delta-endotoxin C (1169 aa)
initn: 4513 initl: 3108 opt: 4365 Z-score: 5137.7 bits: 962.6 E(): 0

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Smith-Waterman score: 5055; 66.134% identity (82.773% similar) in 1190 aa overlap
(5-1182:1-1169)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|274 MEIN-NQNQCVPYNCLNPNPESEILNVA-IFSSEQVAEIHKLITRILELFLPGGSF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFRE
gi|274 AFGLFDLIWGFNEDQWSAFLRQVEELINQRITFARGQAIQRLVGFGRSYDEYILALKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|274 WENDPDNPASKERVRTRFRRTDDALLTGVPVLPMAIPGFELATLSVYAQSANLHLLLRDAV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|274 FFGERGLTQTNTINDLYSRKNSIRDYTNHCVRFYNIGL----GNLNVIRPEYYRQREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|274 TISVLDLVALFPNYDIRTYPIPTKSQLTREIYTDPIIS--PGAQAGYT--LQDVLREPHL
240     250     260     270     280

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|274 MDFLNRLIIYTGEGYRIRHWAGHEVESSRTGMM-TNIRFPLYGTAATAEPTRFITPSTFP
290     300     310     320     330     340

370     380     390     400     410
Cry1Ac GV--YRILSSTLYR-RPFNIGINNQLSVLDGTEFAYGTSSNLP SAVYRKSGTVDLDE
gi|274 GLNLFYRILSAPIFRDEPGANIIIRYRTSLVEGVGFI--QPNGEQLYRVRGTLDSLQ
350     360     370     380     390     400

420     430     440     450     460     470
Cry1Ac IPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSIT
gi|274 LPLEGESSLTE--YSHRLCHVRFAQSLRNAEPLDYARVPMFSWTHRSATPTNTIDPDVIT
410     420     430     440     450     460

480     490     500     510     520     530
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
gi|274 QIPLVKAFNLHSGATVVRGPGFTGGDILRRTNAGNFGDMRVNITAPL----SQRYRVRV
470     480     490     500     510

540     550     560     570     580     590
Cry1Ac RYASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VG

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gi|274 520 530 540 550 560 570
Cry1Ac 600 610 620 630 640 650
VRNFSGTAGVILDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
gi|274 580 590 600 610 620 630
AFSFSNNNEVYIDRIEFVPAEVTTFATESDQDRAQKAVNALFTSSNQIGLKTQVNTYHIDQ
Cry1Ac 660 670 680 690 700 710
VSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGIT
gi|274 640 650 660 670 680 690
VSNLVECLSDEFCLDEKRELSKVKHAKRLCDERNLLQDPNFRGNRREPDRGWRGSTDIT
Cry1Ac 720 730 740 750 760 770
IQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIR
gi|274 700 710 720 730 740 750
IQRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSDLEIYLIR
Cry1Ac 780 790 800 810 820 830
YNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSH
gi|274 760 770 780 790 800 810
YNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCATHLEWNPDLDCSCRDGKCAHSHSH
Cry1Ac 840 850 860 870 880 890
FSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLFLLEEKPLVGEALARVKRAEKKWR
gi|274 820 830 840 850 860 870
FSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLFLLEEKPLVGEALARVKRAEKKWR
Cry1Ac 900 910 920 930 940 950
DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPEL
gi|274 880 890 900 910 920 930
DKREKLELETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPEL
Cry1Ac 960 970 980 990 1000 1010
SVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSV
gi|274 940 950 960 970 980 990
SVIPGVNAAIFEELEGRIFTAYSLSYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNHRSV
Cry1Ac 1020 1030 1040 1050 1060 1070
LVVPEWEAEVSVQEVRCVPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEEI
gi|274 1000 1010 1020 1030 1040 1050
LVVPEWEAEVSVQEVRCVPGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKFSNCVEEEI
Cry1Ac 1080 1090 1100 1110 1120
YPNNTVTCNDYTVNQEEYGAYTSRNRGYNEA---PSPVADYASVYEEKSYTDGRENPE
gi|274 1060 1070 1080 1090 1100 1110
YPNNTVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNT
1130 1140 1150 1160 1170 1180

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Cry1Ac CEFNRYGRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|274 CESNRYGDDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120 1130 1140 1150 1160
>>gi|4097876|gb|AAD10291.1| insecticidal crystal protein (1169 aa)
initn: 4499 initl: 3094 opt: 4351 Z-score: 5121.2 bits: 959.6 E(): 0
Smith-Waterman score: 5041; 65.966% identity (82.689% similar) in 1190 aa overlap
(5-1182:1-1169)
Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|409 MEIN-NQNQCVPYNCLNPNESIELNVA-IFSSEQVAEIHKITRILILENFLPGGSF
10 20 30 40 50
Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|409 AFGLFDLIWIGIFNEDQWSAFLRQVEELINQRIEFAFGQAIQRLVGFGRSYDEYILALKE
60 70 80 90 100 110
Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|409 WENDPDNPASKERVTRFRRTDDALLTGVPMAIPGFELATLSVYAQSANLHLLLRDAV
120 130 140 150 160 170
Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|409 FFGERWGLTQTNINDLYSRLKNSIRDYTNHCVRVFNIGL---GNLNVIRPEYRFQREL
180 190 200 210 220 230
Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHPL
gi|409 TISVLDLVALFPNYDIRTYPIPTKSQLTREIYTDPIIS--PGAQAGYT--LQDVLREPHL
240 250 260 270 280
Cry1Ac 310 320 330 340 350 360
MDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
gi|409 MDFLNRLIITYTGEYRGIRHWAGHEVSSRTGMM-TNIRFPLYGTAATAEPTRFITPSTFP
290 300 310 320 330 340
Cry1Ac 370 380 390 400 410
GV---YRSLSTLYR-RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYKSGTVDSLDE
gi|409 GLNLFYRSLSAPIFRDEPGANIIRYRSLVEGVGFI---QPNGEQLYRVRGTLDSLQDQ
350 360 370 380 390 400
Cry1Ac 420 430 440 450 460 470
IPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSIT
gi|409 LPLGESSLITE--YSHRLCHVRFQAQSLRNAEPLDYARVPMFVSWTHRSATPTNTIDPDVIT
410 420 430 440 450 460
480 490 500 510 520 530

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Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV  
gi|409 QIPLVKAFNLHSGATVVRGPGFTGGDILRRTNAGNFGDMRVNITAPL----SQRYRVRI  
470 480 490 500 510

540 550 560 570 580 590  
Cry1Ac RYASVTPHILNWNWGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VG  
gi|409 RYASTANLQFHTSINGRAINQANFPATMNSGENLQSGSFRVAGFTTPTTFSDALSTFTTIG  
520 530 540 550 560 570

600 610 620 630 640 650  
Cry1Ac VRNFGSTAGVVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ  
gi|409 AFSFSSNNEVYIDGIEFVPAEVTFATESDQDRAQKAVNALFTSSNQIGLKTVDVTNYHIDQ  
580 590 600 610 620 630

660 670 680 690 700 710  
Cry1Ac VSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGIT  
gi|409 VSNLVECLSDEFCLDEKRELSKVKHAKRLCDERNLLQDPNFRGINREPDGRGWRGSTDIT  
640 650 660 670 680 690

720 730 740 750 760 770  
Cry1Ac IQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIR  
gi|409 IQRGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIYLIR  
700 710 720 730 740 750

780 790 800 810 820 830  
Cry1Ac YNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDDLDCSCRDGEKCAHSHSH  
gi|409 YNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCATHLEWNPDDLDCSCRDGEKCAHSHSH  
760 770 780 790 800 810

840 850 860 870 880 890  
Cry1Ac FSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLFLEEKPLVGEALARVKRAEKKWR  
gi|409 FSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLFLEEKPLVGEALARVKRAEKKWR  
820 830 840 850 860 870

900 910 920 930 940 950  
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPEL  
gi|409 DKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSIREAYLPEL  
880 890 900 910 920 930

960 970 980 990 1000 1010  
Cry1Ac SVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSV  
gi|409 SVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNHRSV  
940 950 960 970 980 990

1020 1030 1040 1050 1060 1070  
Cry1Ac LVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGECVTHIEIENNTDELKFSNCEVEEII  
gi|409 LVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGECVTHIEIEDNTDELKFSNCEVEEII  
1000 1010 1020 1030 1040 1050

1080 1090 1100 1110 1120  
Cry1Ac YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRREN  
gi|409 YPNNTVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNT  
1060 1070 1080 1090 1100 1110

1130 1140 1150 1160 1170 1180  
Cry1Ac CEFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|409 CESNRGYGDTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
1120 1130 1140 1150 1160

>>gi|296087|emb|CAA80236.1| crystal protein [Bacillus th (1172 aa)  
initn: 4000 init1: 3055 opt: 4295 Z-score: 5055.1 bits: 947.3 E(): 0  
Smith-Waterman score: 5101; 66.360% identity (82.678% similar) in 1195 aa overlap  
(5-1182:1-1172)

10 20 30 40 50  
Cry1Ac CMQAMDNPNININECIPYNCLSNPEVEVLGGERIETGYTP--IDISLSLTQFLLESEFVPGA  
gi|296 MEIINNQNQYVYPYNCLSNPENEIILDIESLSSRSREQVAEISLGLTRFLLESLLPGA  
10 20 30 40 50

60 70 80 90 100 110  
Cry1Ac GFVLGLVDI IWGIFGSPQWDAFLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESF  
gi|296 SPGFALFDI IWGVIGPDQWNLFLAQIEQLIDQRIEAHVNRNQAISRLEGLGDSVEVYIESL  
60 70 80 90 100 110

120 130 140 150 160 170  
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD  
gi|296 REWEASPNNEALQDDVRNRFNSNTDNALITAIPILREQGFEIPLLSVYVQAANLHLSLLRD  
120 130 140 150 160 170

180 190 200 210 220 230  
Cry1Ac VSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFRR  
gi|296 AVYFGQRWGLDVTVVNHNRLINLINTYSDHCAQWFNRLDNDFFGGVSAR---YLDQFR  
180 190 200 210 220 230

240 250 260 270 280 290  
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQGLEGSIRSP  
gi|296 EVTISVLDIVSLFPNYDIRTYPISTQSQLTREIYTSVPAEP-GASLNANLQNI---LREP  
240 250 260 270 280

300 310 320 330 340 350  
Cry1Ac HLMDDLNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTmgNAApQRIVAQL  
gi|296 HLMDFLTRIVITYGQSGIYHWAGHEISSRTTGNLSNIQFPlyGTAAADRAFNMNIHH  
290 300 310 320 330 340

360 370 380 390 400 410  
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPFA--VYRKSgtVdSLDE  
gi|296 SETIYRTLSAPIY--SVSGGISPNRTRVVEGVRFLIARDNNLDSLpFLYRKEgtLdSFTE  
350 360 370 380 390 400

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420      430      440      450      460      470
Cry1Ac IPPQNNVPPRQGFHSHRLSHVSMFRSGFSNSVSIIRAPMFVSWIHRSAEFNNIIASDSIT
gi|296 LPPPEDESTPPYIGYSHRLCHARFARSPVILEPSNFARLPVFSWTHRSASPTNEVSPSRIT
410      420      430      440      450      460

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480      490      500      510      520      530
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYRV
gi|296 QIPWVKAHTLASGASVIGKPGFTGGDIMTRNN--INLGDGLTLRVTVTGRLPQS--YYI
470      480      490      500      510      520

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540      550      560      570      580      590
Cry1Ac RVRYASVTPIHNLNVNNGNSSIFSNTV-PATATSLDNLQSSDFGYFESANAFSTSSLGNIVG
gi|296 RLRYSASV-----NSSGVFRHLPPQPSYGISFPRTMGTDLEPLTSSRFALTTLFTPTITL
530      540      550      560      570

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600      610      620      630      640
Cry1Ac VR-----NFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTD
gi|296 TRAQEEFNLTIPRGVYIDRIEFPVVDATFEAGYDLERAKAVNALFTSTNQRGLKTDITD
580      590      600      610      620      630

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650      660      670      680      690      700
Cry1Ac YHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGG
gi|296 YHIDQVSNLVECLDEFCLDEKRELSEKVKHAKRLSDGRNLLQDRNFISINGLLDRGWGR
640      650      660      670      680      690

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710      720      730      740      750      760
Cry1Ac STGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLE
gi|296 STDITIQGSDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLE
700      710      720      730      740      750

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770      780      790      800      810      820
Cry1Ac IYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCA
gi|296 IYLIRYNAKHEIVNVPGTGLWPLSVENSIGPCGESNRCAPHLEWNPDLDCSCRDGEKCA
760      770      780      790      800      810

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830      840      850      860      870      880
Cry1Ac HHSHHFSLDIDVGCDDLNLGVLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
gi|296 HHSHHFSLDIDVGCDDLNLGVLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
820      830      840      850      860      870

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890      900      910      920      930      940
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREA
gi|296 EKKWRDKRKKLEFETNIVYKEAKESVDALFVNSQYDKLADTNIAAMIHAADKRVHRIREA
880      890      900      910      920      930

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950      960      970      980      990      1000
Cry1Ac YLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSLSCWNVKGHVDVEEQN
gi|296 YLPELSVIPGVNADIFEELEGRIFTAFSLYDARNVIKNGDFNNGLLSCWNVKGHVDVEEQN
940      950      960      970      980      990

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1010      1020      1030      1040      1050      1060
Cry1Ac NQRSVLVPEWEAEVQSEVVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIENNDELKFSNC
gi|296 NHRSVLVPEWEAEVQSEVVRVCPGRGYILRVYAYKEGYGEGCVTTHIEIEDNDELKFSNC
1000      1010      1020      1030      1040      1050

```

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1070      1080      1090      1100      1110      1120
Cry1Ac VEEIIPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDG
gi|296 VEEEVYPSNTVTCNDYTANQEEYEGTYTSRNRQGYDEAYESNSSVPPANYASVYEEKAYTDG
1060      1070      1080      1090      1100      1110

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1130      1140      1150      1160      1170      1180
Cry1Ac RRENPCFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGFFIVDSVELLMEE
gi|296 RRENPCFNRYRDTPLPAGYVTKELEYFPGTAKVWIEIGETEGFFIVDSVELLMEE
1120      1130      1140      1150      1160      1170

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>>gi|45387401|gb|AAS60191.1| crystal protein [Bacillus t (1170 aa)
initn: 4524 init1: 2478 opt: 4209 Z-score: 4953.7 bits: 928.6 E(): 0
Smith-Waterman score: 4974; 64.815% identity (81.987% similar) in 1188 aa overlap
(5-1182:1-1170)

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10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTP--IDISLSLQFLLSEFVPGA
gi|453 MDNPNKIQECIPYNCLNPESEILDIEGLSTRSREQVAEISLGLTRFLEENLFPGA
10      20      30      40      50

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60      70      80      90      100      110
Cry1Ac GFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESF
gi|453 TPGFGLFDIIWGFGPSQWDAFLVQIEQLIDQRIETVERNRAIQTILGLSNLYQIYAESF
60      70      80      90      100      110

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120      130      140      150      160      170
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|453 KEWENPNPNASQERVRNRFRITDDALITSIPLLAIPNFEIATLSVYVQAANLHLSVLRD
120      130      140      150      160      170

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180      190      200      210      220      230
Cry1Ac VSVFGRQWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRR
gi|453 AVVFFGRWGLTQINVDLRYRLTNNIRKYSDFHARWYNEGLDNISGLS----RSINFOR
180      190      200      210      220      230

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240      250      260      270      280      290
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSIKSP
gi|453 EVTISVLDIVSLFPNYDIRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSIKSP
240      250      260      270      280      290

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300      310      320      330      340      350
Cry1Ac HLMDDILNSITIIDAHARGEYWSGHQIMASPVGFSGPEFTFPYGTMGNAAPQQRIVAQL
gi|453 HLFDFLEKLVITGDRSGIRHWAGHEITSRRRTDSYHGIIRYPLYGTMAAESPYPYTLALQP
290      300      310      320      330      340

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360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP5A-VYRKSQTVSDLEI
gi|453  SESIYRTLSEPIFSQ--TGGLSPHRRRVVEGVF5IVNINNVPSSVFYRKGSLDSFTL
350      360      370      380      390      400

420      430      440      450      460      470
Cry1Ac  PPQNNNPPRQGF5HRLSHVSMFRSGF5N5SV5IIRAPMFSWIHRS5AEFN5NI5ASDSITQ
gi|453  PPEDESVP5PPY5IG5ISHQLCHVGFGR5TNV5IFEP5SNFAR5VPV5FW5THRSAT5PTNT5IDPDRITQ
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGSVISGPGFTGGDLVRLN5SSGNNI5QRNGYIEVPIH5FP5TS--TRYRVRVR
gi|453  IPSVKASSLRN5TVV5SGPGFTGGDIVRM5GAVHQIYATDLSMN5V---RPSVALSRYLIRLR
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac  YASVTP5IHLNVN5WGN5SIF5SNTVP5PATAT5SLDNLQ5SDFGYF5ESANAF5TSSLGNI--VGVR
gi|453  YACRGSSNIV5IH--GPSIR5FV--SLP5TMSN5DEPLTYQ5SFRYASIT5PITRPIY5NMF5NLSIS
530      540      550      560      570

600      610      620      630      640      650
Cry1Ac  NFSGTAGV5IIDRF5EIPV5TATLEA5EYNL5ERAQKAV5NALF5TSTNQLG5LKT5NVT5DYHIDQV5
gi|453  RISGVQNL5FIDRI5EIPV5DANF5EAERDL5ERAQKAV5NALF5TSTNQR5GLKIDV5TDYHIDQV5
580      590      600      610      620      630

660      670      680      690      700      710
Cry1Ac  NLV5TYLS5DEFCL5DEKREL5SEKVKHAKR5LSDERNL5LQD5NF5KIDINR5QPERG5WG5SG5TITQ
gi|453  NLVDCL5SDEFCL5DEKREL5SEKVKHAKR5LSDERNL5LQD5LNF5KIDINR5QPERG5WG5SG5TITQ
640      650      660      670      680      690

720      730      740      750      760      770
Cry1Ac  GGDDV5FKENY5VTL5SGTF5DECYPT5YLYQKID5ESK5LKA5FTRY5QLR5GYI5ED5SQD5LEI5YIR5YN
gi|453  GGDDV5FKENY5VTL5PGTF5DECYPT5YLYQKID5ESK5LKA5YTRY5QLR5GYI5ED5SQD5LEI5YIR5YN
700      710      720      730      740      750

780      790      800      810      820      830
Cry1Ac  AKHETV5NV5PGT5GSL5WPL5SAQ5SPI5GK5CE5PNR5CAP5HLE5WNP5DL5DC5SCR5DGE5KCA5H5SH5H5F5
gi|453  AKHETV5NV5VPG5GSL5WPL5SV5ESS5VGK5CE5PNR5CAS5RM5EWN5PDL5DC5SCR5DGE5KCA5H5SH5H5F5
760      770      780      790      800      810

840      850      860      870      880      890
Cry1Ac  LDIDV5GCT5DLN5EDL5GVV5VIF5KI5KTQ5DGHAR5LGN5LE5FLE5EK5PLV5GEAL5ARV5KRA5EKK5WR5DK
gi|453  LDIDV5GCT5DLN5EDL5GVV5VIF5KI5KTQ5DGHAK5IGN5LE5FL5EK5LL5GEAL5ARV5KKA5EKK5WR5DK
820      830      840      850      860      870

900      910      920      930      940      950
Cry1Ac  REKLEW5ETN5VY5KEAK5ESVD5AL5FVN5SQY5DQL5QAD5TNI5AMI5HAAD5KRV5HSI5REAY5LPEL5SV
gi|453  RDKLEW5ETN5VY5KEAK5ESVD5AL5FV5DS5QY5SRL5QAD5TNI5AMI5HAAD5KRV5HR5IREAY5LPEL5TV

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880      890      900      910      920      930
Cry1Ac  IPGVNA5AIF5EE5LEGR5IFTA5FSLY5DARN5VIK5NGDF5N5NGL5SC5WN5VK5GH5VD5VE5EQ5NN5QR5SVL5V
gi|453  IPGVNA5SIF5EE5LEGR5IFTA5S5LY5GARN5VIK5NGDF5N5NGL5SC5WN5VK5GH5VE5VQ--QI5H5RS5VL5V
940      950      960      970      980      990

1020     1030     1040     1050     1060     1070
Cry1Ac  VP5EWA5EAV5SQ5EVR5VCP5GR5GYI5LR5VT5AY5KE5GY5G5CV5TI5HE5IEN5NT5DEL5K5FS5NC5VE5E5I5YP
gi|453  VP5SWK5TEV5SQ5EVC5PC5PR5GYI5LR5VT5AY5KE5GY5G5GN5VT5I5HE5IEN5NT5DEL5K5FR5N5CE5E5E5V5YP
1000     1010     1020     1030     1040     1050

1080     1090     1100     1110     1120     1130
Cry1Ac  NNTV5TC5ND5Y5TVN5Q5E5Y5GG5AY5TS5RN5RG5Y5NEA---PSV5PAD5Y5AS5VY5E5K5SY5TD5GR5REN5P5CE
gi|453  NNTV5TC5ND5Y5TVN5Q5E5Y5KG5T5CT5SR5NR5GY5DE5S5S5SE5S5E5S5AY5AS5VY5E5E5K5GY5TD5GR5REN5L5CE
1060     1070     1080     1090     1100     1110

1140     1150     1160     1170     1180
Cry1Ac  FNR5GY5RD5Y5T5PL5PV5GY5V5T5KE5LEY5FP5ET5DK5V5W5IE5IG5ET5EG5TF5IV5DS5V5ELL5LM5EE
gi|453  FNR5GY5GD5Y5T5SL5PT5AY5V5T5KE5LEY5FP5ET5DK5V5W5IE5IG5ET5EG5AF5ILD5S5V5ELL5LM5EE
1120     1130     1140     1150     1160     1170

>>gi|295862|emb|CAA80233.1| crystal protein [Bacillus th (1166 aa)
initn: 4348 initl: 3198 opt: 4205 Z-score: 4949.0 bits: 927.7 E(): 0
Smith-Waterman score: 5099; 67.707% identity (83.474% similar) in 1186 aa overlap
(12-1182:7-1166)

10      20      30      40      50      60
Cry1Ac  CMQAM5DNN5PNINE5CIPY5NCL5SNPE5VE5VL5GGER5IET5GY5TPID5ISL5TQ5FLL5SE5FV5PG5AG5F
gi|295  MEIS5DQ5NQ5YIP5YNCL5NPE5SIE5FN5ARN5SN5FGL5VS--QV5SSGL5TR5FL5LEA5AV5PE5AG5F
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGL5VD5II5WG5IF5GPS5QW5DA5FL5V5QIE5QLIN5QR5IE5EF5ARN5QA5ISR5LE5GL5SN5LY5QI5YAE5S5FRE
gi|295  ALGL5FD5II5WG5AL5G5VD5QW5SL5FL5R5QIE5QLIR5QE5ITEL5ERN5R5ATA5ILT5GL5SS5YN5LY5VE5AL5RE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEAD5PT5NP5AL5RE5EM5RI5Q5F5ND5M5NS5ALT5TA5I5PL5FA5V5Q5NY5Q5V5PL5S5VY5QA5AN5L5HL5SL5RD5V5
gi|295  WEND5PN5NP5AS5Q5ER5V5TR5FR5L5T5DD5A5IV5T5GL5PT5LA5IR5N5LE5VV5NL5SV5YT5QA5AN5L5HL5SL5RD5AV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFG5QR5WG5F5DA5AT5INS5RY5NDL5TRL5IGN5Y5TD5H5AV5RW5Y5NT5GL5ER5V5WG5P5D5SR5DW5IR5YN5Q5FR5EL
gi|295  YFGER5NGL5Q5AN5IED5LY5TRL5TS5NI5Q5E5Y5SD5HC5AR5W5YN5Q5GL5NEI--GGI5SR---RYL5DF5QR5DL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac  TLT5VLD5IV5LS5FP5NY5DS5RT5YPI5RT5V5SQL5TRE5I5Y5T5NP5V5LEN5FD5GS5FR5G5SA5Q5GIE5GS5IR5SP5HL
gi|295  TIS5VLD5IVAL5FP5NY5DIR5TYPI5T5Q5SL5TRE5I5Y5T5SP5V5V5AG--NIN5F5GL5SI5AN5V---LR5AP5HL

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      240      250      260      270      280
Cry1Ac MDILNSITTYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORI----V
      310      320      330      340      350
gi|295 MDFIDRIVIYTNVSRSTPYWAGHEVISRRTGQGGNEIRFPLYGVAANAEPVPTIRPTGF
      290      300      310      320      330      340
Cry1Ac AQLGQGVYRTRLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKS-G-TVDS
      360      370      380      390      400      410
gi|295 TDEQRQWYRARSRVVFSR-----SGQDFSLVDAVGFLLTFSA---VSIYRNGFGFNTDT
      350      360      370      380      390
Cry1Ac LDEIPPQNNVPPRQGFSHRSLHVMFRSGFNSVSIIRAPMFSWIHRSAEFNNIIASD
      420      430      440      450      460      470
gi|295 LDEIPIEGTD--PFTGYSHRLCHVGLASSPFISQYA--RAPIFSWTHRSATLNTIAPD
      400      410      420      430      440      450
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYLEVPIHFSTSTRYR
      480      490      500      510      520      530
gi|295 VITQIPLVKAFNLHSGATIVKGPFGTGGDILRRT---NVGSFGDMRVNITAP-LSQRYR
      460      470      480      490      500
Cry1Ac VVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---
      540      550      560      570      580
gi|295 VRIRYAST'DLQFYTNINGTTINIGNFSSTMDSGDLDQYGRFRVAGFTT'PFTFSDANSTF
      510      520      530      540      550      560
Cry1Ac IVGVRNFGSTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
      590      600      610      620      630      640
gi|295 TIGAFGFSPPNNEVYIDRIEFVPAEVTFEAEYDLEKAQKAVNALFTSSNQIGLKTVDYD
      570      580      590      600      610      620
Cry1Ac IDQVSNLVYLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
      650      660      670      680      690      700
gi|295 IDKVSNLVECLSEDFECLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRG
      630      640      650      660      670      680
Cry1Ac GITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
      710      720      730      740      750      760
gi|295 DITIQQGGDDVFKENYVTLPGTFDGCYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
      690      700      710      720      730      740
Cry1Ac SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRNGEKAH
      770      780      790      800      810      820
gi|295 LIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRNGEKAH
      750      760      770      780      790      800
Cry1Ac SHHFSLDIDVGCCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK

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gi|295 SHHFSLDIDVGCCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
      810      820      830      840      850      860
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYL
      890      900      910      920      930      940
gi|295 KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYL
      870      880      890      900      910      920
Cry1Ac PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVEEQNNQ
      950      960      970      980      990      1000
gi|295 PELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVEEQNNH
      930      940      950      960      970      980
Cry1Ac RSVLVVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVE
      1010      1020      1030      1040      1050      1060
gi|295 RSVLVVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVE
      990      1000      1010      1020      1030      1040
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRR
      1070      1080      1090      1100      1110      1120
gi|295 EEVYPNNTVTCNDYTANQEEYKAYTSRNRGYDEAYGNNSVPADYTPVYEEKAYTDGRR
      1050      1060      1070      1080      1090      1100
Cry1Ac ENPCEFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130      1140      1150      1160      1170      1180
gi|295 ENPCESNRGYDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVESVELLLMEE
      1110      1120      1130      1140      1150      1160
>>gi|143227|gb|AAA22613.1| insecticidal endotoxin (1156 aa)
      initn: 5384 initl: 3530 opt: 4163 Z-score: 4899.5 bits: 918.5 E(): 0
Smith-Waterman score: 6357; 83.179% identity (89.992% similar) in 1189 aa overlap
(5-1182:1-1156)
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50      60
gi|143 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      70      80      90      100      110      120
gi|143 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130      140      150      160      170      180
gi|143 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190      200      210      220      230      240

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gi|616 WEEDPNNPATRTRVIDRFRILDGLLERDIPSPRISGFVPLLSVYAQAANLHLAALRDSV
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|616 IFGERWGLTTINVENYENRRLRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290
TLTVLDIVSLFNPYDSRTPYPIRTVSQLTREIYTNVLENFVDFGSRFRSAQG----IEGS-
gi|616 TLTVLDIAAFFPNYDNRYPYIQQVQQLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350
IRSPHLMIDLINSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|616 IRNPHLFDILNLLTFTDFWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQPEPPR
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400
RIVAQLGQGVYRTLSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKS
gi|616 SFT--FNGPVFRTLNSPTLRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac 410 420 430 440 450 460
TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNN
gi|616 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac 470 480 490 500 510 520
IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
gi|616 TIDPERINQIPLVKGRFVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPIT
470 480 490 500 510

Cry1Ac 530 540 550 560 570 580
STRYRVRVRYASVTPIHNLNVWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
gi|616 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTD
520 530 540 550 560 570

Cry1Ac 590 600 610 620 630
NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|616 NPFSPFRANPDIIGISEQPLFGAGSISGELYDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac 640 650 660 670 680 690
FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|616 FTSSNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

Cry1Ac 700 710 720 730 740 750

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Cry1Ac NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLAFT
gi|616 NFRGINRQDRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLAFT
700 710 720 730 740 750

Cry1Ac 760 770 780 790 800 810
RYQLRGIYIEDSQDLEIYSIRYNAKHETVNVVPGTSLWPLSAQSPIGKCGEPNRCAPHLEW
gi|616 RYELRGIYIEDSQDLEIYLIRYNAKHEIVNVVPGTSLWPLSAQSPIGKCGEPNRCAPHLEW
760 770 780 790 800 810

Cry1Ac 820 830 840 850 860 870
NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
gi|616 NPDLDCSCRDGEKCAHSHHFTLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

Cry1Ac 880 890 900 910 920 930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|616 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIA
880 890 900 910 920 930

Cry1Ac 940 950 960 970 980 990
MIHAADKRVHSIREAYLPELSVIPGVNAAIPEELEGRIPTAFSLYDARNVIKNGDFNNG
gi|616 MIHAADKRVHRIREAYLPELSVIPGVNAAIPEELEGRIPTAYSLYDARNVIKNGDFNNG
940 950 960 970 980 990

Cry1Ac 1000 1010 1020 1030 1040 1050
SCWNVKGVHDVEEQNNQSVLVVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTI
gi|616 LCWNVKGVHDVEEQNNHRSVLVPEWEAEVSEVVRVCPGRGYILRVTA
1000 1010 1020 1030 1040

Cry1Ac 1060 1070 1080 1090 1100 1110
HEIENNTDELKFSNCVEEIEYNNVTCTNDYTVNQEEYGGAYTSRNRGYNAPSVADYA
>>gi|2414156|emb|CAA70925.1| delta-endotoxin [Bacillus t (618 aa)
initn: 4102 init1: 4102 opt: 4102 Z-score: 4831.6 bits: 905.1 E(): 0
Smith-Waterman score: 4102; 100.000% identity (100.000% similar) in 618 aa overlap
(5-622:1-618)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|241 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
gi|241 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|241 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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120      130      140      150      160      170
Cry1Ac 190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|241 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180      190      200      210      220      230

250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|241 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
240      250      260      270      280      290

310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|241 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300      310      320      330      340      350

370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
gi|241 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
360      370      380      390      400      410

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|241 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420      430      440      450      460      470

490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|241 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480      490      500      510      520      530

550      560      570      580      590      600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|241 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac GVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|241 GVIIIDRFEFIPVTATLEAEYNL
600      610

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>>gi|22415751|gb|AAM95162.1| insecticidal protein CryIac (618 aa)
  initn: 4064 initl: 4064 opt: 4064 Z-score: 4786.8 bits: 896.8 E(): 0
Smith-Waterman score: 4064; 99.029% identity (99.515% similar) in 618 aa overlap
(5-622:1-618)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|224 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

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10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|224 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|224 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|224 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|224 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|224 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
gi|224 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
360     370     380     390     400     410

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|224 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
gi|224 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIIPPQ
360     370     380     390     400     410

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|224 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420     430     440     450     460     470

490     500     510     520     530     540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|224 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480     490     500     510     520     530

550     560     570     580     590     600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|224 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540     550     560     570     580     590

610     620     630     640     650     660
Cry1Ac GVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|224 GVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

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gi|224 GVIIDRFEFIPVTATLEAEYNL
    600      610

>>gi|1669651|emb|CAA70506.1| delta-endotoxin [Bacillus t (1173 aa)
    inith: 4498 inilt: 2906 opt: 4058 Z-score: 4775.5 bits: 895.6 E(): 0
    Smith-Waterman score: 4871; 65.570% identity (82.025% similar) in 1185 aa overlap
    (12-1179:7-1164)

    10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  MEISDQNYIYPYNCLNNPESEIFNARNSNFGLVS-QVSSGLTRFLLEAAVPEAGF
    10      20      30      40      50

    70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  ALGLFDIIWALGVDQWLSLFLRQIEQLIRQEI TELERNRATAAILGLSSSYNLYVEALRE
    60      70      80      90      100     110

    130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  WENDPNNPASQERVTRFRRLTDDAIVTGLPTLAIRNLEVNVLSVYTAANLHLSLLRDAV
    120     130     140     150     160     170

    190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  YFGERWGLTQANIEDLYTRLTNSIQEYSDHRCARWYNQGLNEI--GGISR---RYLDFQRDL
    180     190     200     210     220     230

    250     260     270     280     290
Cry1Ac TLTVLDIVSLF--PNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPH
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  TISVLDIVAPFSPNYDIRTYPIPTQSQLTREIYTSPPVAG--NINFGLSIANV---LRAPH
    240     250     260     270     280

    300     310     320     330     340     350
Cry1Ac LMDILNSITIIYTDahrgeyywsgHQIMASpVGFs-GPEFTFPlyGTmGNAAPQQRi----
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  LMDFIDRIVIIYTNsVRSTPYWAGHEVISRRTGQAQGNIRFPlyGVAANAEPpVTIRPTG
    290     300     310     320     330     340

    360     370     380     390     400     410
Cry1Ac VAQLGQGVYRTLSSTLYRRPFNIGINNQLSVDLGTefAYGTSSNLpSAVYRKS-G-TVD
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  FTDEQRQWYR--ARSLSRFRSSG---QDFSLVDAVAFLTIFSA--VSIYRNGFGFNFD
    350     360     370     380     390

    420     430     440     450     460     470
Cry1Ac SLDEIPPNVPPRQGFShRLSHVSMFRSGFSNSsvSIIRAPMFSWIHRSAEFNNIIAS
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  TIDEPIEGTD--PFTGYSHRLCHVGLASSPFISQYA--RAPISWThRSATLNTIAP
    400     410     420     430     440     450

    480     490     500     510     520     530
Cry1Ac DSITQIPAVKGNFLFNG-SVISGPFGTGGDLVRLNSSGNNIQNRGyIEVPIHFPSTSTRY
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:

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gi|166 DVITQIPLVKAFNLHSGATIVKGPFGTGGDILRRT---NVRSFRDMRVNITAP-LSQRy
    460      470      480      490      500

    540     550     560     570     580     590
Cry1Ac RVRVRYASVTPiHLNVNWGNSSiFNSNTVPATATSLDNLQSSDFGyFESANAFT--SSLGNI
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  RVRIRYASTTDLQFYTNINGTTINIGNFSSTMDSGDDLQYGRFRVAGFTTPTTFsrCKQT
    510     520     530     540     550     560

    600     610     620     630     640
Cry1Ac VGVRFN---SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTD
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  FHNRSFWFSPKlTEVYIDRIEFVPAEVTFAEYDLEKAQKAVNALFTSSNQIGLKTdVTD
    570     580     590     600     610     620

    650     660     670     680     690     700
Cry1Ac YHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGG
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  YHIDKVSNLVECLSEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQPDrgWRG
    630     640     650     660     670     680

    710     720     730     740     750     760
Cry1Ac STGITIQGGDDVFKENYVTLsGTFDECYPTyLYQKIDESKlKAFTRYQLRGYIEDSODLE
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  STDITIQGGDDVFKENYVTLPGTFDGCYPTyLYQKIDESKlKAYTRYQLRGYIEDSODLE
    690     700     710     720     730     740

    770     780     790     800     810     820
Cry1Ac IYSIRYNAKHETVNVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGEKCA
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  IYLIRYNAKHETVNVPGTGSWPLSAQSPiGKCGEPNRCAPHLEWNPYLDCSCRNGKKA
    750     760     770     780     790     800

    830     840     850     860     870     880
Cry1Ac HSHHFFSLDIDVGCTDLNEDLGVVViFKIKTDGHARLGNLEFLEEKPLVGEALARVKRA
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  HSHHFFSLDIDVGCTDLNEDLGVVViFKIKTDGHARLGNLEFLEEKPLVGEALARVKRA
    810     820     830     840     850     860

    890     900     910     920     930     940
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRvHSIREA
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  EKKWRDKREKLELETNIVYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRvHSIREA
    870     880     890     900     910     920

    950     960     970     980     990     1000
Cry1Ac YLPELSVIPGVNAAIfeELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQN
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  YLPELSVIPGVNAAIfeELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQN
    930     940     950     960     970     980

    1010    1020    1030    1040    1050    1060
Cry1Ac NQRSLVVPPEWAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHEIENNTDELKfSNC
    .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|166  NHRSLVVPPEWAEVsqEVRVCPGRGYILRVtAYKEGYGEGCVTIHE--SRTtQRTEIQQl
    990     1000    1010    1020    1030    1040

    1070    1080    1090    1100    1110    1120
Cry1Ac VEEIYPNNVTVCNDYTVNqEYGGAYTSRNRGyNEA---PSVPADYASVYEEKSYTDG

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gi|166 LEEEVYPNNTVTCNDYTANQEEYKAYTSHNRGYDEAYGNPSPADYTPVYEEKAYTDG
1050 1060 1070 1080 1090 1100

Cry1Ac RRENPCFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLME
1130 1140 1150 1160 1170 1180

gi|166 RRDNPCESTRGYGDTPLPAGYVSKELEYFPETDKVWIEIGETEGTFIVESVNYSLWRNR
1110 1120 1130 1140 1150 1160

gi|166 IRFKM
1170

>>gi|22770982|gb|AAN06817.1| insect toxin CryIA(c) [synt (615 aa)
initn: 4043 initl: 4043 opt: 4043 Z-score: 4762.0 bits: 892.2 E(): 0
Smith-Waterman score: 4043; 99.024% identity (99.675% similar) in 615 aa overlap
(5-619:1-615)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60
gi|227 MDNPNINEWIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120
gi|227 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180
gi|227 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
190 200 210 220 230 240
gi|227 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL
250 260 270 280 290 300
gi|227 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360
gi|227 MDIVNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GYVRTLSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEIPPQ
370 380 390 400 410 420
gi|227 GYVRTLSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|227 420 430 440 450 460 470
NNNVPPRQGFSHRLSHVSMFRSGFSNTSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

Cry1Ac 490 500 510 520 530 540
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

gi|227 480 490 500 510 520 530
VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

Cry1Ac 550 560 570 580 590 600
TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

gi|227 540 550 560 570 580 590
TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA

Cry1Ac 610 620 630 640 650 660
GVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL

gi|227 600 610
GVIIIDRFEFIPVTATLEAE

>>gi|4090435|gb|AAC98807.1| truncated Cry1Ac (613 aa)
initn: 4033 initl: 4033 opt: 4033 Z-score: 4750.2 bits: 890.0 E(): 0
Smith-Waterman score: 4033; 99.021% identity (99.511% similar) in 613 aa overlap
(5-617:1-613)

Cry1Ac 10 20 30 40 50 60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

gi|409 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi|409 60 70 80 90 100 110
VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

gi|409 120 130 140 150 160 170
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL

gi|409 180 190 200 210 220 230
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL

Cry1Ac 250 260 270 280 290 300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL

gi|409 240 250 260 270 280 290
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL



70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE  
 .....  
 gi | 155 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi | 155 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 .....  
 gi | 155 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL  
 .....  
 gi | 155 TLTVLDIVALFPNYDSRRYPPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi | 155 MDILNSITTYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
 .....  
 gi | 155 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 .....  
 gi | 155 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 420 430 440 450 460 470

490 500 510 520 530 540  
 Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....  
 gi | 155 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 480 490 500 510 520 530

550 560 570 580 590 600  
 Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 .....  
 gi | 155 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA  
 540 550 560 570 580 590

610 620 630 640 650 660  
 Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL  
 .....  
 gi | 155 GVIIDRFEFIPVTATLE

600 610  
 >>gi|56579955|gb|AAW01773.1| Sequence 6 from patent US 6 (613 aa)  
 initn: 4033 initl: 4033 opt: 4033 Z-score: 4750.2 bits: 890.0 E(): 0  
 Smith-Waterman score: 4033; 99.021% identity (99.511% similar) in 613 aa overlap  
 (5-617:1-613)

10 20 30 40 50 60  
 Cry1Ac CMQAMDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 .....  
 gi | 565 MDNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 10 20 30 40 50

70 80 90 100 110 120  
 Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE  
 .....  
 gi | 565 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE  
 60 70 80 90 100 110

130 140 150 160 170 180  
 Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 .....  
 gi | 565 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 120 130 140 150 160 170

190 200 210 220 230 240  
 Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 .....  
 gi | 565 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 180 190 200 210 220 230

250 260 270 280 290 300  
 Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL  
 .....  
 gi | 565 TLTVLDIVALFPNYDSRRYPPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIERSIRSPHL  
 240 250 260 270 280 290

310 320 330 340 350 360  
 Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 .....  
 gi | 565 MDILNSITTYTDAHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 300 310 320 330 340 350

370 380 390 400 410 420  
 Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
 .....  
 gi | 565 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ  
 360 370 380 390 400 410

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 .....  
 gi | 565 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 420 430 440 450 460 470

490 500 510 520 530 540  
 Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV  
 .....  
 gi | 565 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV

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480      490      500      510      520      530
Cry1Ac  550      560      570      580      590      600
TPIHLNVNWGSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|565  TPIHLNVNWGSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540      550      560      570      580      590

```

```

610      620      630      640      650      660
Cry1Ac  GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|565  GVIIDRFEFIPVTATLE
600      610

```

>>gi|10063045|gb|AAE38034.1| Sequence 6 from patent US 5 (613 aa)  
 initn: 4033 initl: 4033 opt: 4033 Z-score: 4750.2 bits: 890.0 E(): 0  
 Smith-Waterman score: 4033; 99.021% identity (99.511% similar) in 613 aa overlap  
 (5-617:1-613)

```

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|100  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|100  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|100  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|100  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|100  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac  MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|100  MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac  GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQ
gi|100  GVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQ

```

```

360      370      380      390      400      410
Cry1Ac  430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|100  NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
420      430      440      450      460      470

```

```

490      500      510      520      530      540
Cry1Ac  VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|100  VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
480      490      500      510      520      530

```

```

550      560      570      580      590      600
Cry1Ac  TPIHLNVNWGSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|100  TPIHLNVNWGSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
540      550      560      570      580      590

```

```

610      620      630      640      650      660
Cry1Ac  GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
gi|100  GVIIDRFEFIPVTATLE
600      610

```

>>gi|21517416|gb|AAM60745.1| Sequence 11 from patent US (613 aa)  
 initn: 4033 initl: 4033 opt: 4033 Z-score: 4750.2 bits: 890.0 E(): 0  
 Smith-Waterman score: 4033; 99.021% identity (99.511% similar) in 613 aa overlap  
 (5-617:1-613)

```

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|215  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|215  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|215  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|215  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWVRYNQFRREL
180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|215  TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL

```

```

      240      250      260      270      280      290
Cry1Ac      310      320      330      340      350      360
MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTfPlygTMGNAAPQQRIVaQLGQ
gi|215 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTfPlygTMGNAAPQQRIVaQLGQ
      300      310      320      330      340      350

```

```

      370      380      390      400      410      420
Cry1Ac GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEiPPQ
gi|215 GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEiPPQ
      360      370      380      390      400      410

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNnIIASDSITQIPa
gi|215 NNNVPPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNnIIASDSITQIPa
      420      430      440      450      460      470

```

```

      490      500      510      520      530      540
Cry1Ac VKGNFLfNGSVISGPGfTGGDLVRLnSSGNNIQNRgYIEVPIHfPSTStRYRVRVRYASV
gi|215 VKGNFLfNGSVISGPGfTGGDLVRLnSSGNNIQNRgYIEVPIHfPSTStRYRVRVRYASV
      480      490      500      510      520      530

```

```

      550      560      570      580      590      600
Cry1Ac TPIHLNVnWGNSSIFsNTVPATATSLDNLQSSDFGyFESANaFTSSLGNIVGVRnFSGTA
gi|215 TPIHLNVnWGNSSIFsNTVPATATSLDNLQSSDFGyFESANaFTSSLGNIVGVRnFSGTA
      540      550      560      570      580      590

```

```

      610      620      630      640      650      660
Cry1Ac GVII DRFEfIPVtATLEAEYnLERAQKAVNALfTSTnQLGLKtNVtDYHIDQVSNLVTYL
gi|215 GVII DRFEfIPVtATLEAEYnLERAQKAVNALfTSTnQLGLKtNVtDYHIDQVSNLVTYL
      600      610

```

>>gi|40275|emb|CAA38098.1| unnamed protein product [Baci (618 aa)  
 initn: 2933 initl: 2906 opt: 4033 Z-score: 4750.2 bits: 890.0 E(): 0  
 Smith-Waterman score: 4033; 98.384% identity (99.354% similar) in 619 aa overlap  
 (5-623:1-618)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNnPNINeCIPYnCLSNPEVEVLGGERIEtGYtPIDISLSLTQfLLSEfVPGAGf
gi|402 MDNNPNINeCIPYnCLSNPEVEVLGGERIEtGYtPIDISLSLTQfLLSEfVPGAGf
      10      20      30      40      50

```

```

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESfRE
gi|402 VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESfRE
      60      70      80      90      100      110

```

```

      130      140      150      160      170      180
Cry1Ac WEADPTnPALREEMRIQfNDMNSALtTAIPLFAVQnYQVPLLSVYVQAANLHLSVLRdVS
gi|402 WEADPTnPALREEMRIQfNDMNSALtTAIPLFAVQnYQVPLLSVYVQAANLHLSVLRdVS

```

```

      120      130      140      150      160      170
Cry1Ac      190      200      210      220      230      240
VFGQRWGFDAATINSRYNDLTRLIGNyTDHAvRWYnTGLERVWGpDSRDWIRYnQFRREL
gi|402 VFGQRWGFDAATINSRYNDLTRLIGNyTDHAvRWYnTGLERVWGpDSRDWIRYnQFRREL
      180      190      200      210      220      230

```

```

      250      260      270      280      290      300
Cry1Ac TLTvLDIVSLfPNyDSrTYPIrTVSQtLREIYtNPVLEnFDGSfRGSaQGIeGSIRsPHL
gi|402 TLTvLDIVSLfPNyDSrTYPIrTVSQtLREIYtNPVLEnFDGSfRGSaQGIeGSIRsPHL
      240      250      260      270      280      290

```

```

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTfPlygTMGNAAPQQRIVaQLGQ
gi|402 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTfPlygTMGNAAPQQRIVaQLGQ
      300      310      320      330      340      350

```

```

      370      380      390      400      410      420
Cry1Ac GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEiPPQ
gi|402 GvYrTLsStLYRRPFNIGINnQQLSVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEiPPQ
      360      370      380      390      400      410

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNnIIASDSITQIPa
gi|402 NNNVPPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEFNnIIASDSITQIPa
      420      430      440      450      460      470

```

```

      490      500      510      520      530      540
Cry1Ac VKGNFLfNGSVISGPGfTGGDLVRLnSSGNNIQNRgYIEVPIHfPSTStRYRVRVRYASV
gi|402 VKGNFLfNGSVISGPGfTGGDLVRLnSSGNNIQNRgYIEVPIHfPSTStRYRVRVRYASV
      480      490      500      510      520      530

```

```

      550      560      570      580      590      600
Cry1Ac TPIHLNVnWGNSSIFsNTVPATATSLDNLQSSDFGyFESANaFTSSLGNIVGVRnFSGTA
gi|402 TPIHLNVnWGNSSIFsNTVPATATSLDNLQSSDFGyFESANaFTSSLGNIVGVRnFSGTA
      540      550      560      570      580      590

```

```

      610      620      630      640      650      660
Cry1Ac GVII DRFEfIPVtATLEAEYnLERAQKAVNALfTSTnQLGLKtNVtDYHIDQVSNLVTYL
gi|402 GVII DRFEfIPVtATLEAEYnLERAQKAVNALfTSTnQLGLKtNVtDYHIDQVSNLVTYL
      600      610

```

>>gi|1850365|gb|AAB82749.1| insecticidal crystal protein (911 aa)  
 initn: 4590 initl: 1977 opt: 3999 Z-score: 4707.6 bits: 882.7 E(): 0  
 Smith-Waterman score: 4720; 79.409% identity (86.906% similar) in 947 aa overlap  
 (5-947:1-911)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNnPNINeCIPYnCLSNPEVEVLGGERIEtGYtPIDISLSLTQfLLSEfVPGAGf
gi|185 MDNNPNINeCIPYnCLSNPEVEVLGGERIEtGYtPIDISLSLTQfLLSEfVPGAGf

```

```

          10      20      30      40      50
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
          70      80      90     100     110     120
gi|185  VLGLVDIIWEIFSVLSSDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
          60      70      80      90     100     110

          130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
gi|185  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV--TCNYIIS--SESV
          190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          180     190     200     210     220     230
gi|185  MCGQRSGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
          250     260     270     280     290     300
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIIRSPHL
          240     250     260     270     280     290
gi|185  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIIRSPHL
          310     320     330     340     350     360
Cry1Ac  MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300     310     320     330     340     350
gi|185  MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNSAPQQRIVAQLGQ
          370     380     390     400     410     420
Cry1Ac  GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQ
          360     370     380     390     400     410
gi|185  GVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQ
          430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
          420     430     440     450     460     470
gi|185  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIPSSQITQIPL
          490     500     510     520     530
Cry1Ac  VKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
          480     490     500     510     520
gi|185  TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRILYAS
          540     550     560     570     580     590
Cry1Ac  VTPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
          530     540     550     560     570     580
gi|185  TTNLQFHTSIDGRPINQGNFSATMSSGRNLQSGSLRTVGFTTTPFNFSNGSSVFTLSAHVF
          600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
          ..   : : : : : . . : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi|185  NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTDTVTDYHIDQVSNL
          590     600     610     620     630     640
          660     670     680     690     700     710
Cry1Ac  VTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
          650     660     670     680     690     700
gi|185  VECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRSTDTITQGG
          720     730     740     750     760     770
Cry1Ac  DDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYNAK
          710     720     730     740     750     760
gi|185  DDFQENYVTLGLT-MGFPS-IYIKKWWFEIKSLYPLPIRGYIEDSQDLEIYLIRYNAK
          780     790     800     810     820     830
Cry1Ac  HETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFSLD
          770     780     790
gi|185  HETVNVPGTVPYGRFPQVPIGK-----AHSHHFFSLD
          840     850     860     870     880     890
Cry1Ac  IDVGCTDLNEDLGVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
          810     820     830     840     850     860
gi|185  IDVGCTDLNEDLGVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRE
          900     910     920     930     940     950
Cry1Ac  KLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIP
          870     880     890     900     910
gi|185  KLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREA
          960     970     980     990     1000    1010
Cry1Ac  GVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHV DVEEQNNQRSVLVVP

>>gi|2555147|gb|AAC63055.1| CryIA(c) [synthetic construc (616 aa)
  initn: 3982 init1: 3982 opt: 3982 Z-score: 4690.1 bits: 878.9 E(): 0
Smith-Waterman score: 3982; 98.358% identity (99.343% similar) in 609 aa overlap
(9-617:6-614)
          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50
gi|255  MAMITPSLHACIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          70      80      90     100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
          60      70      80      90     100     110
gi|255  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
          130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
gi|255  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

```

```

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
gi|255 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      180      190      200      210      220      230

```

```

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|255 TLTVLDIVALFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIRSPHL
      240      250      260      270      280      290

```

```

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaapQQRIVAQLGQ
gi|255 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaapQQRIVAQLGQ
      300      310      320      330      340      350

```

```

      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
gi|255 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
      360      370      380      390      400      410

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|255 NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      420      430      440      450      460      470

```

```

      490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYRVRVRYASV
gi|255 VKGNFLFNGSVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYRVRVRYASV
      480      490      500      510      520      530

```

```

      550      560      570      580      590      600
Cry1Ac TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
gi|255 TPIHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590

```

```

      610      620      630      640      650      660
Cry1Ac GVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYL
gi|255 GVIIDRFEFIPVTATLEPP
      600      610

```

>>gi|70673280|gb|AAZ06794.1| truncated insecticidal acti (716 aa)  
 initn: 3979 init1: 3166 opt: 3975 Z-score: 4680.8 bits: 877.4 E(): 0  
 Smith-Waterman score: 3975; 85.021% identity (92.094% similar) in 721 aa overlap  
 (5-721:1-716)

```

      10      20      30      40      50      60
Cry1Ac CMQAMNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|706 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

```

```

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIrSLRLEGLSNLYQIYAESFRE
gi|706 VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIrSLRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

```

```

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNdmNSALTtAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|706 WEADPTNPALREEMRIQFNdmNSALTtAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

```

```

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
gi|706 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQFRREL
      180      190      200      210      220      230

```

```

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|706 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
      240      250      260      270      280      290

```

```

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaapQQRIVAQLGQ
gi|706 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaapQQRIVAQLGQ
      300      310      320      330      340      350

```

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      370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
gi|706 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
      360      370      380      390      400      410

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```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|706 NNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420      430      440      450      460      470

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      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQRgyIEVPIHFPSTSTRYRVRVRYAS
gi|706 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

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```

      540      550      560      570      580      590
Cry1Ac VTP IHLNVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|706 TTNLQPHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFPTFPNFNSGSSVFTLSAHVF
      540      550      560      570      580      590

```

```

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|706 NSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNQIGLKTVDYHIDQVSNL
      600      610      620      630      640      650

```

```

660      670      680      690      700      710
Cry1Ac VTYLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
: .....: .....: .....: .....: .....: .....:
gi|706 VECLSDPEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQGG
      660      670      680      690      700      710

```

```

720      730      740      750      760      770
Cry1Ac DDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAPTRYQLRGYIEDSQDLEIYSIRYNAK
: .....: .....: .....: .....: .....: .....:
gi|706 DDVFK

```

```

>>gi|1171235|gb|AAA86266.1| CryIA(c) (607 aa)
  initn: 2933 initl: 2906 opt: 3970 Z-score: 4676.0 bits: 876.2 E(): 0
Smith-Waterman score: 3970; 98.355% identity (99.342% similar) in 608 aa overlap
(5-612:1-607)

```

```

10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
: .....: .....: .....: .....: .....: .....:
gi|117 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
: .....: .....: .....: .....: .....: .....:
gi|117 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
: .....: .....: .....: .....: .....: .....:
gi|117 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNOFRREL
: .....: .....: .....: .....: .....: .....:
gi|117 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWVRYNOFRREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSI RSPHL
: .....: .....: .....: .....: .....: .....:
gi|117 TLTVLDIVALFPNYDSRRYPRTVSQLTREIYTNVLENFDGSRFGSAQGIERSIRSPHL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
: .....: .....: .....: .....: .....: .....:
gi|117 MDILNSITIYTDahrGYYWsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDLSLDEIPPQ
: .....: .....: .....: .....: .....: .....:
gi|117 GVYRTLSSTFYRRFPNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDLSLDEIPPQ
      360     370     380     390     400     410

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
: .....: .....: .....: .....: .....: .....:
gi|117 NNNVPPRQGFSHRLSHVSMFRSG-SSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      420      430      440      450      460      470

```

```

490      500      510      520      530      540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASV
: .....: .....: .....: .....: .....: .....:
gi|117 VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASV
      480      490      500      510      520      530

```

```

550      560      570      580      590      600
Cry1Ac TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
: .....: .....: .....: .....: .....: .....:
gi|117 TPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTA
      540      550      560      570      580      590

```

```

610      620      630      640      650      660
Cry1Ac GVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL
: .....: .....: .....: .....: .....: .....:
gi|117 GVIIIDRFEFIPV
      600

```

```

>>gi|1022728|gb|AAA79694.1| crystal toxin (1155 aa)
  initn: 4600 initl: 3044 opt: 3918 Z-score: 4610.5 bits: 865.1 E(): 0
Smith-Waterman score: 4945; 65.240% identity (83.048% similar) in 1168 aa overlap
(12-1160:7-1147)

```

```

10      20      30      40      50
Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTP--IDISLSLTQFLLSEFVPGA
: .....: .....: .....: .....: .....: .....:
gi|102 MEVNHQNECPVYNCLKNPKIEMLDIEGISSRSREQVABISLGLTRFLLSLLPGA
      10      20      30      40      50

```

```

60      70      80      90      100     110
Cry1Ac GFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESF
: .....: .....: .....: .....: .....: .....:
gi|102 SFGFLGLFDIIWGFVIGPDQWLSLFLTQIEQLIDQRIEAHVRNQAI SRLEGLGDSYEVYIESL
      60      70      80      90      100     110

```

```

120     130     140     150     160     170
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
: .....: .....: .....: .....: .....: .....:
gi|102 REWEASPNNESLQQDVRNRFNSNTDNALITAIPILREQGFEIPLLTVYVQAANLHLSLLRD
      120     130     140     150     160     170

```

```

180     190     200     210     220     230
Cry1Ac VSVFGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNOFRRR
: .....: .....: .....: .....: .....: .....:
gi|102 AVYFGRWGLDtatvnnhynrlinlntysdhcaqwfNrgLDN-FGVVT---ARYLDFQR
      180     190     200     210     220     230

```

```

240     250     260     270     280     290
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIIEGSI RSP
: .....: .....: .....: .....: .....: .....:
gi|102 EVTISVLDIVALFPNYDIRTYPIQTLSQLTREIYTSVPAEP-GASLNVDLRNI---LREP
      240     250     260     270     280

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300      310      320      330      340      350
Cry1Ac HLMIDLNSITIIYTDHRGGEYVNSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|102 HLMDFLTRLVYITGVQGGIYHWAGHEISSRTTGNLSSNIQFPLYGTSANADRPFNLAIHY
290      300      310      320      330      340

360      370      380      390      400      410
Cry1Ac GQGVYRTLSSITLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSA--VYRSGTVDLSLDE
gi|102 SETIYRTLSPAPIY--SVSGGISPNRTRAVEGVRFILTARDNNLNSLPFLYRKEGSLDSPTFE
350      360      370      380      390      400

420      430      440      450      460      470
Cry1Ac IPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFVSWIHRSAEFNNIIASDSIT
gi|102 LPPEDENEPPIYIGYSHRSLCHARFARSSVLEPSNFARIPVFSWTHRSAGPTNEVSSSRIT
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac QIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYRV
gi|102 QIPWVKAHTLDSGAFVIKPGFTGGDIL----TRPNLGTGLALRVTLTGLPQT---YNI
470      480      490      500      510

540      550      560      570      580
Cry1Ac RVRYASVTPPIHLNVNNGNSSIFS-----TVPATATSLDNLQSSDFGY--FESANAFTS
gi|102 RIRYASIA-----NRGGTLIFSQPPSYGLTFPKTMDIDEPLTSRSFARTTLFTPTITFQ
520      530      540      550      560      570

590      600      610      620      630      640
Cry1Ac SLGNLVGRVNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNV
gi|102 AQAEL---NLTIIQQGVYIDRIEFIPVNATFEAEYDLERAQEAVALFTSSNQLGLKTDL
580      590      600      610      620

650      660      670      680      690      700
Cry1Ac TDYHIDQVSNLVTYLSDFCLEDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGW
gi|102 TDYHIDQVSNLVDCLSDFCLEDEKRELSEKVKHAKRLSDERNLLQDSNFRGINRQPRGW
630      640      650      660      670      680

710      720      730      740      750      760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQD
gi|102 RGSTDITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQD
690      700      710      720      730      740

770      780      790      800      810      820
Cry1Ac LEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGK
gi|102 LEIYLIRYNAKHETVNVPGTGLWPLSVESPIGKCGEPNRCVPQLEWNSNLDLDCSCRDEGK
750      760      770      780      790      800

830      840      850      860      870      880
Cry1Ac CAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVK
gi|102 CAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVK

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810      820      830      840      850      860
Cry1Ac RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIR
gi|102 RAEKKWRDKRETLQLETNIVYKEAKESVDALFANSQYNRLQADTNIAMIHAADKRVHRIR
870      880      890      900      910      920

950      960      970      980      990      1000
Cry1Ac EAYLPELSVIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEE
gi|102 EAYLPELSVIPGVNAGIFEELEGRIFTAFSLYDARNVIKNSDFNGLSCWNVKGVHDVIEE
930      940      950      960      970      980

1010     1020     1030     1040     1050     1060
Cry1Ac QNNQRSVLVPEWEAEVSVQEVVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFS
gi|102 QNNHRSVLVPEWEAEVSKVHVCPGRGYILRVVTAYKEGYGEGCVTIHEIEDHTDELKFR
990     1000     1010     1020     1030     1040

1070     1080     1090     1100     1110     1120
Cry1Ac NCVEEEIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYT
gi|102 NCEEDEVYPNNTRTCNAYPADQEGYEGACTSRNRGYDEVYGMTPSLPADYAPIYEENAYT
1050     1060     1070     1080     1090     1100

1130     1140     1150     1160     1170     1180
Cry1Ac DGRRENPCFENRGRDYTPPLVGYVTKLEYPFETDKVWIEIGETEGTPIVDSVELLME
gi|102 DGRRGNCPCESSRGGYDTPPLPAGYETKELEYPFETDTVWPRNRYSD
1110     1120     1130     1140     1150

Cry1Ac E
>>gi|13173240|gb|AAK14337.1| insecticidal crystal protei (1118 aa)
  initn: 4523 init1: 2642 opt: 3906 Z-score: 4596.6 bits: 862.4 E(): 0
Smith-Waterman score: 5521; 80.166% identity (87.454% similar) in 1084 aa overlap
(5-1080:1-1049)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|131 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
gi|131 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|131 WEADPTNPALREEMRIQFNDMNSALTTAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|131 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREI  
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGIIEGSIIRSPHL  
gi|131 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQGTTERSIRSPHL  
240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNA--PQQRIVAQL  
gi|131 MDILNSITIIYRMHIEDIIIGQGIKRLLLEGFQGGNSLF-LYLGRGEMQLHPNRLLLNKV  
300 310 320 330 340 350

Cry1Ac GQGV--YRTLSSLTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDE  
gi|131 RACIEHYRPL--YIEDLFKEGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDE  
360 370 380 390 400 410

Cry1Ac IPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSIT  
gi|131 IPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIPSSQIT  
420 430 440 450 460 470

Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVV  
gi|131 QIPLTKSNTLGSSTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRI  
480 490 500 510 520 530

Cry1Ac RYASVTPIHNLNVWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSLGNIV---G  
gi|131 RYASTTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRVTVPFNFSSGVSFTLS  
530 540 550 560 570 580

Cry1Ac VRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ  
gi|131 AHVFNNGNEVYIDRIFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQ  
590 600 610 620 630 640

Cry1Ac VSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGIT  
gi|131 VSNLVECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWGSTDIT  
650 660 670 680 690 700

Cry1Ac IQGGDDVFKENYVTLSGTFDECPYTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYISIR  
gi|131 IQGGDDVFKENYVTLTGTDFECFQRIYIKKVDSEKFKAYTRDQLRGYIEDSQDLEIYLIR  
710 720 730 740 750 760

Cry1Ac YNAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSH  
gi|131 YNAKHETVNVPGTGLSLWPLSAPSPIGK-----AHSHSH  
770 780 790 800

Cry1Ac FSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWR  
gi|131 FSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWR  
810 820 830 840 850 860

Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPEL  
gi|131 DKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPEL  
870 880 890 900 910 920

Cry1Ac SVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSV  
gi|131 SVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNHRSV  
930 940 950 960 970 980

Cry1Ac LVVPEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVT IHEIENNTDELKFSNCVVEEIE  
gi|131 LVVPEWAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVT IHEIENNTDELKFSNCVVEEIV  
990 1000 1010 1020 1030 1040

Cry1Ac YPNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFEFN  
gi|131 YPNNTVTCCKIILRLKKNMVRVRLLVIEDMTEPMKAILLYQLIMHQPMKKKHIQMDEETIL  
1050 1060 1070 1080 1090 1100

>>gi|34429675|gb|AAQ72336.1| Sequence 3 from patent US 5 (595 aa)  
initn: 3892 init1: 3892 opt: 3892 Z-score: 4584.1 bits: 859.2 E(): 0  
Smith-Waterman score: 3892; 98.992% identity (99.496% similar) in 595 aa overlap  
(33-627:1-595)

Cry1Ac QAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVL  
gi|344 IETGYTPIDISLSLTQFLLEFVPGAGFVL  
10 20 30 40 50 60

Cry1Ac GLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWE  
gi|344 GLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWE  
70 80 90 100 110 120

Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVF  
gi|344 ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVF  
130 140 150 160 170 180

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190      200      210      220      230      240
Cry1Ac GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT
gi|344 GQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRRELT
160      170      180      190      200      210

250      260      270      280      290      300
Cry1Ac TVLDIVSLFPPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIKSPHLM
gi|344 TVLDIVALFPPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSGFRGSAQGIERSIKSPHLM
220      230      240      250      260      270

310      320      330      340      350      360
Cry1Ac ILNSITIIYTDHRGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
gi|344 ILNSITIIYTDHRGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
280      290      300      310      320      330

370      380      390      400      410      420
Cry1Ac YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSSTVDSLDEIPPQNN
gi|344 YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSSTVDSLDEIPPQNN
340      350      360      370      380      390

430      440      450      460      470      480
Cry1Ac NVPPRQGFSSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
gi|344 NVPPRQGFSSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
400      410      420      430      440      450

490      500      510      520      530      540
Cry1Ac GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYASVTP
gi|344 GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYASVTP
460      470      480      490      500      510

550      560      570      580      590      600
Cry1Ac IHLNWNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGV
gi|344 IHLNWNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGV
520      530      540      550      560      570

610      620      630      640      650      660
Cry1Ac IIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD
gi|344 IIDRFEFIPVTATLEAEYNLERAQK
580      590

>>gi|117518746|gb|ABK35074.1| insecticidal delta endotox (1173 aa)
  initn: 4638 initl: 3000 opt: 3880 Z-score: 4565.6 bits: 856.8 E(): 0
Smith-Waterman score: 5098; 67.058% identity (82.649% similar) in 1193 aa overlap
(5-1182:1-1173)

10      20      30      40      50
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTP--IDISLSLTQFLLSEFVPGA
gi|117 MEIINNQCQVYPYNCLSNPENEILDIESLSSRSREQVAEISLGLTRFLESLLPGA
10      20      30      40      50

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60      70      80      90      100      110
Cry1Ac GFVLGLVDIIWGIIFGSPQWDAFLVQIEQLINQRIIEEFARNQAIISRLGLESLNLYQIYAESF
gi|117 SFGFALFDIIWGVIGPDQWNLFLAQIEQLIDQRIEAHVRNQAIISRLGLESLDSEYEVYIESL
60      70      80      90      100      110

120      130      140      150      160      170
Cry1Ac REWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|117 REWEGSPNNEGLQDVRNRFNSNTDNALITGYLFLREQGFEIPLLSVYVQAANLHLSILRD
120      130      140      150      160      170

180      190      200      210      220      230
Cry1Ac VSVFGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFR
gi|117 VSVFGRWGYDTATINNRYSDLTSLIHVYTNHCVDITYNQGLRRLEGRFLTDWIVYRFR
180      190      200      210      220      230

240      250      260      270      280      290
Cry1Ac ELTLTVLDIVSLFPPNYDSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSGFRGSAQGIIEGS
gi|117 QFTISVLDIVAFPPNYDIRTYPIHTATQLTREIYLDLPPINENLSPAASYPTFSAESA
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac IRSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQR
gi|117 IRSPHLVDFLNSFTIYTDLSLARYAYWGGHLVNCFRGTGTTNLRSPLYGREGNTERPV
300      310      320      330      340      350

360      370      380      390      400      410
Cry1Ac VAQLGQGVYRTLSSTLYRRPFNIGINNQQ-LSVLDGTEFAYGTSSNLPSSAVYRKSSTVDS
gi|117 TASPSVPIFRTLS-----YITGLDNSNPVAGIEGVEF----QNTISRSIYRKSQPIDS
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac LDEIPPQNNVPPRQGFSSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASD
gi|117 FNLPPQDASVSPSIGYSHRLCHAT-FLERISGPRIAGV---VFPWTHRSASPTNEVSSS
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYR
gi|117 RKTQIPWVKAHTLASGASVIKGGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYR
470      480      490      500      510

540      550      560      570      580      590
Cry1Ac VRVRYASVPIHLNWNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNIV-
gi|117 VRIRYASTNLQFHTSIDGRPINQGNFSATMSSGNNLQSGSFRTVGFPTPFNFNSGSSVF
520      530      540      550      560      570

600      610      620      630      640
Cry1Ac --GVRNFGSTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|117 TLAHVFNKSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVNELFTSSNIGLKTVDVTDYH
580      590      600      610      620      630

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650      660      670      680      690      700
Cry1Ac IDQVSNLVYTLSEDFCLDEKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 IDQVSNLVCELSDFCLDEKRELSSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGST
640      650      660      670      680      690

```

```

710      720      730      740      750      760
Cry1Ac GITIQQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 DITIQQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSDLEIY
700      710      720      730      740      750

```

```

770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 LIRYNAKHEIVNVPGTGLWPLSVENQIGPCGEPNRCAPHLEWNPDLHCSRDGENVPII
760      770      780      790      800      810

```

```

830      840      850      860      870      880
Cry1Ac SHHFSLDIDVCGTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 PIISPWDIDVCGTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEK
820      830      840      850      860      870

```

```

890      900      910      920      930      940
Cry1Ac KWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 KWRDKREKLELETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYL
880      890      900      910      920      930

```

```

950      960      970      980      990      1000
Cry1Ac PELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 PELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNH
940      950      960      970      980      990

```

```

1010     1020     1030     1040     1050     1060
Cry1Ac RSVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFNVCVE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 RSVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFNVCVE
1000     1010     1020     1030     1040     1050

```

```

1070     1080     1090     1100     1110     1120
Cry1Ac EEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 EEVYPNNTVTCINYTATQEEYEGTYTSRNRGYDEAYGNNPSVPADYASVYEEKSYTDRRR
1060     1070     1080     1090     1100     1110

```

```

1130     1140     1150     1160     1170     1180
Cry1Ac ENPCEFNRGRYDTPPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 ENPCESNRGYDTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120     1130     1140     1150     1160     1170

```

```

>>gi|1022696|gb|AAB00376.1| Cry1K (1215 aa)
initn: 3452 initl: 2239 opt: 3827 Z-score: 4502.8 bits: 845.2 E(): 0
Smith-Waterman score: 4154; 57.070% identity (78.323% similar) in 1181 aa overlap
(38-1182:54-1215)

```

```

10      20      30      40      50      60
Cry1Ac NPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSITQFLLSEF-VPGAGFVLGLVD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 SAQMDLSPDARIEDSLCVAEGNNDIPFVSASTVQTGISIAGRILGVLGVPFAGQLASFYS
30      40      50      60      70      80

```

```

70      80      90      100     110     120
Cry1Ac IIWGIFGPS---QWDAFLVQIEQLI-NQRIEEFARNQAI SRLLEGLSNLYQIYAESPREWE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 FLVGEVLPSSGRDPWEIFMEHVEQIVRQQQITDSVRDTA IARLEGLGRGYRSYQQALETWL
90      100     110     120     130     140

```

```

130     140     150     160     170     180
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 DNRNDARSRSIIRERYIALELDITTAIPLFSIRNEEVPLLMVYAANLHLLLLLRDASLF
150     160     170     180     190     200

```

```

190     200     210     220     230     240
Cry1Ac GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 GSEWGMSSADVNYQYQEIRIYTEEYSNHCVQWYNTGLNRLRGTTAETWVRYNQFRDLTL
210     220     230     240     250     260

```

```

250     260     270     280     290
Cry1Ac TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNP--VLENFDGS-FRGSQA--GIEGSI-R
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 GVLDLVALFPYSYDTRTYPIPTAQLTREVYTDPNQVAGPNNWFRNGASFSAIENAIIR
270     280     290     300     310     320

```

```

300     310     320     330     340     350
Cry1Ac SPHLMIDLNSITITD-AHRGEY---WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 QPHLYDFLNLNLTYYTRRSQVGTIMNLWAGHRIITFNRI--QGGSTSEMVGAIITNPVSVS
330     340     350     360     370     380

```

```

360     370     380     390     400     410
Cry1Ac RIVAQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSNLPASAVYRKSGTV-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 DI-PFVNRDVYRTVSLAGGLGSLG-GIR-YGLTRVD-FDMIFRNHPDIVTGLFYHPGHAG
390     400     410     420     430

```

```

420     430     440     450     460
Cry1Ac -----DSLDEIPPNQNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 IATQVKDSDELPPETTEQPNYRAFSHLLSHISM---GPTTQDVP----PVYSWTHQSAD
440     450     460     470     480     490

```

```

470     480     490     500     510     520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 RTNTINSDRITQIPLVKAHTLQSGTTVVKGPFTGGDILRRTSGGP----FAFSNVNLDLF
500     510     520     530     540

```

```

530     540     550     560     570     580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|102 -NLSQRYSRIRYASTTNLRIYVTVAGERIFAGQFDKTM DAGAPLTFQFSFYATINTAFT

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550      560      570      580      590      600
Cry1Ac ---SSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      590      600      610      620      630      640
gi|102 FPERSSSLTIGADTFSSGNEVYVDRFELIQVTATFEAESDLERARKAVNALFTSTNPRGL
      610      620      630      640      650      660
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
      650      660      670      680      690      700
gi|102 KTDVTDYHIDQVSNLVECLSDEFCLDKKRELLEEVKYAKRLSDERNLLQDPTFTSISGQT
      670      680      690      700      710      720
Cry1Ac ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIE
      710      720      730      740      750      760
gi|102 DRGWIGSGTGISIQGGDDIFKENYVRLPGTVDECYPTYLYQKIDESQLKSYTRYQLRGYIE
      730      740      750      760      770      780
Cry1Ac DSQDLLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLWPNPDLDCSCR
      770      780      790      800      810      820
gi|102 DSQDLLEIYLIRYNAKHETLSVPGTESPPWSSGVYPSGRCGEPNRCAPRIEWNPDLDCSCR
      790      800      810      820      830      840
Cry1Ac DGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEKPLVGEAL
      830      840      850      860      870      880
gi|102 YGEKCVHSHHFLSLDIDVGCTDLNEDLGVVWIFKIKTQDGHAKLGNLEFIEKPLLGKAL
      850      860      870      880      890      900
Cry1Ac ARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRV
      890      900      910      920      930      940
gi|102 SRVKRAEKKWRDKYKLEKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRV
      910      920      930      940      950      960
Cry1Ac HSIREAYLPELSPVPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVH
      950      960      970      980      990      1000
gi|102 HRIREPYSLELSPVPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGVH
      970      980      990      1000      1010      1020
Cry1Ac DVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVTAAYKEGYEGCVTTHEIENNTDE
      1010      1020      1030      1040      1050      1060
gi|102 DVQ-QNHRSVLVPEWEAEVSVQEVVRCVPCDRGYILRVTAAYKEGYEGCVTTHEIENNTDV
      1030      1040      1050      1060      1070      1080
Cry1Ac LKFSNCVEEIEYPPNNTVTCNDYTVNQEEYGG--AYTSRNRGYNEA-----PSVPADY
      1070      1080      1090      1100      1110      1120
gi|102 LKFRNFVEEIEYPPNNTVTCNDYTTNQSAEGSTDAACNSYRNGYEDGYENRYEPPNPAPVNY
      1090      1100      1110      1120      1130      1140
Cry1Ac ASVYEEKSYTDGRRNCPCEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFI
      1120      1130      1140      1150      1160      1170

```

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gi|102 TPTYEEGMYTDTQGYNHCVSDRGRYRNHTPLPAGYVTLLELYFPETEQQVWIEIGETEGTFI
      1150      1160      1170      1180      1190      1200
Cry1Ac VDSVELLLMEE
      1180
gi|102 VGSVELLLMEE
      1210
>>gi|5916230|gb|AAD55947.1| Cry 1Ac insecticidal toxin [ (587 aa)
      initn: 3819 init1: 3819 opt: 3819 Z-score: 4498.1 bits: 843.3 E(): 0
      Smith-Waterman score: 3819; 98.803% identity (99.316% similar) in 585 aa overlap
      (33-617:3-587)
Cry1Ac QAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVL
      10      20      30      40      50      60
gi|591 MAIETGYTPIDISLSLTQFLLESEFVPGAGFVL
      10      20      30
Cry1Ac GLVDIHWGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWE
      70      80      90      100      110      120
gi|591 GLVDIHWGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWE
      40      50      60      70      80      90
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
      130      140      150      160      170      180
gi|591 ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
      100      110      120      130      140      150
Cry1Ac GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRYNQFRRELTL
      190      200      210      220      230      240
gi|591 GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRYNQFRRELTL
      160      170      180      190      200      210
Cry1Ac TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHLM
      250      260      270      280      290      300
gi|591 TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQGIERSIRSPHLM
      220      230      240      250      260      270
Cry1Ac ILNSITIIYTDHARGYYWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
      310      320      330      340      350      360
gi|591 ILNSITIIYTDHARGYYWWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
      280      290      300      310      320      330
Cry1Ac YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQNN
      370      380      390      400      410      420
gi|591 YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSGETVDSLDEIPPQNN
      340      350      360      370      380      390
Cry1Ac NVPQRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
      430      440      450      460      470      480

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gi|591 NVPPRQGF... 400 410 420 430 440 450

Cry1Ac GNFLFNGSVISGPGFTGGDLVRLN... 490 500 510 520 530 540

gi|591 GNFLFNGSVISGPGFTGGDLVRLN... 460 470 480 490 500 510

Cry1Ac IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGSTAGV... 550 560 570 580 590 600

gi|591 IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGSTAGV... 520 530 540 550 560 570

Cry1Ac IIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS... 610 620 630 640 650 660

gi|591 IIDRFEFIPVTATLE 580

>>gi|13173242|gb|AAK14338.1| insecticidal crystal protei (1118 aa)
initt: 5175 initt1: 2529 opt: 3817 Z-score: 4491.6 bits: 843.0 E(): 0
Smith-Waterman score: 5432; 79.482% identity (86.784% similar) in 1082 aa overlap
(5-1080:1-1049)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF... 10 20 30 40 50 60

gi|131 MDNNPNINEFLIVEVTLLEEKYC--GERIETGYTPIDISLSLTQFLLESEFVPGAGF... 10 20 30 40 50

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEIEFARNQAIISRLGLESLNLYQIYAESFRE... 70 80 90 100 110 120

gi|131 ELGLVDIIWGFPGSQWDAFLVQIEQLINQRIEIEFARNQAIISRLGLESLNLYQIYEPSFRE... 60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNMDNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS... 130 140 150 160 170 180

gi|131 WEADPTNPALREEMRIQFNMDNSALTTAIPLFAVQNYQVPLLSVYVQAAMVCVSGGRFGG... 120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGDSDRWIRYNQFRREL... 190 200 210 220 230 240

gi|131 PRALSSRFNALNLRHWTTLRLIGNCTDHPGYWYNTGLGRVWGRDSRDWIRYNQFRREL... 180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIKRSRPHL... 250 260 270 280 290 300

gi|131 TLTVLDIVSLFPNYDSRTYPIRTVSQLTEIYTNVPLENFDGSGFRGSAQGIIEGSIKRSRPHL... 240 250 260 270 280 290

Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFGSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ... 310 320 330 340 350 360

gi|131 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFGSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ... 300 310 320 330 340 350

Cry1Ac GVYR... 370 380 390 400 410 420

gi|131 GVYR... 360 370 380 390 400 410

Cry1Ac NNNVPPRQGF... 430 440 450 460 470 480

gi|131 NTTVKPRQGF... 420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLN... 490 500 510 520 530

gi|131 TKSTNLGSGT... 480 490 500 510 520

Cry1Ac VTP... 540 550 560 570 580 590

gi|131 TTNLQFHTS... 530 540 550 560 570 580

Cry1Ac SGTAGV... 600 610 620 630 640 650

gi|131 NSGNEVY... 590 600 610 620 630 640

Cry1Ac VTYS... 660 670 680 690 700 710

gi|131 VECLS... 650 660 670 680 690 700

Cry1Ac DDVFKENY... 720 730 740 750 760 770

gi|131 DDVFKENY... 710 720 730 740 750 760

Cry1Ac AKHETVNV... 780 790 800 810 820 830

gi|131 AKHETVNV... 770 780 790 800

Cry1Ac LDIDVGCT... 840 850 860 870 880 890

gi|131 LDIDVGCT... 810 820 830 840 850 860

Cry1Ac REKLEWETN... 900 910 920 930 940 950

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gi|131 REKLEWEFNIVYKEAKESVDALFVNSQVDRLQADTNIAIHAADKRVHSIREAYLPELSV
      870      880      890      900      910      920
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLV
      960      970      980      990      1000     1010
gi|131 IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVLV
      930      940      950      960      970      980
Cry1Ac VPEWEAEVSQEVVPCPRGYLLRV TAYKEGYGEGCVTTIHEIENNTDELKFSNCV EEEIYP
      1020     1030     1040     1050     1060     1070
gi|131 VPEWEAEVSQEVVPCPRGYLLRV TAYKEGYGEGCVTTIHEIENNTDELKFSNCV EEEVYP
      990      1000     1010     1020     1030     1040
Cry1Ac NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVVEEKS YTDGRRENPCFEFNRG
      1080     1090     1100     1110     1120     1130
gi|131 NNTVTCNKIILRLKKNMVRV TLLVIEDMTEPMKAILLYQLIMHQPMKKKH IQMDEETILVN
      1050     1060     1070     1080     1090     1100

```

>>gi|34423557|gb|AAQ68986.1| Sequence 4 from patent US 5 (1165 aa)  
 initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0  
 Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap  
 (5-1182:1-1165)

```

Cry1Ac CMQAMDNPNINECIPY NCLSNPEVEVLGGERIETGYTP IDISLSLTQ FLLSEFVPGAGF
      10      20      30      40      50      60
gi|344 MEIN-NQNQCVPYNCLSNPK EIIILGEERLETGNTVADISLGLINFL YSNFVPGGGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFGPSQWD AFLVQIEQLINQRIEEFARNQ AISRLEGLSNLYQ IYAESFRE
      70      80      90      100     110     120
gi|344 IVGLLELIWGFGPSQWD IFLAQIEQLISQRIEEFARNQ AISRLEGLSNLYK VYVRAFSD
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRI QFNDMNSALITTAIPLFAVQ NYQVPLLSVYVQA ANLHLSVLRDVS
      130     140     150     160     170     180
gi|344 WEKDPNTPALREEMRI QFNDMNSALITAIPLFRVQ NYEVALLSVYVQA ANLHLSILRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSR YNDLTRLIGNYTDHAVRWYNTGL ERVWGPDSRDWIRY NQFRREL
      190     200     210     220     230     240
gi|344 VFGERWGYDTATINN RYSDLTSLIHVYTNHCVDTYN QGLRRLEGRFLSDWIVY NFRFRQL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYSR TYPIRTVSQLTREIYTN-PVL-ENFD --GSFRGSAQGI EGSIR
      250     260     270     280     290
gi|344 TISVLDIVAFFPNYD IRTYPIQTATQLTREVYLDL PFINENLSPAASYP TFFSAESAIR
      240     250     260     270     280     290
Cry1Ac SPHLM DILNSIT IYTD AHRGEYYWSGHQIMASPVG FSGPEFTF PLYGTMGNAAPQRIVA
      300     310     320     330     340     350

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gi|344 SPHLVDFLNSFTIY TDSLARYAYWGGHLVNSFR TGTNTLIRSPLYGREGNTERPV TITA
      300     310     320     330     340     350
Cry1Ac QLQGGVYRVLSTLYRR PPNIGINNQQ-LSVLDGTEFAYGTSS NLPSAVYRKS GVTVDSDL
      360     370     380     390     400     410
gi|344 SPSVPIFRTLS----- YITGLDNSNPVAGIEGVEF ---QNTISRSIYRKS GPIDSF S
      360     370     380     390     400
Cry1Ac EIPPNNNVPPRQGF SHRLSHVSMFRSGFSNSSVSI IIRAPMFSWIHRSAEFNNII ASDSI
      420     430     440     450     460     470
gi|344 ELPPQDASVSPAIGY SHRLCHAT-FLERISGPRIA-- GTVFSWTHRSASPT NEVSPSRI
      410     420     430     440     450     460
Cry1Ac TQIPAVKGNFLFNG-SV ISGPGFTGGDLVRLNSSGNNI QNRGYIEVPI--HFPSTSTRYR
      480     490     500     510     520     530
gi|344 TQIPVWKAHTLASGAS VIKGPGFTGGDILTRNSMGE ---LGTLRVFTFTRLPQS ---YY
      470     480     490     500     510
Cry1Ac VRVRYASVTPIH LNVNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS -SLGNIV
      540     550     560     570     580     590
gi|344 IRFRYASVANRSGTFR YRSQPPSYGISFPKTM DAGEPLTSRSPAH---TTLFTPTIF SRAQ
      520     530     540     550     560     570
Cry1Ac GVRNFSGTAGV IIDREFIPVTATLEAEYNLERAQKAVNALFTSTNQ LGLKTNVTDYHID
      600     610     620     630     640     650
gi|344 EEFDLYIQSGVYIDR IEFIPVTATFEAEYDLERAQKV VNALFTSTNQ LGLKTDVTDYHID
      580     590     600     610     620     630
Cry1Ac QVSNLVTYLSDEFCL DEKRELSEKVKHAKRLSDERNLLQDSNFKD INRQPERGWGGSTGI
      660     670     680     690     700     710
gi|344 QVSNLVACLSEDEFCL DEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDRGWRGSTD I
      640     650     660     670     680     690
Cry1Ac TIQGGDDVFKENYV TLSPGTFDECYPTYLYQK IDESKLKAFTRYQLR GYIEDSQDLEIYSI
      720     730     740     750     760     770
gi|344 TIQGGDDVFKENYV TLSPGTFDECYPTYLYQK IDESKLKAYTRYQLR GYIEDSQDLEIYLI
      700     710     720     730     740     750
Cry1Ac RYNAKHETVNVPGT GSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLH CSRDGKCAHSH
      780     790     800     810     820     830
gi|344 RYNAKHEIVNVPGT GSLWPLSVENQIGPCGEPNRCAPHLEWNPDLH CSRDGKCAHSH
      760     770     780     790     800     810
Cry1Ac HFSLDIDVGTDLNED LGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      840     850     860     870     880     890
gi|344 HFSLDIDVGTDLNED LGVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKKW
      820     830     840     850     860     870
Cry1Ac SPHLM DILNSIT IYTD AHRGEYYWSGHQIMASPVG FSGPEFTF PLYGTMGNAAPQRIVA
      900     910     920     930     940     950

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Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPE
gi|344 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHRIREAYLPE
      880      890      900      910      920      930

      960      970      980      990      1000     1010
Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRS
gi|344 LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVEEQNNHRS
      940      950      960      970      980      990

      1020     1030     1040     1050     1060     1070
Cry1Ac VLVVPEWEAEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEE
gi|344 VLVVPEWEAEVSQEVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFNNCVEEEE
      1000     1010     1020     1030     1040     1050

      1080     1090     1100     1110     1120
Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|344 IYPNNTVTCINYTATQEEYEGTYTSRNRGYDEAYGNNPSVPADYASVYEEKSYTDGRRRN
      1060     1070     1080     1090     1100     1110

      1130     1140     1150     1160     1170     1180
Cry1Ac PCFNRGRYRDYTPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|344 PCESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120     1130     1140     1150     1160

>>gi|12819674|gb|AAE47788.1| Sequence 4 from patent US 6 (1165 aa)
  initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|128  MEIN-NQNQCVPYNCLSNPKEIILGEERLETGNTVADISLGLINFLYVVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESPFE
gi|128  IVGLLELIWGFQPSQWDFLAQIEQLISQRIEEFARNQAISRLEGLSNLYKVVYVRAFSD
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128  WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|128  VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDYTNQGLRRLEGRFLSDWIVYVNRFRRL
      180     190     200     210     220     230

      250     260     270     280     290

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Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIIEGSIR
gi|128 TISVLVDIVAFFPNYDIRTYPIQTATQLTREIVYLDLDFPINENLSPAASYPTFSAESAIIIR
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac SPHLMIDLNSITTYTDAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|128 SPHLVDFLNSFTIYTDLSLARYAYWGGHLVNSFRTGTTNLRSPLYGREGNTERPVTITA
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac QLGQGVYRTLSSTLYRRPFNIGINNQQ-LSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLD
gi|128 SPSVPIFRTLS-----YITGLDNSNPVAGIEGVEF---QNTISRSIYRKSQPIIDFSFS
      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac EIPPQNNVPPRQGFHSHLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
gi|128 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFVSWTHRSASPTNEVSPSRI
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
gi|128 TQIPWVKAHTLASGASVIKGPFTGGDILTRNSMGE---LGTLRVFTFGRLPQS---YY
      470      480      490      500      510

      540      550      560      570      580      590
Cry1Ac VVRVYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
gi|128 IRFRYASVANRSGTFRYSQPPSYGISFPKTMUDGEPLTSRSPAH---TTLFTPIITFSRAQ
      520      530      540      550      560      570

      600      610      620      630      640      650
Cry1Ac GVRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
gi|128 EEFDLIQSGVYIDRIEFIPVTATFEAEYDLERAQKVVNALFTSTNQLGLKTDVTDYHID
      580      590      600      610      620      630

      660      670      680      690      700      710
Cry1Ac QVSNLVITYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|128 QVSNLVACLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDWRGWRSTDI
      640      650      660      670      680      690

      720      730      740      750      760      770
Cry1Ac TIQGGDDVFKENYVTLSPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
gi|128 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLI
      700      710      720      730      740      750

      780      790      800      810      820      830
Cry1Ac RYNAKHETVNPVPGTGSWLPWSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHS
gi|128 RYNAKHEIVNPVPGTGSWLPWSVENQIGPCGEPNRCAPHLEWNPDLHCSCRDGKCAHSHS
      760      770      780      790      800      810

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      840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|128 HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      820      830      840      850      860      870

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      900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
gi|128 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHRIREAYLPE
      880      890      900      910      920      930

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      960      970      980      990     1000     1010
Cry1Ac LSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRS
gi|128 LSVIPGVNAAIPEELEERIFTAFSLYDARNVIKNGDFNNGLLCWNVKGHVVEEQNNHRS
      940      950      960      970      980      990

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     1020     1030     1040     1050     1060     1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVYTAYKEGYEGCVTIHEIENNTDELKFSNCVEEEE
gi|128 VLVVPEWEAEVSEQEVRVCPGRGYILRVYTAYKEGYEGCVTIHEIENNTDELKFNCCVEEEE
     1000     1010     1020     1030     1040     1050

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     1080     1090     1100     1110     1120
Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|128 VYPNNTVTCINYTATQEEYEGTYTSRNRGYDEAYGNNSVPADYASVYEEKSYTDRRREN
     1060     1070     1080     1090     1100     1110

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     1130     1140     1150     1160     1170     1180
Cry1Ac PCEFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|128 PCESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
     1120     1130     1140     1150     1160

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>>gi|118907897|gb|ABL55895.1| Sequence 4 from patent US (1165 aa)  
 initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0  
 Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap  
 (5-1182:1-1165)

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      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|118 MEIN-NQNCVPYNCLSNPKEIILGEEERLETGNTVADISLGLINFLYNSFVPGGGF
      10      20      30      40      50

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      70      80      90     100     110     120
Cry1Ac VLGLVDIIWGIWGFQSDAFLVQIEQLINQRIEEFARNQAI SRL EGLSNLYQIYAESFRE
gi|118 IVGLLELIWGFQSDAFLVQIEQLINQRIEEFARNQAI SRL EGLSNLYQVYVRAFSD
      60      70      80      90     100     110

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     130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSVLRDVS
gi|118 WEKDPNTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
     120     130     140     150     160     170

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     190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|118 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDYTNQGLRRLREGRFLSDWIVYNNRFRQL
     180     190     200     210     220     230

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     250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN-PVL-ENFP--GSFRGSAQGI EGSIR
gi|118 TISVLDIVAFFPNYDIRTYPIQTATQLTREYVLDLFPINENLSPAASYPTFSAESAIIIR
     240     250     260     270     280     290

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     300     310     320     330     340     350
Cry1Ac SPHLM DILNSIT IYTD AHRGEY YWSGHQIMASPVGSGPEFTFP LYGTMGNAAPQQRIVA
gi|118 SPHLVDFLNSFTIYTD SLARYAYWGGHLVNSFRGTGTTN LIRSPLYGREGNTERPVTTA
     300     310     320     330     340     350

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     360     370     380     390     400     410
Cry1Ac QLGQGVYR T L S S T L Y R R P F N I G I N N Q Q - L S V L D G T E F A Y G T S S N L P S A V Y R K S G T V D S L D
gi|118 S P S V P I F R T L S - - - - - Y I T G L D N S N P V A G I E G V E F - - - Q N T I S R S I Y R K S G P I D S F S
     360     370     380     390     400

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     420     430     440     450     460     470
Cry1Ac E I P P Q N N V P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A P M F S W I H R S A E F N N I I A S D S I
gi|118 E L P P Q D A S V P A I G Y S H R L C H A T - F L E R I S G P R I A - - - G T V F S W T H R S A P T N E V S P S R I
     410     420     430     440     450     460

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     480     490     500     510     520     530
Cry1Ac T Q I P A V K G N F L F N G - S V I S G P G F T G G D L V R L N S S G N N I Q N R G Y I E V P I - - H F P S T S T R Y R
gi|118 T Q I P W W K A H T L A S G A S V I K G P G T G G D I L T R N S M G E - - - L G T L R V T F T G R L P Q S - - - Y Y
     470     480     490     500     510

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     540     550     560     570     580     590
Cry1Ac V R V R Y A S V T P I H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D F G Y F E S A N A F T S - S L G N I V
gi|118 I R F R Y A S V A N R S G T F R Y S Q P P S Y G I S F P K T M D A G E P L T S R S F A H - - - T T L F T P I T F S R A Q
     520     530     540     550     560     570

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     600     610     620     630     640     650
Cry1Ac G V R N F S G T A G V I I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F T S T N Q L G L K T N V T D Y H I D
gi|118 E E F D L Y I Q S G V Y I D R I E F I P V T A T F E A E Y D L E R A Q K V V N A L F T S T N Q L G L K T D V T D Y H I D
     580     590     600     610     620     630

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     660     670     680     690     700     710
Cry1Ac Q V S N L V T Y L S D E F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N F K D I N R Q P E R G W G G S T G I
gi|118 Q V S N L V A C L S D E F C L D E K R E L S E K V K H A K R L S D E R N L L Q D P N F R G I N R Q P D R G W R S T D I
     640     650     660     670     680     690

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     720     730     740     750     760     770
Cry1Ac T I Q G G D D V F K E N Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R Y Q L R G Y I E D S Q D L E I Y S I
gi|118 T I Q G G D D V F K E N Y V T L P G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q L R G Y I E D S Q D L E I Y L I
     700     710     720     730     740     750

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640      650      660      670      680      690
Cry1Ac  720      730      740      750      760      770
TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSI
gi|337  720      730      740      750      760      770
TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQDLEIYLI
700      710      720      730      740      750

800      810      820      830
Cry1Ac  780      790      800      810      820      830
RYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSH
gi|337  780      790      800      810      820      830
RYNAKHEIVNVPGTGSWPLSVENQIGPCGEPNRCAPHLEWNPDLHCSRDEKCAHSH
760      770      780      790      800      810

840      850      860      870      880      890
Cry1Ac  840      850      860      870      880      890
HFSLDIDVGCETDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|337  840      850      860      870      880      890
HFSLDIDVGCETDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
820      830      840      850      860      870

900      910      920      930      940      950
Cry1Ac  900      910      920      930      940      950
RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIAMIHAADKRKRVHSIREAYLPE
gi|337  900      910      920      930      940      950
RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADNTNIAMIHAADKRVRHIREAYLPE
880      890      900      910      920      930

960      970      980      990      1000     1010
Cry1Ac  960      970      980      990      1000     1010
LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQRS
gi|337  960      970      980      990      1000     1010
LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLLCWVVKGHVEVEEQNNHRS
940      950      960      970      980      990

1020     1030     1040     1050     1060     1070
Cry1Ac  1020     1030     1040     1050     1060     1070
VLVVPWEAEVVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEE
gi|337  1020     1030     1040     1050     1060     1070
VLVVPWEAEVVSQEVVRCVGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFNCCVEEE
1000     1010     1020     1030     1040     1050

1080     1090     1100     1110     1120
Cry1Ac  1080     1090     1100     1110     1120
IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|337  1080     1090     1100     1110     1120
IYPNNTVTCINYTATQEEYEGTYTSRNRGYDEAYGNNPSPADYASVYEEKSYTDGRREN
1060     1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac  1130     1140     1150     1160     1170     1180
PCFNRGRYRDYTPLVGYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE
gi|337  1130     1140     1150     1160     1170     1180
PCESNRGYGDYTPLVGYVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE
1120     1130     1140     1150     1160

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>>gi|62771821|gb|AA01598.1| Sequence 6 from patent US 6 (1165 aa)  
 initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0  
 Smith-Waterman score: 5358; 69.941% identity (84.215% similar) in 1191 aa overlap  
 (5-1182:1-1165)

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10      20      30      40      50      60
Cry1Ac  10      20      30      40      50      60
CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|627  10      20      30      40      50      60
MEIN-NQNQCVPYNCLSNPKIILGGERLETGNTVADISLGLINFLYNSFVPGGGF

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10      20      30      40      50
Cry1Ac  70      80      90      100     110     120
VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISREGLSNLYQIYAESFRE
gi|627  70      80      90      100     110     120
IVGLLELIWGFIGPSQWDIFLAQIEQLISQRIEEFARNQAIISREGLSNLYKVYVRAFSD
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|627  130     140     150     160     170     180
WEKDPNTPALREEMRIQFNDMNSALTTAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
gi|627  190     200     210     220     230     240
VFGQRWGYDTATINNRYSDLTSLIHVYTNHCVDVTYNQGLRRLRLEGRFLSDWIVYVRRQL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  250     260     270     280     290
TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQIEGSIR
gi|627  250     260     270     280     290
TISVLDIVAFFPNYDIRTYPIQTATQLTREVYLDLFFINQNLSPAASYPTFSAAESAIR
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac  300     310     320     330     340     350
SPHLMIDLNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVA
gi|627  300     310     320     330     340     350
SPHLVDFLNSFTTYTDSLARYAYWGGHLVNSFRGTGTTNLRSLRSGREGNTERPVTITA
300     310     320     330     340     350

360     370     380     390     400     410
Cry1Ac  360     370     380     390     400     410
QLGQGVYRTLSSTLYRRPFPNIGINNQQ-LSVLDGTEFAYGTSSNLPASVYRKSQVDSLD
gi|627  360     370     380     390     400     410
SPSVPIFRTLS-----YITGLDNSNPVAGIEGVF---QNTISRSYRKSQVDSVDS
360     370     380     390     400

420     430     440     450     460     470
Cry1Ac  420     430     440     450     460     470
EIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMPFSWIHRSAEFNIIASDSI
gi|627  420     430     440     450     460     470
ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFSWTHRSASPTNEVSPSRI
410     420     430     440     450     460

480     490     500     510     520     530
Cry1Ac  480     490     500     510     520     530
TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPI--HFPSTSTRYR
gi|627  480     490     500     510     520     530
TQIPVWKAHTLASGASVIKPGFTGGDILTRNSMGE---LGLTRVTFTRGLPQS---YY
470     480     490     500     510

540     550     560     570     580     590
Cry1Ac  540     550     560     570     580     590
VRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
gi|627  540     550     560     570     580     590
IRFRYASVANRSGTFRYSQPPSYGIFPKTMDAGEPLTSRFAH---TTLFTPIITFSRAQ
520     530     540     550     560     570

600     610     620     630     640     650
Cry1Ac  600     610     620     630     640     650
GVRNFGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID

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gi|412 IRFRYASVANRSGTFRYSQPPSYGISFPKTM DAGEPLTSRSFAH---TTLFTPTITFSRAQ
      520      530      540      550      560      570

Cry1Ac GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHID
      600      610      620      630      640      650
gi|412 EEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAKVVALFTSTNQLGLKTDVTDYHID
      580      590      600      610      620      630

Cry1Ac QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
      660      670      680      690      700      710
gi|412 QVSNLVACLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPRGRWGRSTDI
      640      650      660      670      680      690

Cry1Ac TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSI
      720      730      740      750      760      770
gi|412 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKAYTRYQLRGYIEDSQDLEIYLI
      700      710      720      730      740      750

Cry1Ac RYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSH
      780      790      800      810      820      830
gi|412 RYNAKHEIVNVPGTGLWPLSVENQIGPCGEPNRCAPHLEWNPDLHDCSCRDGEKCAHSH
      760      770      780      790      800      810

Cry1Ac HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      840      850      860      870      880      890
gi|412 HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      820      830      840      850      860      870

Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
      900      910      920      930      940      950
gi|412 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHRIREAYLPE
      880      890      900      910      920      930

Cry1Ac LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRS
      960      970      980      990      1000     1010
gi|412 LSVIPGVNAAIFFEELEERIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHEVEEQNNHRS
      940      950      960      970      980      990

Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEE
      1020     1030     1040     1050     1060     1070
gi|412 VLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFNNCVEEEE
      1000     1010     1020     1030     1040     1050

Cry1Ac IYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
      1080     1090     1100     1110     1120
gi|412 VYPNNTVTCINYTATQEEYEGTYTSRNRGYDEAYGNNPSVPADYASVYEEKSYTDRREN
      1060     1070     1080     1090     1100     1110

      1130     1140     1150     1160     1170     1180

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Cry1Ac PCEFNRGYRDYTPLPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      ::: :
gi|412 PCBSNRGYDYPPLPAGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120     1130     1140     1150     1160

>>gi|490266|emb|CAA01235.1| bt4 [Bacillus thuringiensis] (1165 aa)
      initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50      60
gi|490 MEIN-NQNQCVPYNCLSNPKEIILGEEERLETGNTVADISLGLINFLYSNFPVGGGF
      10      20      30      40      50

Cry1Ac VLGVDVLIWGFIPGSPQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
      70      80      90      100     110     120
gi|490 IVGLLELIWGFIPGSPQWDFLAQIEQLISQRIEAFARNQAISRLEGLSNLYKVYVRAFSD
      60      70      80      90      100     110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|490 WEKDPTNPALREEMRIQFNDMNSALTAIPLFRVQNYEVALLSVYQAANLHLSILRDVS
      120     130     140     150     160     170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRREL
      190     200     210     220     230     240
gi|490 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRRLRLEGRFLSDWIVYNRFRQL
      180     190     200     210     220     230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN-PVL-ENPD--GSFRGSAQGIEGSIR
      250     260     270     280     290
gi|490 TISVLDIVAFFPNYDIRTYPIQTATQLTREYVLDLDFINENLSPAASYPTFSAESAIIIR
      240     250     260     270     280     290

Cry1Ac SPHLMIDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVA
      300     310     320     330     340     350
gi|490 SPHLVDLNSFTIYTDLSLARYAYWGGHLVNSFRGTGTTNLRSLYRGENTERPVTIITA
      300     310     320     330     340     350

Cry1Ac QLGQGVYRSLTSSTLYRRFPNIGINNQQ-LSVLDGTEFAYGTSSNLPSAVYRKSGETVDSL
      360     370     380     390     400     410
gi|490 SPSVPIFRTLS-----YITGLDNSNPVAGIEGVEF---QNTISRSYRKSGETVDSL
      360     370     380     390     400

Cry1Ac EIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
      420     430     440     450     460     470
gi|490 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA--GTVFVSWTHRSASPTNEVSPSRI
      410     420     430     440     450     460

      480     490     500     510     520     530

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Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR  
gi|490 TQIPWVKHAHTLASGASVIKGPGFTGGDLTRNSMGE---LGLTRVFTGRLPQS---YY  
470 480 490 500 510

540 550 560 570 580 590  
Cry1Ac VRVRYASVTPHILNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV  
gi|490 IRFRVYASVANRSGTFRYSQPPSYGISFPKTM DAGEPLTSRSFAH---TTLFTPIITFSRAQ  
520 530 540 550 560 570

600 610 620 630 640 650  
Cry1Ac GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID  
gi|490 EEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAQKVVNALFTSTNQLGLKTDVTDYHID  
580 590 600 610 620 630

660 670 680 690 700 710  
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI  
gi|490 QVSNLVACLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRGWRGSDTI  
640 650 660 670 680 690

720 730 740 750 760 770  
Cry1Ac TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSI  
gi|490 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKAYTRYQLRGYIEDSQDLEIYLI  
700 710 720 730 740 750

780 790 800 810 820 830  
Cry1Ac RYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCS CRDGEKCAHSH  
gi|490 RYNAKHEIVNVPGTGLSWPLSVENQIGPCGEPNRCAPHLEWNPDLHCS CRDGEKCAHSH  
760 770 780 790 800 810

840 850 860 870 880 890  
Cry1Ac HFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW  
gi|490 HFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW  
820 830 840 850 860 870

900 910 920 930 940 950  
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPE  
gi|490 RDKRETTQLQETTIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHRIREAYLPE  
880 890 900 910 920 930

960 970 980 990 1000 1010  
Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLCWNVKGVHVDVEEQNNQRS  
gi|490 LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLCWNVKGVHVEVEEQNNHRS  
940 950 960 970 980 990

1020 1030 1040 1050 1060 1070  
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFNCSNVEE  
gi|490 VLVVPEWEAEVSEQEVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFNCSNVEE  
1000 1010 1020 1030 1040 1050

1080 1090 1100 1110 1120  
Cry1Ac IYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN  
gi|490 VYPNNVTVCIN YATQEEYEGTYTSRNRGYDEAYGNNPSPADYASVYEEKSYTDGRREN  
1060 1070 1080 1090 1100 1110

1130 1140 1150 1160 1170 1180  
Cry1Ac PCEFNRGRYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|490 PCESNRGYDGYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1120 1130 1140 1150 1160

>>gi|40280|emb|CAA38099.1| unnamed protein product [Baci (1165 aa)  
initn: 4919 init1: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0  
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap  
(5-1182:1-1165)

10 20 30 40 50 60  
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|402 MEIN-NQNQCVPYNCLSNPKEIILGEERLETGNTVADISLGLINFLYVYVPGGDF  
10 20 30 40 50

70 80 90 100 110 120  
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE  
gi|402 IVGLLELIWIGIFGPSQWDFLAQIEQLISQRIEEFARNQAISRLEGLSNLYQIYVYRAFSD  
60 70 80 90 100 110

130 140 150 160 170 180  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLDRVDS  
gi|402 WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSVLDRVDS  
120 130 140 150 160 170

190 200 210 220 230 240  
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|402 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRRLREGFLSDWIVYVYRFRRL  
180 190 200 210 220 230

250 260 270 280 290  
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIIEGSIR  
gi|402 TISVLDIVAFPNYDRTYPIQTATQLTREYVLDLPPFINENLSPAASYPTFSAAESAIIR  
240 250 260 270 280 290

300 310 320 330 340 350  
Cry1Ac SPHLMDILNSITTYTDAHRGEYWSGHQIMASPVGFSPEFTFPLYGTMGNAAPQRIVA  
gi|402 SPHLVDFLNSFTTYTDSLARYAYWGGHLVNSFRTGTTTLIRSPLYGREGNTERPVTITA  
300 310 320 330 340 350

360 370 380 390 400 410  
Cry1Ac QLGGQVYR TLSSTLYRRPFNIGINNQQ-LSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLD  
gi|402 SPSVPIFR TLS-----YITGLDNSNPVAGIEGVF---QNTISRSYRKS GPIDSPS  
360 370 380 390 400

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420      430      440      450      460      470
Cry1Ac EIPPNQNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWHRSAEFNNI IASDSI
gi|402 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA--GTVFSWTHRSASPNEVSPSRI
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
gi|402 TQIPVWKAHTLASGASVIKGPFTGGDILTRNSMGE---LGTLRVFTTGRLPQS---YY
470      480      490      500      510

540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
gi|402 IRFRYASVANRSGTFRYSQPPSYGISFPKTMUDGEPLTSSRSFAH--TTLFTPIITFSRAQ
520      530      540      550      560      570

600      610      620      630      640      650
Cry1Ac GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQGLKTNVTDYHID
gi|402 EEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAQKVVNALFTSTNQGLKTDVTDYHID
580      590      600      610      620      630

660      670      680      690      700      710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|402 QVSNLVAQLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQDRGRWGSSTDI
640      650      660      670      680      690

720      730      740      750      760      770
Cry1Ac TIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
gi|402 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLI
700      710      720      730      740      750

780      790      800      810      820      830
Cry1Ac RYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHS
gi|402 RYNAKHEIVNVPGTGSWPLSVENQIGPCGEPNRCAPHLEWNPDLHCSCRDGEKCAHSHS
760      770      780      790      800      810

840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|402 HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
820      830      840      850      860      870

900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPE
gi|402 RDKRETQLLETTIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHRIREAYLPE
880      890      900      910      920      930

960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCMNKGVHVDVEEQNNQRS
gi|402 LSVIPGVNAAIFFEELEERIFTAFSLYDARNVIKNGDFNNGLLCWNKGVHVEEQNNHRS
940      950      960      970      980      990

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1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEE
gi|402 VLVVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFNKNCVEEE
1000      1010      1020      1030      1040      1050

1080      1090      1100      1110      1120
Cry1Ac IYPNNTVTNCDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|402 VYPNNTVTNCDYTVNQEEYGGAYTSRNRGYDEAYGNPSPVPADYASVYEEKSYTDRREN
1060      1070      1080      1090      1100      1110

1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|402 PCESNRGYDTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120      1130      1140      1150      1160

>>gi|53932144|gb|AAV00426.1| Sequence 4 from patent US 6 (1165 aa)
initn: 4919 init1: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|539 MEIN-NQNQCVPYNCLSNPKEIILGEEERLETGNTVADISLGLINFLYSNFVPGGGF
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFIPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|539 IVGLLELIWGFIPGSQWDIFLAQIEQLISQRIEEFARNQAISRLEGLSNLYKVYVRAFSD
60      70      80      90      100      110

130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
120      130      140      150      160      170

190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFRREL
gi|539 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDVTYNQGLRRLREGFLSDWIVYVYVFRRL
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIIEGSIR
gi|539 TISVLDIVAFFPNYDRTYPIQTATQTLTREVYLDLFFINENLSPAASYPTFSAAESAIIR
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac SPHLMIDLNSITITDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|539 SPHLVDFLNSFTITITDRLARYAYWGGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITA
300      310      320      330      340      350

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360      370      380      390      400      410
Cry1Ac  QLQGVYVYRTLSSTLYRRPFNIGINNQQ--LSVLDGTEFAYGTSSNLPNAVYRKSQVTVDSLD
gi|539  SPSVPIFRTLS-----YITGLDNSNPVAGIEGVEF---QNTISRSIYRKSGPIDSFSS
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac  EIPPNNNVPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSI
gi|539  ELPPQDASVSPAIGYSHRLCHAT--FLERISGPRIA---GTVFSWTHRSASPTNEVSPSRI
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac  TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPI--HFPSTSTRYR
gi|539  TQIPVVKAHTLASGASVIKGPFTGGDILTRNSMGE---LGTLRVTFTRGLPQS---YY
470      480      490      500      510

540      550      560      570      580      590
Cry1Ac  VRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFS--SLGNIV
gi|539  IRFRYASVANRSGTFRYSQPPSYGISFPKMTDAGEPLTRSFAH---TTLFTPTFSRAQ
520      530      540      550      560      570

600      610      620      630      640      650
Cry1Ac  GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSNQLGLKTNVTDYHID
gi|539  EEFDLIYIQSGVYIDRIEFPVPTATFEAEYDLERAQKVVNALFTSTNQLGLKTDVTDYHID
580      590      600      610      620      630

660      670      680      690      700      710
Cry1Ac  QVSNLVTYLSDDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|539  QVSNLVACLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWRGSTDII
640      650      660      670      680      690

720      730      740      750      760      770
Cry1Ac  TIQGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSI
gi|539  TIQGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQDLEIYLI
700      710      720      730      740      750

780      790      800      810      820      830
Cry1Ac  RYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDLDCSCRDGEKCAHSHS
gi|539  RYNAKHEIVNVPGTGSWPLSVENQIGPCGEPNRCAPHEWNPDLHCSCRDGEKCAHSHS
760      770      780      790      800      810

840      850      860      870      880      890
Cry1Ac  HFSLDIDVGCETDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|539  HFSLDIDVGCETDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
820      830      840      850      860      870

900      910      920      930      940      950
Cry1Ac  RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPE
gi|539  RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHRIREAYLPE

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880      890      900      910      920      930
Cry1Ac  LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQVNVKGVHVDVEEQNNQRS
gi|539  LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLLCWNVKGHVEVEEQNNHRS
940      950      960      970      980      990

1020     1030     1040     1050     1060     1070
Cry1Ac  VLWVPEWEAEVSVQEVRCVGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEE
gi|539  VLVIPEWEAEVSVQEVRCVGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFNVCVEEE
1000     1010     1020     1030     1040     1050

1080     1090     1100     1110     1120
Cry1Ac  IYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|539  VYPNNVTVCINYTATQEEYEGTYTSRNRGYDEAYGNNPSVPADYASVYEEKSYTDRREN
1060     1070     1080     1090     1100     1110

1130     1140     1150     1160     1170     1180
Cry1Ac  PCEFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|539  PCESNRGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120     1130     1140     1150     1160

>>gi|3012930|gb|AAC11773.1|I76776 Sequence 4 from patent (1165 aa)
initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|301  MEIN-NQNQCVPYNCLSNPKEIILGEERLETGNTVADISLGLINFLYSNFPVGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFIPGSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|301  IVLLELIWGFIPGSQWDAFLVQIEQLISQRIEAFARNQAISRLEGLSNLYKVYVRAFSD
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALITAIPLFVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|301  WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|301  VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDVTYNQGLRRLRLEGRFLSDWIVYVYRFRQL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIIEGSIR
gi|301  TISVLDIVAFFPNYDIRTYPIQTATQLTREYVLDLFPINENLSPAASYPTFSAESAIR

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240      250      260      270      280      290
Cry1Ac SPHLMIDLNSITIIYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|301 SPHLVDFLNSFTIYDLSLARYAYWGGHLVNSFRGTNTLNLRSPLYGREGNTERPVTITA
300      310      320      330      340      350
Cry1Ac QLGQGVYRVLSSSTLYRRPFNIGINNQQ-LSVLDGTEFAYGTSSNLPSSAVYRKSQGVDSLD
gi|301 SPSVPIFRITLS-----YITGLDNSNPVAGLEGVEF---QNTISRSIYRKSQGPIDSFS
360      370      380      390      400      410
Cry1Ac EIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
gi|301 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFSWTHRSASPINEVSPSRI
420      430      440      450      460      470
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
gi|301 TQIPVVKAKHTLASGASVKGPGFTGGDLITRNSMGE---LGTLRVTFTGRLPQS---YY
480      490      500      510      520      530
Cry1Ac VRRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
gi|301 IRFRYASVANRSGTFRYSQPPSYGISFPKTM DAGEPLTSRFAH---TTLFTPIFSAQA
540      550      560      570      580      590
Cry1Ac GVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHID
gi|301 EFDLYIQSGVYIDRIEPIPVTTATFEAEYDLERAKVVALFTSTNQLGLKTDVTDYHID
600      610      620      630      640      650
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
gi|301 QVSNLVAQLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRGWRGSDI
660      670      680      690      700      710
Cry1Ac TIQGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYI
gi|301 TIQGGDDVFKENYVTLPGTDFDECYPTYLYQKIDESKLLKAYTRYQLRGYIEDSQDLEIYLI
720      730      740      750      760      770
Cry1Ac RYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSH
gi|301 RYNAKHEIVNVPGTGLSWPLSVENQIGPCGEPNRCAPHLEWNPDLHDCSCRDEKCAHSH
780      790      800      810      820      830
Cry1Ac HFSLDIDVGCITDNLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|301 HFSLDIDVGCITDNLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
840      850      860      870      880      890

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gi|301 HFSLDIDVGCITDNLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
820      830      840      850      860      870
900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPE
gi|301 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAMHAADKRVHRIREAYLPE
880      890      900      910      920      930
960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQVNVKGVHVDVEEQNNQRS
gi|301 LSVIPGVNAAIFEELEERIFTAFSLYDARNIKNKDFNNGLLCWNVKGHVEVEEQNNHRS
940      950      960      970      980      990
1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNVCVEEE
gi|301 VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFNVCVEEE
1000      1010      1020      1030      1040      1050
1080      1090      1100      1110      1120
Cry1Ac IYPNNVTVCNDYTVNQEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRREN
gi|301 VYPNNVTVCINYTATQEEYEGTYTSRNRGYDEAYGNPSPADYASVYEEKSYTDRREN
1060      1070      1080      1090      1100      1110
1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|301 PCESNRGYDGYTLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1120      1130      1140      1150      1160
>>gi|1411120|gb|AAE57660.1| Sequence 6 from patent US 6 (1165 aa)
initn: 4919 initl: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E( ): 0
Smith-Waterman score: 5358; 69.941% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)
10      20      30      40      50      60
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|141 MEIN-NQNQCVPYNCLSNPKKEIILGEERLETGNTVADISLGLINFLYVYVPGGGF
10      20      30      40      50
70      80      90      100      110      120
Cry1Ac VLGLVDIINGIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLEGLSNLYQIYAESFRE
gi|141 IVGLLELWIFGPSQWDFLAQIEQLISQRIEERFARNQAIISRLEGLSNLYQIYVYVRAFS
60      70      80      90      100      110
130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|141 WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
120      130      140      150      160      170
190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|141 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

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gi|141 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDVTYNQGLRRLLEGRFLSDWIVVYNRFRRLQ
180      190      200      210      220      230

          250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQIGEGSIR
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 TISVLDIVAFFPNYDIRTYPIQTATQLTREVYLDLPPFINQNLSPAASYPTFSAESAIR
240      250      260      270      280      290

          300      310      320      330      340      350
Cry1Ac SPHLMIDILNSITTYDAHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 SPHLVDFLNSFTIYTDLSLARYAYWGGHLVNSFRTGTTNLIRSPLYGREGNTERPVTITA
300      310      320      330      340      350

          360      370      380      390      400      410
Cry1Ac QLGQGVYRITLSSTLYRRPFNIGINNQQ-LSVLDGTFEAYGTSSNLPASAVYRKSGTVDSLD
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 SPSVPPIFRITLS-----YITGLDNSNPVAGIEGVF----QNTISRSIYRKSQPIDSF
360      370      380      390      400

          420      430      440      450      460      470
Cry1Ac EIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFSWTHRSASPINEVSPSRI
410      420      430      440      450      460

          480      490      500      510      520      530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 TQIPVVKHAHTLASGASVIKPGFTGGDLTRNSMGE---LGTLRVTFTRGLPQS---YY
470      480      490      500      510

          540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHLLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 IRFRYASVANRSGTFRYSQPPSYGISFPKTMUDGEPLTSSRFAH---TTLFTPIITFSRAQ
520      530      540      550      560      570

          600      610      620      630      640      650
Cry1Ac GVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 EEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAQKVVNALFTSTNQLGLKTDVTDYHID
580      590      600      610      620      630

          660      670      680      690      700      710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 QVSNLVACLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPRDGRWRSSTDI
640      650      660      670      680      690

          720      730      740      750      760      770
Cry1Ac TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 TIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLI
700      710      720      730      740      750

          780      790      800      810      820      830
Cry1Ac RYNAKHETVNVPGTSSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSH

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:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 RYNAKHEIVNVPGTSSLWPLSVENQIGPCGEPNRCAPHLEWNPDLHCSCRDEKCAHSH
760      770      780      790      800      810

          840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKW
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 HFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKW
820      830      840      850      860      870

          900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHADKRVHSIREAYLPE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAMIHADKRVHIREAYLPE
880      890      900      910      920      930

          960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNKGVHDVVEEQNNQRS
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLLCWNKGVHVEVEEQNNHRS
940      950      960      970      980      990

          1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 VLVVPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFNCCVEEE
1000      1010      1020      1030      1040      1050

          1080      1090      1100      1110      1120
Cry1Ac IYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 VYPNNVTVCINYTATQEEYEGTYTSRNRGYDEAYGNPSPADYASVYEEKSYTDRREN
1060      1070      1080      1090      1100      1110

          1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGRYDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|141 PCESNRGYDYPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1120      1130      1140      1150      1160

>>gi|1247715|emb|CAA01885.1| bt4 [Bacillus thuringiensis (1165 aa)
initn: 4919 init1: 3109 opt: 3774 Z-score: 4440.6 bits: 833.6 E(): 0
Smith-Waterman score: 5362; 70.025% identity (84.215% similar) in 1191 aa overlap
(5-1182:1-1165)

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|124 MEIN-NQNCQVYPYNCLSNPKEIILGEERLETGNTVADISLGLINFLYVYVPGGGF
10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac VLGLDVDIWGFIPGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFRE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|124 IVGLLELIWGFIPGSPQWDFLAQIEQLISQRIEEFARNQAIISRLGSLNLYKYVYVRAFSD
60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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gi|124 WEKDPNTPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVVAANLHLSILRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      .....
gi|124 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRLEGRFLSDWIVYNRFRQL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIEGSIR
      .....
gi|124 TISVLDIVAFFPNYDIRTYPIQTATQLTREVYLDLFPINENLSPAASYPTFSAAESAIIR
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac SPHLMILNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVA
      .....
gi|124 SPHLVDFLNSFTIYDLSLARYAWGGHLVNSFRGTGTTNLRSPLYGREGNTERPVTITA
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac QLQGVYRTLSSTLYRRPFNIGINNQQ-LSVLDGTFEAYGTSSNLPASAVYKSGTVDSLD
      .....
gi|124 SPSVPIFRTLS-----YITGLDNSNPVAGIEGVEF---QNTISRSIYRKSGPIDSF
      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac EIPPNQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSI
      .....
gi|124 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA--GTVFSWTHRSASPINEVSPSRI
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
      .....
gi|124 TQIPWVKAHTLASGASVIKPGFTGGDILTRNSMGF---LGTLRVTFTRLPQS---YY
      470      480      490      500      510

      540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFPS-SLGNIV
      .....
gi|124 IRFRYASVANRSGTFRYSQPPSYGISFPKTMUDGEPLTSRSFAH---TTLFTPIITFSRAQ
      520      530      540      550      560      570

      600      610      620      630      640      650
Cry1Ac GVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQGLKTNVTDYHID
      .....
gi|124 EEFDLIYIQSGVYIDRIEFIPVTATFPAEYDLERAQKVVNALFTSTNQGLKTNVTDYHID
      580      590      600      610      620      630

      660      670      680      690      700      710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI
      .....
gi|124 QVSNLVACLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRGWSDDI
      640      650      660      670      680      690

      720      730      740      750      760      770

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Cry1Ac TIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSI
      .....
gi|124 TIQGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLI
      700      710      720      730      740      750

      780      790      800      810      820      830
Cry1Ac RYNAKHETVNVPGTGLSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGEKCAHSH
      .....
gi|124 RYNAKHEIVNVPGTGLSWLPLSVENQIGPCGEPNRCAPHLEWNPDLHCSRDGEKCAHSH
      760      770      780      790      800      810

      840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      .....
gi|124 HFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
      820      830      840      850      860      870

      900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPE
      .....
gi|124 RDKRETLQLETTIVYKEAKESVDALFVNSQYDRLQADTNIAMHAADKRVHIREAYLPE
      880      890      900      910      920      930

      960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRS
      .....
gi|124 LSVIPGVNAAIFEELEERIFTAFSLYDARNVIKNGDFNNGLLCWNVKGVHVEEQNNHRS
      940      950      960      970      980      990

      1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEE
      .....
gi|124 VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEE
      1000      1010      1020      1030      1040      1050

      1080      1090      1100      1110      1120
Cry1Ac IYPNNTVTCDNYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
      .....
gi|124 IYPNNTVTCDNYTVNQEEYEGTYTSRNRGYDEAYGNPNVSPADYASVYEEKSYTDRRRRN
      1060      1070      1080      1090      1100      1110

      1130      1140      1150      1160      1170      1180
Cry1Ac PCFENRGRYDYPPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|124 PCENRGRYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1120      1130      1140      1150      1160

>>gi|911501|gb|AAA70955.1| Sequence 5 from patent US 542 (695 aa)
      initn: 3753 init1: 3174 opt: 3753 Z-score: 4419.1 bits: 828.9 E(): 0
      Smith-Waterman score: 3753; 85.044% identity (92.375% similar) in 682 aa overlap
      (5-682:1-677)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      .....
gi|911 MDNPNININECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120

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Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|911 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|911 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|911 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|911 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
      240     250     260     270     280     290

      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|911 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

      370     380     390     400     410     420
Cry1Ac GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIIPPQ
gi|911 GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIIPPQ
      360     370     380     390     400     410

      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|911 NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470

      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|911 TKSTNLGSGTSPVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

      540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV--GVRNF
gi|911 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTTPFNFSNGSSVFTLSAHVF
      540     550     560     570     580     590

      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|911 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNL
      600     610     620     630     640     650

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      660     670     680     690     700     710
Cry1Ac VTLYSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGG
      :      :      :      :      :      :
gi|911 VECLSDEFCLDEKRELSKVKHANDLVMGSIYFKIQTLGESSIDN
      660     670     680     690

>>gi|33765721|gb|AAQ52372.1| Sequence 22 from patent US (1168 aa)
      initn: 5026 init1: 3036 opt: 3755 Z-score: 4418.2 bits: 829.5 E(): 0
      Smith-Waterman score: 5149; 66.917% identity (81.788% similar) in 1197 aa overlap
      (5-1182:1-1168)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 MEIN-NQNQCIPYNCLSNPEVEVFLDGERILPDIDPLEVSLSLQLFLNNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 ISGLLDKIWALRPSDWELFLAQIEQLIDRRRIERTVRAKAIAELEGLGRSYQLYGEAFKE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 WEKTPDNTAARSVRTFRFRIDAQIEANIPSPRVSGFEVPLLVYTYQAANLHLLALRDSV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 VFGERGLTNTVNDIYNRQVNRIGEYKHCVDTYKTELERLGRSIAQWRIYNQFRREL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 TLTVLDIVAVFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac PHLMDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 PHLMDIFNSMIMYTSNDRREHYWSGLEMTATNT--EGHQRSFPLAGTIGNSAPPVTVRNN
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac LQGGVYRRTLSSSTLYRRPFNIGINNQQLSVLD--GTEFAYG--TSSNLPSSAVYRKSGETVDS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 -GEGIYRILSEPFYSAPP-LGT----SVLGSRGEEFAPASNTTSLPSTIYRNRGTVDS
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac LDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 LVSIPPQDYVPPHRYSHLLSHVTM----RNSS-----PIFHWTHRSATPRNTIDPD
      410     420     430     440     450

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480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNNGSVISGPGFTGGDLVRLNLSGNNIQNRGYIEVPIHFPSTST-RYR
gi|337 SITQIPAVKGAYIFNSPVIITGPGHTGGDIIRFNP--NTQNN--IRIP--FQSNVQRYSR
460      470      480      490      500

540      550      560      570      580
Cry1Ac VRVRYAS---VTPIHLLNVNWNSSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSL
gi|337 IRMRVAAEADCILESGVNIIVTGAGVTRFRPIPIKATMTPGSPLTYYSFYQADLNINLTAPI
510      520      530      540      550      560

590      600      610      620      630      640
Cry1Ac --GNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNV
gi|337 RPNNFVSIIRSNQPGNLYIDRIEFIPIDPIREAEHDLERAKAVNALFTSSNQLGLKTDV
570      580      590      600      610      620

650      660      670      680      690      700
Cry1Ac TDYHIDQVSNLVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGW
gi|337 TDYHIDQVSNLVACLDEFCLDEKRELESEKVKHAKRLSDERNLLQDNFTGINRQVDRGW
630      640      650      660      670      680

710      720      730      740      750      760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQD
gi|337 RGSTDITIQGMDVFKENYVTLPGTFDECYPTYLYQKIDESKLLKPYTRYELRGYIEDSQD
690      700      710      720      730      740

770      780      790      800      810      820
Cry1Ac LEIYSIRYNAKHETVNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK
gi|337 LEVYLIRYNAKHETLNVPGTGSLLWPLAESSIGRCGEPNRCAPHLEWNPDLDCSCRDGEK
750      760      770      780      790      800

830      840      850      860      870      880
Cry1Ac CAHSHHFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVK
gi|337 CAHSHHFSLDIDVGCTDLNEDLGVVVIFKIKTQDGYARLGNLEFLEEKPLVGEALARVK
810      820      830      840      850      860

890      900      910      920      930      940
Cry1Ac RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIR
gi|337 RAEKKWRDKRDKLEWETNIVYKEAKESVDALFVDSQYNRLQTDNTIAMIHVADKRVHRI
870      880      890      900      910      920

950      960      970      980      990      1000
Cry1Ac EAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEE
gi|337 EAYLPELSVIPGVNAAIFFEELEGLIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEE
930      940      950      960      970      980

1010     1020     1030     1040     1050     1060
Cry1Ac QNNQRSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGGCVTIHEIENNTDELKFS
gi|337 QNNHRSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGGCVTIHEIEDHTDELKFR
990     1000     1010     1020     1030     1040

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1070     1080     1090     1100     1110     1120
Cry1Ac NCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEKSYT
gi|337 NCEEEEVYPNNTVTCNDYPANQEEYRAAETSRRNGYGESYESNSSIPAAYAPIYE-KAYT
1050     1060     1070     1080     1090     1100

1130     1140     1150     1160     1170     1180
Cry1Ac DGRRENPCFNRGRDYTPLPVGYVTKELEYFPETDKVWIEIETEGTFIVDSVELLME
gi|337 DGRKENSCESNRGYNYTLPAGYVTKELEYFPETDKVWIEIETEGTFIVDSVELLME
1110     1120     1130     1140     1150     1160

Cry1Ac E
:
gi|337 E

>>gi|13537904|emb|CAC35765.1| unnamed protein product [B (1168 aa)
initn: 5026 init1: 3036 opt: 3755 Z-score: 4418.2 bits: 829.5 E(): 0
Smith-Waterman score: 5149; 66.917% identity (81.788% similar) in 1197 aa overlap
(5-1182:1-1168)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|135  MEIN-NQNQCIPYNCLSNPEEVLGGERILDPIDPLEVSLSLQLLNNFVPGGGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|135  ISGLLDKIWALRPSDWELFLAQIEQLIDRRIERTVRAKAIAELEGLGRSYQLYGEAFKE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|135  WEKTPDNTAARSRVTERFRIIDAQIEANIPSPFRVSGFEVPLLLVYTAANLHLALLRDSV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|135  VFGERWGLTTTNNVDIYNRQVNRIGEYSKHCVDTYKTELERLGFRIAQWRIYNYQFRREL
180     190     200     210     220     230

250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGS---AQGIEGSIRS
gi|135  TLTVLDIVAVFPNYDSRLYPIRTISQLTREIYTSVSEFYGVINSNNIIGTLTEQQIRR
240     250     260     270     280     290

300     310     320     330     340     350
Cry1Ac PHLMDILNSITITDAHRGEBYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQ
gi|135  PHLMDFFNSMIMYTSNRRHEHYWSGLEMTATNT--EGHQRSFPLAGTIGNSAPPVTVRRN
300     310     320     330     340     350

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180      190      200      210      220      230
Cry1Ac  TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSGFRGS--AQGIEGSIRS
gi|112  TLTVLDIVAVFPNYSRSLYPIRTISQLTREIYTSVPSEFYGVINSNNIIGTLTEQQIRR
240      250      260      270      280      290
Cry1Ac  PHLMDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQ
gi|112  PHLMDFNNSMIMYTSNRRREHYWSGLEMTATNT--EGHQRSFPLAGTIGNSAPPVTVRNN
300      310      320      330      340      350
Cry1Ac  PHLMDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQ
gi|112  PHLMDFNNSMIMYTSNRRREHYWSGLEMTATNT--EGHQRSFPLAGTIGNSAPPVTVRNN
360      370      380      390      400      410
Cry1Ac  LGQGVYRTLSSTLYRRPFNIGINNQQLSVLD--GTEFAYG--TSSNLPASVYRKSQTVDS
gi|112  -GEGIYRILSEPFYSAPF-LGT----SVLGSRGEEFASFASNTTSLPSTIYRNRGTVDS
380      390      400      410      420      430
Cry1Ac  LDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASD
gi|112  LVSIPPQDYSVPPHRGYSHLLSHVTM----RNSS-----PIFHWTHRSATPRNTIDPD
440      450      460      470
Cry1Ac  SITQIPAVKGNFLFNQSVISGPGFTGGDLVRLNLSGNNIQNRGYIEVPIHFPSTST-RYR
gi|112  SITQIPAVKGAIFNRPVITGPGHTGGDIIRFNP--NTQNN--IRIP--FQSNVQRYR
480      490      500      510      520      530
Cry1Ac  VRVRYAS---VTPIHNLVNWGNSSIFSNT-VPATATSLDNLQSSDFGYFESANAFTSSL
gi|112  IRMRYAAEADCILESVNIIVTGAGVTRFRPIPIKATMTPGSPLTYYSFQYADLNINLTAPI
540      550      560      570      580
Cry1Ac  --GNIVGVNRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNV
gi|112  RPNNFVSIIRSNQPGNLYIDRIEFIPIDPIREAEHDLERAQKAVNALFTSSNQLGLKTDV
590      600      610      620      630      640
Cry1Ac  TDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGW
gi|112  TDYHIDQVSNLVACLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDNFTGINRQVDRGW
650      660      670      680      690      700
Cry1Ac  GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQD
gi|112  RGSTDITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKPYTRYELRGYIEDSQD
710      720      730      740      750      760
Cry1Ac  LEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGK
gi|112  LEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGK

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gi|112  LEVYLIRYNAKHETLNVPGTGSWPLAAESSIGRCGEPNRCAPHLEWNPDLDCSCRDGK
750      760      770      780      790      800
Cry1Ac  CAHSHHFFSLDIDVGCITDLNEDLGVVVFIFKIKTQDGHARLGNLEFLEEKPLVGEALARVK
gi|112  CAHSHHFFSLDIDVGCITDLNEDLGVVVFIFKIKTQDGYARLGNLEFLEEKPLLGEALARVK
810      820      830      840      850      860
Cry1Ac  RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIR
gi|112  RAEKKWRDKRDKLEWETNIVYKEAKESVDALFVNSQYRNLQDQDTNIAMIHVADKRVHRIR
870      880      890      900      910      920
Cry1Ac  EAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEE
gi|112  EAYLPELSVIPGVNAAIFFEELEGLIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEE
930      940      950      960      970      980
Cry1Ac  QNNQRSVLVPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGECVTIHEIENNTDELKFS
gi|112  QNNHRSVLVPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGECVTIHEIEDHTDELKFR
990      1000      1010      1020      1030      1040
Cry1Ac  NCVEEIIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYT
gi|112  NCVEEIVPNNTVTCDYTPANQEEYRAAETSRRNGYGESYESSNSSIPAEYAPIYE-KAYT
1050      1060      1070      1080      1090      1100
Cry1Ac  DGRRENPCFNRGRDYTPLVGYVTKLEYPFETDKVWIEIGETEGTFIVDSVELLLME
gi|112  DGRKENSCESNRGYNYTLPAGYVTKLEYPFETDKVWIEIGETEGTFIVDSVELLLME
1110      1120      1130      1140      1150      1160
Cry1Ac  E
gi|112  E
>>gi|3410670|gb|AAC31092.1|I90730 Sequence 6 from patent (1168 aa)
initn: 4975 init1: 2994 opt: 3713 Z-score: 4368.6 bits: 820.3 E(): 0
Smith-Waterman score: 5098; 66.332% identity (81.119% similar) in 1197 aa overlap
(5-1182:1-1168)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|341  MEIN-NQQCIPYNCLSNPEEVFLDGERILPDIDPLEVLSLLQFLNNFVPGGGF
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGSLNLYQIYAESFRE

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initn: 5087 init1: 3065 opt: 3702 Z-score: 4355.7 bits: 817.9 E(): 0
Smith-Waterman score: 5251; 68.992% identity (83.445% similar) in 1190 aa overlap
(5-1182:1-1160)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|295 MDINHQ-NQCIPYNCLSNPDAILLDAERLETGNTVADISLGLINFLYSNFVPGGGF
Cry1Ac VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|295 IVGELLEHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|295 WEKDPSPALREEMRTQFNVMSALIAAIPLLRVRNYEVALLSVYVQAANLHLSVLRDVS
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|295 VYGQRWGFDPATVNSRYSDLTRLIHVYTDHCVDTYNDGLKLEGSRLSDWVYVNRFRRL
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTN-P-VLENFD--GSFRGSAQGI EGSI R
gi|295 TISVLDI AAFP NYDIEAYPIQTASQLTREVYLDLFPVNETLSPASYP TFSAAESA IIR
Cry1Ac SPHLM DILNSIT IYTD AHRGEY YW SGHQIMASPVGFSGPEFTFP LYGTMGNAAPQQRIVA
gi|295 SPHLVDFLNSFTIYTD SLASAYWGGHLVNSFR TGT TNLIRSPLYGREGNTERPVTISA
Cry1Ac QLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDE
gi|295 SPSVP IFR TLS ---YFTGLN---NNNPVAGIEGVEF---QNTISR SIYRKSGPIDSFSE
Cry1Ac IPPQNNVPPRQGF SHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNI IASDSIT
gi|295 LPPQDVSVSPAIGYSHRLCHAT-FLERISGPRIA---GTVF SWTHRSASPINEVSPSRIT
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGIEVPI--HFPSTSTRYRV
gi|295 QIPWVKAHTL ASGASVIKGP GFTGGDILTRNSMGD----LGALRVTFTRGLPQS---YYI

Cry1Ac RVRVYASVTP IHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTS-SLGNIVG
gi|295 RFRYASVANRSGTFRYSQPPSYGISFPKTM DAGEALTSRSFAH---TTLFTPI TFSRAQE
Cry1Ac VRNFSGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
gi|295 EFDLYIQSGVYIDRIEFIPVDATFESEINLERAQKAVNALFTSTNQLGLKTDVTDYHIDQ
Cry1Ac VSNLVTYLSD EFC LDEKRELS EKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGIT
gi|295 VSNLVECLSD EFC LDEKRELS EKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGRGSTDTIT
Cry1Ac IQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESK LKAFTRYQLRGIYEDSQDLEIYSIR
gi|295 IQGGDDVFKENYVTLTGTFTDECYPTYLYQKIDESK LKAYTRYQLRGIYEDSQDLEIYLIR
Cry1Ac YNAKHETVNVPGTGS L WPLSAQSP I GKC GEPNRCAPHLEWNPDLDCSCRDGEC AHHSHH
gi|295 YNAKHEIVNVPGTGS L WPLSVQSP I GKC GEPNRCAPHLEWNPDLDCSCRDEEKCAHHSHH
Cry1Ac FSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWR
gi|295 FSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWR
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPEL
gi|295 DKREKLELETNIVYKEAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPEL
Cry1Ac SVIPGVNA AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSV
gi|295 SVIPGVNAGIFEELEGRIFTAYS LYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSV
Cry1Ac LVVPEWAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEV DNNTD ELKFSNCEKEQV
gi|295 LVVPEWAEV SQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEV DNNTD ELKFSNCEKEQV
Cry1Ac YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPADYASVYEEKSYTDGRREN P
gi|295 YPGNTVACNDY---NKNHGANACSSRNRGYDESYESNSSIPADYAPVYEEEA YTDGQRGNP



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1080      1090      1100      1110      1120
Cry1Ac YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|138 YPGNTVACNDY--NKNHGANACSSRRNGYDESYESNSSIPADYAPVYEEEAAYTDGQRGNP
1060      1070      1080      1090      1100

1130      1140      1150      1160      1170      1180
Cry1Ac CEFNRRGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|138 SEFNRRGH---TLPAGYVTALEYFPETDTVWVEIGETEGTFIVDSVELLLMEE
1110      1120      1130      1140      1150      1160

>>gi|53984837|gb|AAV26513.1| Sequence 12 from patent US (1242 aa)
  initn: 3650  initl: 3093  opt: 3604  Z-score: 4239.6  bits: 796.5  E(): 0
Smith-Waterman score: 4298; 58.039% identity (75.241% similar) in 1244 aa overlap
(5-1182:26-1242)

```

```

10      20      30
Cry1Ac CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSQNSSIILN--WINIIGDAAKE
10      20      30      40      50

```

```

40      50      60      70      80      90
Cry1Ac TGYPIDISLSLTQFLLEFVPG-AGFVLGLVD-IIWGIFGSPQWDAFLVQIEQLINQRI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 A---VSIQTTIVSLITAPSLTGLISIVYDLIGKVLGSSGQGISDLSICDLLSIIDLRV
60      70      80      90      100      110

```

```

100      110      120      130      140
Cry1Ac EEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQF---NDMNSALT--
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 SQSVLNDGIADFNQSVLLYRNYLEALDSWNKNP-NSASAEELRTRFRRIADSEFDRILTRG
120      130      140      150      160      170

```

```

150      160      170      180      190      200
Cry1Ac --TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWG-FDAATINSRYNDLTRL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 SLTNGGSLARQNAQILLPSFASAAFFHLLLRDTRYGTNWGLYNATPFINYQSKLVEL
180      190      200      210      220      230

```

```

210      220      230      240      250      260
Cry1Ac IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRELTTLTVLDIVSLFPNYDSRTYPI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 IELYTDYCVHWYNRGFNLRQRGTSATAWLEFHRYSRREMTLMVLDIVASFSSLDITNYPI
240      250      260      270      280      290

```

```

270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPVLNFDGSGFRGSA-----QIEGSIRSPHMDILNSITIYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 ETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNRRANFSDLENAIPNRPSPWFLNMIIST
300      310      320      330      340      350

```

```

320      330      340      350      360
Cry1Ac DA-----HRGEYWSGHQIMASPVGSGPEFTFPYLGTMGNAAPQORIVAQLGQGV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 GSLTLPVSPSTRARV-WYGSRRDISP---ANSQFITEILISGQHTTAQ---TILGRNI
360      370      380      390      400

```

```

370      380      390      400      410
Cry1Ac YRTLSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSGT----VDSLDE-I
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 FRVDSQACNLNDTTYGVN-RAVFYHDASE---GSQRSVYEGYIRTTGIDNPRVQINITYL
410      420      430      440      450      460

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```

420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNNIIASD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 PGENSDIPTPEDYTHILSTTINLTGGLRQVASNRRSSLV---MYGWTHTKSLARNNTINPD
470      480      490      500      510

```

```

480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 RITQIPLVKGFRVWGGTSTVITGPGFTGGDILRRNTPFGDFVS---LQVNINSPIQ-RYR
520      530      540      550      560      570

```

```

540      550      560      570      580
Cry1Ac VRVRYASVTPIHNLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAFTS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 LRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDSNPFPSF
580      590      600      610      620      630

```

```

590      600      610      620      630
Cry1Ac SLG-NIVGVNR---F---SGTAG-VIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 RANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSN
640      650      660      670      680      690

```

```

640      650      660      670      680      690
Cry1Ac QLGLKTNVTDYHIDQVSNLVTVLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 QIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGI
700      710      720      730      740      750

```

```

700      710      720      730      740      750
Cry1Ac NRQPERGWGGSTGITIQGGDDVFKENYVTLVSGTFFDECYPTLYQKIDESKLFKAFTRYQLR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 NRQPDGRWRGSTDITIQGGDDVFKENYVTLVPGTVDECYPTLYQKIDESKLFKAYTRYELR
760      770      780      790      800      810

```

```

760      770      780      790      800      810
Cry1Ac GYIEDSQDLEIYIRYNKAKHEIVNVPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 GYIEDSQDLEIYIRYNKAKHEIVNVPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
820      830      840      850      860      870

```

```

820      830      840      850      860      870
Cry1Ac CSCRDGEKCAHSHHFLSLDIDVGTDLNEDLGWVWVIFKIKTDGCHARLGNLEFLEKPLV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 CSCRDGEKCAHSHHFLSLDIDVGTDLNEDLGWVWVIFKIKTDGCHARLGNLEFLEKPLL
880      890      900      910      920      930

```

```

880      890      900      910      920      930
Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAA

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          940      950      960      970      980      990
Cry1Ac  DKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWV
gi|539  DKRVHRIREAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLSWV
          1000      1010      1020      1030      1040      1050
Cry1Ac  KGHVDVVEEQNNQSRVSLVVPWEAEVSVQEVVRCVCPGRGYILRVTAAYKEGYEGECVTTIHEIEN
gi|539  KGHVDVVEEQNNHRSVSLVPEWEAEVSVQEVVRCVCPGRGYILRVTAAYKEGYEGECVTTIHEIBD
          1060      1070      1080      1090      1100      1110
Cry1Ac  NTDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYAS
gi|539  NTDELKFSNCVEEEVYPNNTVTCNNTYGTQEEYEGTYTSRNQGYDEAYGNNPSVPADYAS
          1120      1130      1140      1150      1160      1170
Cry1Ac  VYEEKSYTDGRRENPCFNNGRYDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVD
gi|539  VYEEKSYTDGRRENPCSNRQYGDYTPPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVD
          1180
Cry1Ac  SVELLLMEE
gi|539  SVELLLMEE
          1240
>>gi|15105607|gb|AAE66201.1| Sequence 12 from patent US (1242 aa)
  initn: 3650 initl: 3093 opt: 3604 Z-score: 4239.6 bits: 796.5 E(): 0
Smith-Waterman score: 4298; 58.039% identity (75.241% similar) in 1244 aa overlap
(5-1182:26-1242)
          10      20      30
Cry1Ac  CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
gi|151  MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSQCNSSILN--WINIIGDAAKE
          10      20      30      40      50
Cry1Ac  TGYTPIDISLSLTQFLLSEFVPG-AGFVLGLVD-IIWIGIFGSPQWDAFLVQIEQLINQRI
gi|151  A---VSI GTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQSISDLSICDLLSIIDLRV
          60      70      80      90      100      110
Cry1Ac  EEFARNQAI SRL EGLSNLYQIYAESFREWEADPTNPALREEMRIQF---NDMNSALT--
gi|151  SQSVLNDGIADFNQSVLLYRNYLEALDSWKNP-NSASAEELRTRFRFIADSEFDRILTRG
          120      130      140      150      160      170
Cry1Ac  --TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWG-FDAATINSRYNDLTRL
gi|151  SLTNGGSLARQNAQILLLPSFASAAFFHLLLRDATRYGTNWGLYNATPFFINYQSKLVLEL

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          180      190      200      210      220      230
Cry1Ac  IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|151  IELYTDYCVHWYNRGPNELRQRGTSATAWLEFHRYRREMTLMVLDIVASFSSLDITNYPFI
          240      250      260      270      280      290
Cry1Ac  RTVSQLTREIYTNPVLNFDGSRGSA-----QGIIEGSI RSPHMLDILNLSITIIYT
gi|151  ETDQFLSRVIYTDPIGFVHRSSLRGESWFSFVNANFSDLENAIPNRPSPWFLNMIIST
          300      310      320      330      340      350
Cry1Ac  DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGV
gi|151  GSLTLPLVSPSTDRARV-WYGSRDRI SP---ANSQFITE LISGQHTTATQ---TILGRNI
          360      370      380      390      400      410
Cry1Ac  YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GT---VDSLDE-I
gi|151  FRVDSQACNLNDTTYGVN-RAV FYHDASE---GSQRSVYEGYIRTTGIDNPRVQNTIYTL
          420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGF SHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|151  PGENSDIPTPEDYTHILSTINLTGGLRQVASNRRSSLV---MYGWTHKSLARNNTINPD
          480      490      500      510      520      530
Cry1Ac  SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|151  RITQIPLVKGFRVWGTSVITGPGFTGGDILRNTFPGDFVS---LQVNINSPITQ-RYR
          540      550      560      570      580
Cry1Ac  VRVRYASVTPIHNLVNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAFTS
gi|151  LRFYASSRDARVIVLTGAASTGVGGQVSVNMP LQKTMEIGENLTSRTFRYTD FSNPFSF
          590      600      610      620      630
Cry1Ac  SLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTN
gi|151  RANPDIIGISEQPLFGAGSISSGELYDKIEIILADATFEAESDLERAQKAVNALFTSSN
          640      650      660      670      680      690
Cry1Ac  QLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDI
gi|151  QIGLKTVDVTDYHIDQVSNLVDCSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGI
          700      710      720      730      740      750
Cry1Ac  NRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECPYTYLQKIDESKLFKAFTRYQLR

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. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTNGLGLKTDVTDYQIDQV
      580      590      600      610      620      630
Cry1Ac 660      670      680      690      700      710
SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 SNLVECLSDDEFCLDEKRELSKVKHAKRLSDKRNLLQDPNFTSINRQLDRGWRGSTDITI
      640      650      660      670      680      690
Cry1Ac 720      730      740      750      760      770
QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 QGGNDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEVYLIRY
      700      710      720      730      740      750
Cry1Ac 780      790      800      810      820      830
NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 NAKHETVNVPGTGSWPLSVESPIGRGCEPNRCVPHIEWNPDLDCSCRDGEKCAHSHHF
      760      770      780      790      800      810
Cry1Ac 840      850      860      870      880      890
SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKKWRD
      820      830      840      850      860      870
Cry1Ac 900      910      920      930      940      950
KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELS
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 KREQLQFETNIVYKEAKESVDALFVDSHYNRLQADTNITMIHAADKRVHRIREAYLPELS
      880      890      900      910      920      930
Cry1Ac 960      970      980      990      1000     1010
VIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHDVVEQNNQRSVL
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 VIPGVNADIFEELEGLIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDIQ-QNDHRSVL
      940      950      960      970      980      990
Cry1Ac 1020     1030     1040     1050     1060     1070
VPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIY
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 VPEWESEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCIEEVEVY
      1000     1010     1020     1030     1040     1050
Cry1Ac 1080     1090     1100     1110     1120
PNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 PTDT--GNDYTAHQGTTCADACNSRNNGYEDGYEINTTASVNYKPTYEEMMYTDVRRDN
      1060     1070     1080     1090     1100     1110
Cry1Ac 1130     1140     1150     1160     1170     1180
PCEFNRYRDTYPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|300 HCEYDRGYGNHTPLPAGYVTKLEYFPETDTVWIEIGETEGTFIVDSVELLMEE
      1120     1130     1140     1150     1160

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>>gi|2096162|gb|AAB54994.1| Sequence 2 from patent US 56 (1167 aa)

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initn: 4235 init1: 2446 opt: 3566 Z-score: 4195.2 bits: 788.2 E(): 0
Smith-Waterman score: 4986; 65.155% identity (81.864% similar) in 1191 aa overlap
(5-1182:1-1167)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 MEIN-NQKQCIPYNCLSNPEEVLDDGERILPDIDPLEVLSLSLQFLLNNFVPGGGF
      10      20      30      40      50
Cry1Ac 70      80      90      100     110     120
VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESNLYQIYAESFRE
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 ISGLVDKIWALRPSWDLFLAQIERLIDQRIEATVRAKAITELEGLGRNYQIYAEAFKE
      60      70      80      90      100     110
Cry1Ac 130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 WESDDPNEAASRVIDFRILDLGLIEANIPSFRIIGFEVPLLSVVYQAAANLHLLLRDSV
      120     130     140     150     160     170
Cry1Ac 190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 IFGERWGLTTKVNVDIYNRQIREIHEYSNHCVDTYNTELERLGRFSIAQWRIYNQFREL
      180     190     200     210     220     230
Cry1Ac 250     260     270     280     290
TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGFSFR-GSAQGI--EGSIRS
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 TLTVLDIVALFPNYSRLYPIQTFSQLTREIVTSPVSEFYGVINGSGNIIGTLTEQQIRR
      240     250     260     270     280     290
Cry1Ac 300     310     320     330     340     350
PHLMDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQ
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 PHLMDFFNSMIMYTSNRRHEHYWSGLEMTAYFTGFAGAQSFPPLVGTGRGESAPPLT-VRS
      300     310     320     330     340     350
Cry1Ac 360     370     380     390     400     410
LGQGVYRTLSSSTLYRRPFNIGINNQLSVDLGTTEFAYGTSSNLPSAVYRKSQVTSVLSDEI
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 VNDGIYRILSAPFYSAPP-LGTIVLG-SRGEKFDALNNSIPPPSTIYRHPGTVDSLVSII
      360     370     380     390     400     410
Cry1Ac 420     430     440     450     460     470
PPQNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 PPQDNSVPPHRGSSHRLSHVTMRAS-----SPIFHWTHRSAATTTNTINPNAIIQ
      420     430     440     450     460
Cry1Ac 480     490     500     510     520     530
IPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 IPLVKAFNLHSGATVVRGPGFTGGDILRRNTGTGFADMRVNIITGPL----SQRYRVRIR
      470     480     490     500
Cry1Ac 540     550     560     570     580     590

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Cry1Ac YASVTPIHLNVNWNWGNSSIFSNTVDPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGV  
 gi|209 YASTTDLQFFTRINTGTSVNVQGNFQRTMNRGDNLESGNFRTAGFSTPFSSNAQSTFTLGT  
 520 530 540 550 560 570

Cry1Ac RNFSGTAGVVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQV  
 gi|209 QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTNQLGLKTDVTDYQIDQV  
 580 590 600 610 620 630

Cry1Ac SNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI  
 gi|209 SNLVECLSDDEFCLDEKRELSEKVKHAKRLSDKRNLLQDPNFTSINRQLDRGWRGSTDITI  
 640 650 660 670 680 690

Cry1Ac QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY  
 gi|209 QGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGIYEDSQDLEVYLIRY  
 700 710 720 730 740 750

Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF  
 gi|209 NAKHETVNVPGTGSWPLSVESPIGRCEPNRCVPHIEWNPDLDCSCRDGEKCAHSHHF  
 760 770 780 790 800 810

Cry1Ac SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
 gi|209 SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKKWRD  
 820 830 840 850 860 870

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS  
 gi|209 KREQLQFETNIVYKEAKESVDALFVDSHYNRLQADTNITMIHAADKRVHRIREAYLPELS  
 880 890 900 910 920 930

Cry1Ac VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDVEEQNNQRSVL  
 gi|209 VIPGVNADIFEELEGLIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDIQ-QNDHRSVL  
 940 950 960 970 980 990

Cry1Ac VVPEWEAEVSVQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEY  
 gi|209 VVPEWEAEVSVQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELKFSNCEVEEY  
 1000 1010 1020 1030 1040 1050

Cry1Ac PNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN  
 gi|209 PTDT--GNDYTAHQGTTCACADACNSRNVGYEDGYEINTTASVNYKPTYEEEMYTDVRRDN  
 1060 1070 1080 1090 1100 1110

Cry1Ac 1130 1140 1150 1160 1170 1180  
 PCFEFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 gi|209 HCEYDRGRYGNHTPLPAGYVTKLEYFPETDVTWVIEIGETEGTFIVDSVELLMEE  
 1120 1130 1140 1150 1160

>>gi|6001559|gb|AAE22521.1| Sequence 2 from patent US 58 (1167 aa)  
 initn: 4235 init1: 2446 opt: 3566 Z-score: 4195.2 bits: 788.2 E(): 0  
 Smith-Waterman score: 4986; 65.155% identity (81.864% similar) in 1191 aa overlap  
 (5-1182:1-1167)

Cry1Ac 10 20 30 40 50 60  
 CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|600 MEIN-NQKQICIPYNCLSNPEEVLDDGERILPDIDPLEVSLLLQFLNNFVPGGGF  
 10 20 30 40 50

Cry1Ac 70 80 90 100 110 120  
 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE  
 gi|600 ISGLVDKIWALRPSWDLFLAQIERLIDQRIEATVRAKAITTELEGLGRNYQIYAEAFKE  
 60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180  
 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAANLHLSVLRDVS  
 gi|600 WESDDPNEAAKSRVIDRFRILDGLEANIPSPRIIGFEVPLLSVYVQAAANLHLLALRDSV  
 120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 gi|600 IPGERWGLTKNVNDIYNRQIREIHEYSNHCVDTYNTELERLGRFIAQWRIYNQFRREL  
 180 190 200 210 220 230

Cry1Ac 250 260 270 280 290  
 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGFSFR-GSAQGI--EGSIRS  
 gi|600 TLTVLDIVALFPNYDSRLYPIQTFSQLTREIYVSPVSEFYGVINSGNIIGTLTEQQIRR  
 240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350  
 PHLMDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQ  
 gi|600 PHLMDIFNSMIMYTSNDRREHYWGLEMTAYFTGFAGAVSFPVLTGRGESAPPLT-VRS  
 300 310 320 330 340 350

Cry1Ac 360 370 380 390 400 410  
 LQGGVYRTLSSSTLYRRPFNIGINNQLSVDLGTTEFAFGTSSNLPSAVYRKSQVSDSLDEI  
 gi|600 VNDGVIYRILSAPFYSAPF-LGTIVLG-SRGEKFDALNNISPPPTIYRHPGTVDSLVI  
 360 370 380 390 400 410

Cry1Ac 420 430 440 450 460 470  
 PPQNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNIIASDSITQ  
 gi|600 PPQDQNSVPPHRGSSHRLSHVTMRAS-----SPIFHWHRSATTTNTINPNAIIQ  
 420 430 440 450 460

```

480          490          500          510          520          530
Cry1Ac IPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR
gi|600 IPLVKAFNLHSGATVVRGPGFTGGDILRRTNTGTADMRVNTGPL-----SQRYVRIR
          470          480          490          500          510

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540          550          560          570          580          590
Cry1Ac YASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDF--GYFESANAFSTSLGNI-VGV
gi|600 YASTTDLQFFTRINGTSVNQGNFQRTMNRGDNLESGNFRTAGFSTPFSFSAQSTFTLGT
          520          530          540          550          560          570

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```

600          610          620          630          640          650
Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|600 QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTNQLGLKTDVTDYQIDQV
          580          590          600          610          620          630

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660          670          680          690          700          710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|600 SNLVECLSDEFCLDEKRELSEKVKHAKRLSDKRNLQDPNFTSINRQLDRGWRGSTDITI
          640          650          660          670          680          690

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720          730          740          750          760          770
Cry1Ac QGGDDVFKENYVTLSTGTFDECYPTLYLQKIDESKLFKAFTRYQLRGIYEDSODLEIYSIRY
gi|600 QGGNDVFKENYVTLSTGTFDECYPTLYLQKIDESKLFKAYTRYELRGIYEDSODLEVYLIRY
          700          710          720          730          740          750

```

```

780          790          800          810          820          830
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
gi|600 NAKHETVNVPGTGSWPLSVESPIGRGCEPNRCVPHIEWNPDLDCSCRDGEKCAHSHSHF
          760          770          780          790          800          810

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```

840          850          860          870          880          890
Cry1Ac SLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|600 SLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKKWRD
          820          830          840          850          860          870

```

```

900          910          920          930          940          950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|600 KREQLQFETNIVYKEAKESVDALFVNSHYNRLQADTNIAMIHAADKRVHRIREAYLPELS
          880          890          900          910          920          930

```

```

960          970          980          990          1000         1010
Cry1Ac VIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNQRSVL
gi|600 VIPGVNADIFEELEGLIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDIQ-QNDHRSVL
          940          950          960          970          980          990

```

```

1020         1030         1040         1050         1060         1070
Cry1Ac VVPEWEAEVSEQEVRVCPGRGYLLRVYAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEYI
gi|600 VVPEWEAEVSEQEVRVCPGRGYLLRVYAYKEGYGEGCVTIHEIEDNTDELKFSNCEVEEYI
          1000         1010         1020         1030         1040         1050

```

```

1080         1090         1100         1110         1120
Cry1Ac PNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|600 PDTT--GNDYTAHQGTTGCADACNSRVNGYEDGYEINTTASVNYKPTYEEEMYTDVRRDN
          1060         1070         1080         1090         1100         1110

1130         1140         1150         1160         1170         1180
Cry1Ac PCEFNRGYRDYPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|600 HCEYDRGYGNHTPLPAGYVTKLEYFPETDVTWVIEIGETEGTFIVDSVELLLMEE
          1120         1130         1140         1150         1160

```

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>>gi|474892|gb|AAA22341.1| crystal protein (1167 aa)
initn: 4235 initl: 2446 opt: 3566 Z-score: 4195.2 bits: 788.2 E(): 0
Smith-Waterman score: 4986; 65.155% identity (81.864% similar) in 1191 aa overlap
(5-1182:1-1167)

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10          20          30          40          50          60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|474 MEIN-NQKQCIPYNCLSNPEEVLDDGERILPDIDPLEVLSLLQFLLNFPVGGGF
          10          20          30          40          50

```

```

70          80          90          100         110         120
Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
gi|474 ISGLVDKIWALRPSWDLFLAQIERLIDQRIEATVRAKAITLEGLGRNYQIYAEAFKE
          60          70          80          90          100         110

```

```

130         140         150         160         170         180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|474 WESDDPNEAAKSRVIDRFRILDGLIEANIPSFRIIGFEVPLLSVYVQAANLHLLALRDSV
          120         130         140         150         160         170

```

```

190         200         210         220         230         240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|474 IFGERWGLTTKNVNDIYNRQIREIHEYSNHCVDTYNTELERLGFRSIAQWRIYNQFRREL
          180         190         200         210         220         230

```

```

250         260         270         280         290
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLNFDGFSFR-GSAQGI--EGSIRS
gi|474 TLTVLVDIVALFPNYDSRLYPIQTFSQTLREIYVTSVSEFYGYGVINSGNIIGTLTEQQIRR
          240         250         260         270         280         290

```

```

300         310         320         330         340         350
Cry1Ac PHLMDILNSITIIYDHAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ
gi|474 PHLMDFFNSMIMYTSNRRHEYWSGLEMTAYFTGFAGAQVSPFLVGTGESAPPLT-VRS
          300         310         320         330         340         350

```

```

360         370         380         390         400         410
Cry1Ac LQGGVYRSLSSLYRRFPNIGINNQLSVDLGTGFAYGTSSNLPASAVYRKSQGTVDLSDEI
gi|474 VNDGIYRILSAPFYSAPF-LGTIVLG-SRGEKFDALNNISPPPSTIYRHPGTVDLSVSI
          360         370         380         390         400         410

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420      430      440      450      460      470
Cry1Ac  PFQNNVPPRQGFSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|474  PFQDNSVPPHRRGSSHRLSHVMTMRAS-----SPIFHWTNRSATTTNTINPNAIIQ
      420      430      440      450      460

```

```

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYVRVR
gi|474  IPLVKAFNLHSGATVVRGPGFTGGDILRRNTGTGTFADMVRVITGTP-----SQRYRVRIR
      470      480      490      500      510

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540      550      560      570      580      590
Cry1Ac  YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFSTSLGNI-VGV
gi|474  YASTTDLQFFTRINGTSVNGQNFQRTMNRGDNLESGNFRTAGFSTPFSSNAQSTFTLGT
      520      530      540      550      560      570

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```

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|474  QAFSNQE-VYIDRIEFVPAEVTFEAESDLERAQKAVNALFTSTNQLGLKTVTDYQIDQV
      580      590      600      610      620      630

```

```

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|474  SNLVECLSDEFCLDEKRELSKVKHAKRLSDKRNLLQDPNFTSINRQLDRGWRGSTDITI
      640      650      660      670      680      690

```

```

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|474  QGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEVYLIRY
      700      710      720      730      740      750

```

```

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
gi|474  NAKHETVNVPGTGLWPLSVESPIGRGCEPNRCVPHIEWNPDLDCSCRDGEKCAHSHSHF
      760      770      780      790      800      810

```

```

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|474  SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLLGEALARVKRAEKKWRD
      820      830      840      850      860      870

```

```

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELS
gi|474  KREQLQFETNIVYKEAKESVDALFVNSQYDQLQADTNITMIHAADKRVHRIREAYLPELS
      880      890      900      910      920      930

```

```

960      970      980      990      1000     1010
Cry1Ac  VIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVL
gi|474  VIPGVNADIFEELEGLIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDIQ-QNDHRSVL

```

```

940      950      960      970      980      990
Cry1Ac  1020      1030      1040      1050      1060      1070
gi|474  VVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIY
      1000      1010      1020      1030      1040      1050
Cry1Ac  1080      1090      1100      1110      1120
gi|474  PNNTVTCNDYTVNQEYEG--GAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
      1060      1070      1080      1090      1100      1110
Cry1Ac  1130      1140      1150      1160      1170      1180
gi|474  PCEFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1120      1130      1140      1150      1160

```

>>gi|125172655|gb|ABN37587.1| Sequence 4 from patent US (1168 aa)  
initn: 4723 init1: 2414 opt: 3534 Z-score: 4157.5 bits: 781.2 E(): 0  
Smith-Waterman score: 4957; 64.613% identity (81.432% similar) in 1201 aa overlap  
(5-1182:1-1168)

```

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|125  MEIN-NQNCIPYNCLSKPEEVFLDGERILPDIDPLEVLSLLQLFLNNFVPGGGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFPARNQAIISRLGLSNLYQIYAESFRE
gi|125  ISGLIDKIWALRPEWELFLAQIEQLIDRRIEATVRAKAI AELEGLGRSYQLYGEAFKE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|125  WEKTPDNTAARSVTERFRIIDAQIEANIPSRVSGFVPLLSVYVQAANLHLLLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERWVGPDSRDWRIRYQFREL
gi|125  IFGERWGLSTTNVNDIYNRQVKRIHEYSDDHCVDITYKTELEFRSIAQWRIYQFREL
      180     190     200     210     220     230

```

```

250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLENFDGS-FRGSAGQ--IEGSIRS
gi|125  TLTVLDIVALFPNYDGRLYPIRTISQLTREIYTSVPSEFYGYGFIYNNHMIGTFIERQLRR
      240     250     260     270     280     290

```

```

300     310     320     330     340     350
Cry1Ac  PHLMDILNSITIYTDHAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ
gi|125  PHLMDFFNSMTMYTSDNRREYWSGLEMTATLT--SGNQVSPFLAGTRGNSAPPVS-VRK

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300      310      320      330      340      350
Cry1Ac  LGQGVYRTLSSLTLYRRPFNIGINNQQLSVLD--GTEFAYG--TSSNLPASVYRKSQTVDS
gi|125  TGEGIYRILSEPFYSAPF-LGT----SVLGSRGEFAPASNTTSLPSTIYRNRGTVDS
      360      370      380      390      400      410
Cry1Ac  LDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|125  LVSIPPQDYVPPHRGYSHLLSHVTMH----NSS-----PIFHWTHRSATPRNIYPD
      420      430      440      450      460      470
Cry1Ac  SITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRV
gi|125  SITQIPVVKASHLSSGGSVIKGGHTGGDLISLP----VNNFTHFRIPFQ-ANTPQRYRI
      480      490      500      510      520      530
Cry1Ac  RVRYASVTP-----IHLNVNNGNSSIFSNT-VPATATSLDNLQSSDFGYFESANAFTSS
gi|125  RICYAADSDGTLDSGVFLSAAAGDG--FNNTSYRATMSPEGSLSRDFQLDLNLSFTSD
      540      550      560      570      580
Cry1Ac  LGNIVGVR--NFSGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|125  VASNLWLHFIRYIRPGNLYIDRAEFIPVDATFEAGYNLERAQKAVNALFTSTNQKGLQTD
      590      600      610      620      630      640
Cry1Ac  VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|125  VTDYHIDQVSNLVDCLSDDEFCLDEKRLSEKVKQAKRLSDERNLLQDSNFRGINREQDRG
      650      660      670      680      690      700
Cry1Ac  WGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
gi|125  WRGSTDITIQGGNDVFKENYVTLPGTFDACYPTYLYQKVDSEKLFKAYTRYQLRGYIEDSQ
      710      720      730      740      750      760
Cry1Ac  DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|125  DLEVLIIRYNAKYETLNVPGMGLWPLSVESPIGKCGEPNRCVPLEWNPDPDCSCRDGE
      770      780      790      800      810      820
Cry1Ac  KCAHSHHFFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLFLEEKPLVGEALARV
gi|125  KCAHSHHFFSLDIDVGCTDLNENLGIWVIFKIKTQDGHARLGNLFLEEKPLLGEALARV
      830      840      850      860      870      880
Cry1Ac  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSI
gi|125  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSI

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gi|125  KRAEKKWRDKREILQSETNIVYKEAKEAVDGLFVDSQYERLQSDTNIAMIHAAKRVHRI
      870      880      890      900      910      920
      950      960      970      980      990      1000
Cry1Ac  REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVE
gi|125  REAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGVHVDIK
      930      940      950      960      970      980
      1010      1020      1030      1040      1050      1060
Cry1Ac  EQNNQRSVLVPEWEAEVSQEVVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKF
gi|125  -QNGHRSVLVIPEWEAQVVSQEVVRVCPGRGYILRVATANKEGYGEGCVTIHEIENHTEKLF
      990      1000      1010      1020      1030      1040
      1070      1080      1090      1100      1110
Cry1Ac  SNCVEEIIYPNNVTVCNDYTVNQEYGG---AYTSRNRGYNEA---PSVPADYASVYEE
gi|125  RNCEEEVYPNNVTGTCNDYTAHQGTAGCADACNTRNVGYEDAYEMNTTTSVNYKPTYEE
      1050      1060      1070      1080      1090      1100
      1120      1130      1140      1150      1160      1170
Cry1Ac  KSYTDGRRNPNCEFNRGYRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVEL
gi|125  EYVTDGRRNPNCEMERGY---TLPVGYVTKLELYFPETNTVWIEIGETEGKFIIVDSVEL
      1110      1120      1130      1140      1150      1160
      1180
Cry1Ac  LLMEE
      ....
gi|125  LLMEE

>>gi|15143041|emb|CAC50779.1| unnamed protein product [B (1168 aa)
      initn: 4723 init1: 2414 opt: 3534 Z-score: 4157.5 bits: 781.2 E(): 0
Smith-Waterman score: 4957; 64.613% identity (81.432% similar) in 1201 aa overlap
(5-1182:1-1168)
      10      20      30      40      50      60
Cry1Ac  CMQAMNPNINECIPYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|151  MEIN-NQNQCIPYCNLSKPEEVFLDGERILPDIDPLEVLSLLQFLNLFVPGGFF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGIQGFPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|151  ISGLIDKIWALRPSWELFLAQIEQLIDRRIEATVRAKAIAELEGGRSYQLYGEAFKE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151  WEKTPDNTAARSRVTERFRIIDAQIEANIPSRVSGFEVPLLSVYVQAANLHLLLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      ....

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gi|215 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|215 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190     200     210     220     230     240
gi|215 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLVDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
      250     260     270     280     290     300
gi|215 TLTVLVDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      310     320     330     340     350     360
gi|215 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      370     380     390     400     410     420
gi|215 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      360     370     380     390     400     410
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      430     440     450     460     470     480
gi|215 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490     500     510     520     530
gi|215 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac VTIPIHLNWNWGSSIFSNTPVATATSLDNLQSSDFGFESANAFSSSLGNIV---GVRNF
      540     550     560     570     580     590
gi|215 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFSGSSVFTLSAHVF
      540     550     560     570     580     590
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      600     610     620     630     640     650
gi|215 NSGNEVYIDRIEFVPAEVTFEAEY
      600     610
>>gi|208155|gb|AAA72985.1| cryIA(a) (615 aa)

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initn: 3419 initl: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
(5-620:1-615)
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50      60
gi|208 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
      70      80      90     100     110     120
gi|208 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90     100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|208 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190     200     210     220     230     240
gi|208 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLVDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
      250     260     270     280     290     300
gi|208 TLTVLVDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLENFDGSGFRGSAQGLEGSIRSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      310     320     330     340     350     360
gi|208 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      370     380     390     400     410     420
gi|208 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      360     370     380     390     400     410
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      430     440     450     460     470     480
gi|208 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490     500     510     520     530
gi|208 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      430     440     450     460     470     480
gi|208 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490     500     510     520     530
gi|208 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      540     550     560     570     580     590

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Cry1Ac VTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|208 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFSGSSVFTLSAHVF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|208 NSGNEVYIDRIEFVPAEVTFEAEY

>>gi|33736852|gb|AAQ40697.1| Sequence 10 from patent US (615 aa)
initn: 3419 initl: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
(5-620:1-615)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|337 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|337 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLSVLRDVS
gi|337 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|337 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL
gi|337 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL

Cry1Ac MDILNSITTYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|337 MDILNSITTYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDLDEIPPQ
gi|337 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDLDEIPPQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDLDEIPPQ

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|337 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|337 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS

Cry1Ac VTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|337 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFSGSSVFTLSAHVF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|337 NSGNEVYIDRIEFVPAEVTFEAEY

>>gi|15119962|gb|AAE72056.1| Sequence 10 from patent US (615 aa)
initn: 3419 initl: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
(5-620:1-615)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|151 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|151 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL
gi|151 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQIEGSIIRSPHL

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Cry1Ac MDILNSITYYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|151 MDILNSITYYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
          370      380      390      400      410      420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|151 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360      370      380      390      400      410
          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|151 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420      430      440      450      460      470
          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|151 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480      490      500      510      520      530
          540      550      560      570      580      590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|151 TTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRVTGFTTFFNFNSNGSSVFTLSAHVF
      540      550      560      570      580      590
          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|151 NSGNEVYIDRIEFVPAEVTFAEAY
      600      610
>>gi|20230203|gb|AAE91346.1| Sequence 10 from patent US (615 aa)
  initn: 3419 init1: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
(5-620:1-615)
          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|202 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50
          70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|202 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110
          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|202 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170
          190     200     210     220     230     240

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|202 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
          250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSAQIEGSIKSPHL
gi|202 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSAQIEGSIKSPHL
      240     250     260     270     280     290
          310     320     330     340     350     360
Cry1Ac MDILNSITYYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|202 MDILNSITYYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
          370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|202 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
      360     370     380     390     400     410
          430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|202 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470
          490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|202 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
          540     550     560     570     580     590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|202 TTNLQFHTSIDGRPINQGNFSAATMSSGSLQSGSFRVTGFTTFFNFNSNGSSVFTLSAHVF
      540     550     560     570     580     590
          600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|202 NSGNEVYIDRIEFVPAEVTFAEAY
      600     610
>>gi|12827415|gb|AAE50565.1| Sequence 10 from patent US (615 aa)
  initn: 3419 init1: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
(5-620:1-615)
          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40      50
          70      80      90      100     110     120

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Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIIRSPHL
gi|128 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
gi|128 GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 TKSTNLGSGTSPVVKPGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530
      540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV--GVRNF
gi|128 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFTTTPFNFSNGSSVFTLSAHVF
      540     550     560     570     580     590
      600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 NSGNEVYIDRIEFVPAEVTFEAEY
      600     610

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>>gi|15119964|gb|AAE72058.1| Sequence 10 from patent US (615 aa)
      initn: 3419 init1: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215
      Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap
      (5-620:1-615)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|151 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|151 VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
      250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIIRSPHL
gi|151 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIIRSPHL
      240     250     260     270     280     290
      310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|151 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
gi|151 GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|151 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
      370     380     390     400     410     420
Cry1Ac GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
gi|151 GYRRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQ
      360     370     380     390     400     410
      430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPL
gi|151 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
      420     430     440     450     460     470
      490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|151 TKSTNLGSGTSPVVKPGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRYAS
      480     490     500     510     520     530

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540      550      560      570      580      590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151  TTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRVTGFTTTPFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

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600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151  NSGNEVYIDRIEFVPAEVTFEAEY
      600      610

```

>>gi|15117049|gb|AAE70575.1| Sequence 10 from patent US (615 aa)  
 initn: 3419 initl: 3174 opt: 3423 Z-score: 4030.7 bits: 756.9 E(): 1.4e-215  
 Smith-Waterman score: 3423; 85.161% identity (92.258% similar) in 620 aa overlap  
 (5-620:1-615)

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFRE
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIKRSRPHL
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIKRSRPHL
      240     250     260     270     280     290

```

```

310     320     330     340     350     360
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ
      300     310     320     330     340     350

```

```

370     380     390     400     410     420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQ
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQ
      360     370     380     390     400     410

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420      430      440      450      460      470

```

```

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIAPL----SQRYRVRIRYAS
      480      490      500      510      520      530

```

```

540      550      560      570      580      590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|151  TTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRVTGFTTTPFNFSNGSSVFTLSAHVF
      540      550      560      570      580      590

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151  NSGNEVYIDRIEFVPAEVTFEAEY
      600      610

```

>>gi|36244769|gb|AAQ85125.1| Cry1Abl [synthetic construc (617 aa)  
 initn: 3412 initl: 3164 opt: 3420 Z-score: 4027.1 bits: 756.2 E(): 2.2e-215  
 Smith-Waterman score: 3420; 84.887% identity (92.122% similar) in 622 aa overlap  
 (5-622:1-617)

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|362  MANNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFRE
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|362  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|362  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|362  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIKRSRPHL
.: ..... : . . . : . . : . . . . . : . . . . . : . . . . .
gi|362  TLTVLDIVSLFPNYSRTPYIRTVSQLTREIYTNPVLNFDGSRGSAQIEGSIKRSRPHL
      240     250     260     270     280     290

```

```

          310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|362 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

```

```

          370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPPQ
gi|362 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPPQ
          360      370      380      390      400      410

```

```

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|362 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
          420      430      440      450      460      470

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|362 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
          480      490      500      510      520      530

```

```

          540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|362 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFNSGSSVFTLSAHVF
          540      550      560      570      580      590

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|362 NSGNEVYIDRIEFVPAEVTFEAEYDL
          600      610

```

>>gi|111983520|gb|ABH85230.1| Sequence 1 from patent US (617 aa)  
 initn: 3410 initl: 3167 opt: 3418 Z-score: 4024.8 bits: 755.8 E(): 2.9e-215  
 Smith-Waterman score: 3418; 85.000% identity (92.258% similar) in 620 aa overlap  
 (6-621:3-617)

```

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|111 MADNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

```

```

          70      80      90      100     110     120
Cry1Ac VLGLVDIIGWIFGSPQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|111 VLGLVDIIGWIFGSPQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100     110

```

```

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|111 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120     130     140     150     160     170

```

```

          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVWGPDSRDWIRYNQFRREL
gi|111 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERLVWGPDSRDWIRYNQFRREL
          180      190      200      210      220      230

```

```

          250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
gi|111 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHL
          240      250      260      270      280      290

```

```

          310      320      330      340      350      360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|111 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
          300      310      320      330      340      350

```

```

          370      380      390      400      410      420
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPPQ
gi|111 GVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEIPPPQ
          360      370      380      390      400      410

```

```

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|111 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
          420      430      440      450      460      470

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|111 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
          480      490      500      510      520      530

```

```

          540      550      560      570      580      590
Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|111 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFTTFFNFNSGSSVFTLSAHVF
          540      550      560      570      580      590

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|111 NSGNEVYIDRIEFVPAEVTFEAEYD
          600      610

```

>>gi|809635|emb|CAA01733.1| bt2 (cryIAb)=bt884 [Escheric (622 aa)  
 initn: 3388 initl: 3167 opt: 3396 Z-score: 3998.8 bits: 751.0 E(): 8.2e-214  
 Smith-Waterman score: 3396; 84.380% identity (91.948% similar) in 621 aa overlap  
 (6-622:4-619)

```

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|809 MDPDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

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              70          80          90          100          110          120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|809 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
              60          70          80          90          100          110

              130          140          150          160          170          180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|809 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120          130          140          150          160          170

              190          200          210          220          230          240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|809 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              180          190          200          210          220          230

              250          260          270          280          290          300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|809 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
              240          250          260          270          280          290

              310          320          330          340          350          360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|809 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
              300          310          320          330          340          350

              370          380          390          400          410          420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
gi|809 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
              360          370          380          390          400          410

              430          440          450          460          470          480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|809 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
              420          430          440          450          460          470

              490          500          510          520          530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|809 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
              480          490          500          510          520          530

              540          550          560          570          580          590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|809 TTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTTPFNFSNGSSVFTLSAHVF
              540          550          560          570          580          590

              600          610          620          630          640          650
Cry1Ac SGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|809 NSGNEVYIDRIEFVPAEVTFDLQPSLLID
              600          610          620

```

```

>>gi|155103227|gb|ABT03519.1| Sequence 8 from patent US (614 aa)
  initn: 3280 initl: 3136 opt: 3370 Z-score: 3968.2 bits: 745.3 E(): 4.2e-212
Smith-Waterman score: 3370; 84.006% identity (91.599% similar) in 619 aa overlap
(5-619:1-614)

```

```

              10          20          30          40          50          60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|155 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
              10          20          30          40          50

              70          80          90          100          110          120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|155 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
              60          70          80          90          100          110

              130          140          150          160          170          180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|155 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120          130          140          150          160          170

              190          200          210          220          230          240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|155 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              180          190          200          210          220          230

              250          260          270          280          290          300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|155 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIIRSPHL
              240          250          260          270          280          290

              310          320          330          340          350          360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|155 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
              300          310          320          330          340          350

              370          380          390          400          410          420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
gi|155 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQ
              360          370          380          390          400          410

              430          440          450          460          470          480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|155 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIIPSSQITQIPL
              420          430          440          450          460          470

              490          500          510          520          530          540
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
              480          490          500          510          520          530

              540          550          560          570          580          590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|155 TTNLQFHTSIDGRPINQGNFSATMSSGNLQSGSFRFTVGFTTPFNFSNGSSVFTLSAHVF
              540          550          560          570          580          590

              600          610          620          630          640          650
Cry1Ac SGTAGVIIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 NSGNEVYIDRIEFVPAEVTFDLQPSLLID
              600          610          620

```

```

540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGSSIFSNTPVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTPFNFNSGSSVFTLSAHVF
      540      550      560      570      580      590

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 NSGNEVYIDRIEFVPAEVTFELE
      600      610

```

>>gi|56579956|gb|AAW01774.1| Sequence 8 from patent US 6 (614 aa)  
 initn: 3280 initl: 3136 opt: 3370 Z-score: 3968.2 bits: 745.3 E(): 4.2e-212  
 Smith-Waterman score: 3370; 84.006% identity (91.599% similar) in 619 aa overlap  
 (5-619:1-614)

```

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

```

```

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

```

```

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

```

```

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

```

```

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 TLTVLDIVALFPNYDSRRYPRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 MDILNSITIYTDHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350

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370     380     390     400     410     420
Cry1Ac GVYRTLSSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIPPQ
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 GVYRTLSSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQTVDLDEIPPQ
      360     370     380     390     400     410

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430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPL
      420     430     440     450     460     470

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490      500      510      520      530
Cry1Ac VKGNFLFNG-SVLSGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 TKSTNLGSGTSVVKGPGFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRYAS
      480     490     500     510     520     530

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540      550      560      570      580      590
Cry1Ac VTPIHNLVNWGSSIFSNTPVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 TTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTPFNFNSGSSVFTLSAHVF
      540      550      560      570      580      590

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600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|565 NSGNEVYIDRIEFVPAEVTFELE
      600      610

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>>gi|10063046|gb|AAE38035.1| Sequence 8 from patent US 5 (614 aa)  
 initn: 3280 initl: 3136 opt: 3370 Z-score: 3968.2 bits: 745.3 E(): 4.2e-212  
 Smith-Waterman score: 3370; 84.006% identity (91.599% similar) in 619 aa overlap  
 (5-619:1-614)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|100 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|100 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|100 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|100 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
      . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|100 TLTVLDIVALFPNYDSRRYPRTVSQLTREIYTNVLENFDGSRGSAQGIERSIRSPHL
      240     250     260     270     280     290

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              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|566 VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
              60      70      80      90      100     110

              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|566 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
              120     130     140     150     160     170

              190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|566 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
              180     190     200     210     220     230

              250     260     270     280     290     300
Cry1Ac TLTVLVDIVSLFPNYDSRTPRTVSQLTREIYTNVLENFDFGSRGSAQGI EGSIRSPHL
gi|566 TLTVLVDIVSLFPNYDSRTPRTVSQLTREIYTNVLENFDFGSRGSAQGI EGSIRSPHL
              240     250     260     270     280     290

              310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|566 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
              300     310     320     330     340     350

              370     380     390     400     410     420
Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
gi|566 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
              360     370     380     390     400     410

              430     440     450     460     470     480
Cry1Ac NNNVPPRQGF SHRLSHVSMFRSGFNS SVSII RAPMFSWIHRS AEFNNI IASDSITQIPA
gi|566 NNNVPPRQGF SHRLSHVSMFRSGFNS SVSII RAPMFSWIHRS AEFNNI IASDSITQIPA
              420     430     440     450     460     470

              490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|566 TKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRYAS
              480     490     500     510     520     530

              540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNF
gi|566 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFPTTFNFNSGSSVFTLSAHVF
              540     550     560     570     580     590

              600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|566 NSGNEVYIDRIEFVPAEVTFELE

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              600     610
>>gi|1297290|gb|AAA98959.1| delta-endotoxin CryET1 (1170 aa)
initn: 4373 initl: 2256 opt: 3353 Z-score: 3943.9 bits: 741.7 E(): 9.3e-211
Smith-Waterman score: 4778; 62.876% identity (80.017% similar) in 1196 aa overlap
(5-1182:1-1170)

              10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|129 MEIN-NQNQCIPYNCLSNPEEVLDDGERILPDIDPLEVSMSSLQFLLNNFVPGGGF
              10      20      30      40      50

              70      80      90      100     110     120
Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|129 ISGLFDKIWGALRPSDWELFLAQIEQLIDQRIEATVRAKAI AELEGLGRSFQLYVEAFKE
              60      70      80      90      100     110

              130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|129 WEETPDNTAARSRVTERFRIDAQIEANIPSPFRIPGFVEVPLLSVYAQAANLHLALLRDSV
              120     130     140     150     160     170

              190     200     210     220     230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR-DWIRYNQFRRE
gi|129 IFGERWGLTTTNNVDIYNRQVKRIHEYS DHCVD TYKTELERL -GFTSRAQWKIYNQFRRE
              180     190     200     210     220     230

              240     250     260     270     280     290
Cry1Ac LTLTVLDIVSLFPNYDSRTPRTVSQLTREIYTNVLENFDFGSRGSAQ-GI--EGSIR
gi|129 LTLTVLDIVAVFPNYDGKLYPIQTKSEL TREIY TSPVSEY YGAINN YNQNQIGQTERQIR
              240     250     260     270     280     290

              300     310     320     330     340     350
Cry1Ac SPHLM DILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVA
gi|129 QPHLMDFFNTMTMYTSYNRREYYWGLEMTAYFTGFAGPQVSFPLAGTRGDAAPPFN-VR
              300     310     320     330     340     350

              360     370     380     390     400     410
Cry1Ac QLGQGVYRTLSTLYRRPFNIGINNQQLSVLD--GTEFAYGTSS--SNLPSAVA YRKS GTVD
gi|129 SVNDGIYRILSAPFYSAPF-LGT----SVLGSRGEEFMFALNNISPPPSARYRNP GTVD
              360     370     380     390     400

              420     430     440     450     460     470
Cry1Ac SLDEIPPQNNVPPRQGF SHRLSHVSMFRSGFNS SVSII RAPMFSWIHRS AEFNNI IAS
gi|129 SLVSIPPQDNSVPPHRGSSHRLSHVTM----RNSS-----PIFWHTRSATTTNRINS
              410     420     430     440     450

              480     490     500     510     520     530
Cry1Ac DSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRY
gi|129 DVITQIPMVKAYNLHAGATVVRGPGFTGGDILRRTSNGMVTLR--VDASA---VRNQR

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gi|151 NNNVPPRQGFHSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSATLTNTIDPERINQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRYAS
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 VKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIITQ-RYRLRFYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|151 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDFSNPFSFRANPDII
      540      550      560      570      580      590

      600      610      620      630      640
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|151 GISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTD
      600      610      620      630      640      650

      650      660      670      680      690      700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRG
      660      670      680      690      700      710

      710      720      730      740      750      760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
      720      730      740      750      760      770

      770      780      790      800      810      820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      780      790      800      810      820      830

      830      840      850      860      870      880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 KCAHSHHFSLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
      840      850      860      870      880      890

      890      900      910      920      930      940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHHSI
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAAKRVHHSI
      900      910      920      930      940      950

      950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVE
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHV DVE
      960      970      980      990      1000      1010

      1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSVLVVPEWAEAVSQEVRVCPGRGYILRVITAYKEGYGEGCVTTHEIENNTDELKLF

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      1020      1030      1040      1050      1060      1070
gi|151 EQNNHRSVLVPEWAEAVSQEVRVCPGRGYILRVITAYKEGYGEGCVTTHEIENNTDELKLF
      1070      1080      1090      1100      1110      1120
Cry1Ac SNCVEEIIYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 SNCVEEIVPNNVTTCNNYTGTQEEYEGTYTSRNQGYDEAYGNNPSPVPADYASVYEEKSY
      1080      1090      1100      1110      1120      1130

      1130      1140      1150      1160      1170      1180
Cry1Ac TDGRRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|151 TDGRRENPCESNRGYDYPPLPAGVYTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
      1140      1150      1160      1170      1180      1190

Cry1Ac EE
::
gi|151 EE

>>gi|2298890|emb|CAA02752.1| unnamed protein product [un (1193 aa)
  initn: 6305 init1: 3146 opt: 3339 Z-score: 3927.3 bits: 738.7 E(): 7.8e-210
Smith-Waterman score: 6852; 87.062% identity (92.571% similar) in 1198 aa overlap
(5-1182:1-1193)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|229 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|229 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|229 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|229 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH
      ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
gi|229 TLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLH
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITITYDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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gi|229 MDILNSITLYTDAHRGEYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420
GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAFGTSSNLPSSAVYRKSGTVDSLDEIIPPQ
gi|229 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAFGTSSNLPSSAVYRKSGTVDSLDEIIPPQ
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|229 NNVVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFLNNTIDPERINQIPL
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|229 VKGFRVWGGTSSVITGPGFTGGDILRRNTFGDFVS----LQVNINSPITQ-RYRLRFRYAS
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
VPIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSSLG-NIV
gi|229 SRDARVIVLVTGAASTGVGGQVSVNMPQLQKTEIGENLTSRTFRYTFDFSNPFSFRANPDII
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640
GVRN---F---SGTAG-VIIDRFEPVATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|229 GISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTD
600 610 620 630 640

Cry1Ac 650 660 670 680 690 700
VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|229 VTDYHIDQVSNLVDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRG
660 670 680 690 700 710

Cry1Ac 710 720 730 740 750 760
WGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
gi|229 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
720 730 740 750 760 770

Cry1Ac 770 780 790 800 810 820
DLEIYSIRYNAKHETVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|229 DLEIYLIRYNAKHEIVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
780 790 800 810 820 830

Cry1Ac 830 840 850 860 870 880
KCAHSHHFLSLDIDVGCSDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|229 KCAHSHHFTLSDIDVGCSDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
840 850 860 870 880 890

Cry1Ac 890 900 910 920 930 940

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Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSI
gi|229 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMHAADKRVHRI
900 910 920 930 940 950

Cry1Ac 950 960 970 980 990 1000
REAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLCWNVKGVHDVDE
gi|229 REAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLCWNVKGVHDVDE
960 970 980 990 1000 1010

Cry1Ac 1010 1020 1030 1040 1050 1060
EQNNQRSVLVPWEAEVSEQVVRVCPGRGYILRVTAKEGYEGGCVTIHEIENDTDELKF
gi|229 EQNNHRSVLVIPWEAEVSEQVVRVCPGRGYILRVTAKEGYEGGCVTIHEIENDTDELKF
1020 1030 1040 1050 1060 1070

Cry1Ac 1070 1080 1090 1100 1110 1120
SNCVEEIVPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|229 SNCVEEIVPNNVTVCNNYTGTYEYEGTYTSRNRQGYDEAYGNPSPVPADYASVYEEKSY
1080 1090 1100 1110 1120 1130

Cry1Ac 1130 1140 1150 1160 1170 1180
TDGRRNCPCEFNRGRDYTPPLVGVYTKLELYFPETDKVWIEIGETEGFFIVDSVELLLM
gi|229 TDGRRNCPESNRGYDYPPLPAGYVTKDLEYFPETDKVWIEIGETEGFFIVDSVELLLM
1140 1150 1160 1170 1180 1190

Cry1Ac EE
gi|229 EE

>>gi|53984835|gb|AAV26511.1| Sequence 8 from patent US 6 (1193 aa)
initn: 6305 initl: 3146 opt: 3339 Z-score: 3927.3 bits: 738.7 E(): 7.8e-210
Smith-Waterman score: 6852; 87.062% identity (92.571% similar) in 1198 aa overlap
(5-1182:1-1193)

Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
gi|539 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240

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Regulatory Product Characterization Team

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
gi|539 250 260 270 280 290 300

Cry1Ac 310 320 330 340 350 360  
gi|539 310 320 330 340 350 360

Cry1Ac 370 380 390 400 410 420  
gi|539 370 380 390 400 410 420

Cry1Ac 430 440 450 460 470 480  
gi|539 430 440 450 460 470 480

Cry1Ac 490 500 510 520 530  
gi|539 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590  
gi|539 540 550 560 570 580 590

Cry1Ac 600 610 620 630 640  
gi|539 600 610 620 630 640 650

Cry1Ac 650 660 670 680 690 700  
gi|539 650 660 670 680 690 700 710

Cry1Ac 710 720 730 740 750 760  
gi|539 710 720 730 740 750 760 770

Cry1Ac 770 780 790 800 810 820  
gi|539 770 780 790 800 810 820 830

Cry1Ac 830 840 850 860 870 880  
gi|539 830 840 850 860 870 880 890

Cry1Ac 890 900 910 920 930 940  
gi|539 890 900 910 920 930 940 950

Cry1Ac 950 960 970 980 990 1000  
gi|539 950 960 970 980 990 1000 1010

Cry1Ac 1010 1020 1030 1040 1050 1060  
gi|539 1010 1020 1030 1040 1050 1060 1070

Cry1Ac 1070 1080 1090 1100 1110 1120  
gi|539 1070 1080 1090 1100 1110 1120 1130

Cry1Ac 1130 1140 1150 1160 1170 1180  
gi|539 1130 1140 1150 1160 1170 1180 1190

Cry1Ac EE  
gi|539 EE

>>gi|19700901|emb|CAD29021.1| unnamed protein product [s (1193 aa)  
initn: 6305 init1: 3146 opt: 3339 Z-score: 3927.3 bits: 738.7 E(): 7.8e-210  
Smith-Waterman score: 6852; 87.062% identity (92.571% similar) in 1198 aa overlap  
(5-1182:1-1193)

Cry1Ac 10 20 30 40 50 60  
gi|197 10 20 30 40 50

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Cry1Ac 70 80 90 100 110 120  
VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|197 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180  
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|197 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|197 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290 300  
TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL  
gi|197 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGI EGSIRSPHL  
240 250 260 270 280 290

Cry1Ac 310 320 330 340 350 360  
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ  
gi|197 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQRIVAQLGQ  
300 310 320 330 340 350

Cry1Ac 370 380 390 400 410 420  
GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
gi|197 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ  
360 370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNIIASDSITQIPA  
gi|197 NNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNIIASDSITQIPA  
420 430 440 450 460 470

Cry1Ac 490 500 510 520 530  
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYAS  
gi|197 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPI TQ-RYRLRFRYAS  
480 490 500 510 520 530

Cry1Ac 540 550 560 570 580 590  
VPIHLNVWNGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV  
gi|197 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTD FSNPFSFRANPDI I  
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640  
GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQ LGLKTN  
gi|197 GISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQ IGLKTD  
600 610 620 630 640 650

Cry1Ac 650 660 670 680 690 700  
VTDYHLDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG  
gi|197 VTDYHLDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD RG  
660 670 680 690 700 710

Cry1Ac 710 720 730 740 750 760  
WGGSTGITIQGGDDVFKENYVTL SGTDFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQ  
gi|197 WRGSTDITIQGGDDVFKENYVTL SGTDFDECYPTYLYQKIDESK LKAYTRYELRGYIEDSQ  
720 730 740 750 760 770

Cry1Ac 770 780 790 800 810 820  
DLEIYSIRYNAKHETVNVPGTGLSWPLSAQSP I GKC GEPNRCAPHLEWNPDLDCSCRDGE  
gi|197 DLEIYLIRYNAKHEIVNVPGTGLSWPLSAQSP I GKC GEPNRCAPHLEWNPDLDCSCRDGE  
780 790 800 810 820 830

Cry1Ac 830 840 850 860 870 880  
KCAHSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV  
gi|197 KCAHSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV  
840 850 860 870 880 890

Cry1Ac 890 900 910 920 930 940  
KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTN IAMIHAADKRVHSI  
gi|197 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTN IAMIHAADKRVHRI  
900 910 920 930 940 950

Cry1Ac 950 960 970 980 990 1000  
REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVE  
gi|197 REAYLPELSVIPGVNAAIFEELEGRIFTAYS LYDARNVIKNGDFNGLSCWNVKGHVDVE  
960 970 980 990 1000 1010

Cry1Ac 1010 1020 1030 1040 1050 1060  
EQNNQRSVLVVPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKF  
gi|197 EQNNHRSVLVIPWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKF  
1020 1030 1040 1050 1060 1070

Cry1Ac 1070 1080 1090 1100 1110 1120  
SNCVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY  
gi|197 SNCVEEIVPNNTVT CNNYTGTEEYEGTYTSRNQGYDEAYGNP SVPADYASVYEEKSY  
1080 1090 1100 1110 1120 1130

Cry1Ac 1130 1140 1150 1160 1170 1180  
TDGRRENPC EFNRGYRDYTPLPVGYVTK ELEYFPETDKVWIEIGETEGTFIVDSVELLLM  
gi|197 TDGRRENPCESNRGYDYTPLPAGYVTK DLEYFPETDKVWIEIGETEGTFIVDSVELLLM  
1140 1150 1160 1170 1180 1190

Cry1Ac EE  
gi|197 EE

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>>gi|3990786|gb|AAC84213.1|AR000636 Sequence 8 from pate (1193 aa)
initn: 6305 initl: 3146 opt: 3339 Z-score: 3927.3 bits: 738.7 E(): 7.8e-210
Smith-Waterman score: 6852; 87.062% identity (92.571% similar) in 1198 aa overlap
(5-1182:1-1193)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|399 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

Cry1Ac VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
gi|399 VLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|399 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|399 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSI RSPHL
gi|399 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSI RSPHL

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIV AQLGQ
gi|399 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIV AQLGQ

Cry1Ac GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ
gi|399 GVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIP PQ

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|399 NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

Cry1Ac VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS
gi|399 VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS

480 490 500 510 520 530
540 550 560 570 580 590
Cry1Ac VTPIHNLVNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
gi|399 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTDVSNPFSFRANPDII
600 610 620 630 640
Cry1Ac GVRN---F---SGTAG-VI IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|399 GISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT D
650 660 670 680 690 700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|399 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPRG
710 720 730 740 750 760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLPGTVEFCYPTLYQKIDESKCLKAFTRYQLRGYIEDSQ
gi|399 WRGSTDITIQGGDDVFKENYVTLPGTVEFCYPTLYQKIDESKCLKAYTRYELRGYIEDSQ
770 780 790 800 810 820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGE
gi|399 DLEIYLIRYNAKHEIVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGE
830 840 850 860 870 880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLEKPLLGEALARV
gi|399 KCAHSHHFSLDIDVGCTDLNEDLGWVVFKIKTQDGHARLGNLEFLEKPLLGEALARV
890 900 910 920 930 940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHAADKRVHSI
gi|399 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNAMIHAADKRVHRI
950 960 970 980 990 1000
Cry1Ac REAYPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHDVDE
gi|399 REAYPELSVIPGVNAAIFEELEGRIFTAYS LYDARNVIKNGDFNGLSCWNKGVHDVDE
1010 1020 1030 1040 1050 1060
Cry1Ac EQNNQSRVSLVVPWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKF
gi|399 EQNNHRSVSLVVIPEWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIEDNTDELKF
1070 1080 1090 1100 1110 1120
Cry1Ac SNCVEEIIYPNNITVTNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY

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gi|399 SNCVEEEVYPNNTVTCNNYGTQEEYEGTYTSRNQGYDEAYGNNPSVPADYASVYEEKSY
1080 1090 1100 1110 1120 1130

Cry1Ac TDGRENPCFNRGYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
1130 1140 1150 1160 1170 1180

gi|399 TDGRENPCSNRGYDGYTLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
1140 1150 1160 1170 1180 1190

Cry1Ac EE
::

gi|399 EE

>>gi|19700905|emb|CAD29023.1| unnamed protein product [s (1193 aa)
initn: 6348 initl: 3146 opt: 3336 Z-score: 3923.8 bits: 738.0 E(): 1.2e-209
Smith-Waterman score: 6869; 87.479% identity (92.654% similar) in 1198 aa overlap
(5-1182:1-1193)

Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50 60

gi|197 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|197 VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|197 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|197 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGLEGSIRSPHL
250 260 270 280 290 300

gi|197 TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGLEGSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaaPQRiVAQLGQ
310 320 330 340 350 360

gi|197 MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPlygtmgnaaPQRiVAQLGQ
300 310 320 330 340 350

Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
370 380 390 400 410 420

gi|197 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ

gi|197 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFShRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|197 NNNVPPRQGFShRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEATLNTIDPERINQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|197 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVnINSPITQ-RYRLRFRYAS
480 490 500 510 520 530

Cry1Ac VTPIHlnVNWGNSSi----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
540 550 560 570 580 590

gi|197 SRDARVIVLTGAASTGVGGQVSVNMP LQKtMEIGENLTSRTFRYtDFSNPFSFRANPDII
540 550 560 570 580 590

Cry1Ac GVRN---F---SGTAG-VIIDRFEPVtATLEAEYNLERAQKAVNALFTSTNQLGLKtN
600 610 620 630 640

gi|197 GISeQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKtD
600 610 620 630 640 650

Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
650 660 670 680 690 700

gi|197 VTDYHIDQVSNLVDCLSEDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRG
660 670 680 690 700 710

Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAFTRYQLRGYIEDSQ
710 720 730 740 750 760

gi|197 WRGSTDITIQGGDDVFKENYVTLQGTfDECYPTYLYQPIDESKLKAYTRYQLRGYIEDSQ
720 730 740 750 760 770

Cry1Ac DLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPiGKCGEPNRCAPHLEWNPDLDCSCRdGE
770 780 790 800 810 820

gi|197 DLEIYLIRYNAKHETVNVPGTGSWLPPSAPSPiGKCGEPNRCAPHLEWNPDLDCSCRdGE
780 790 800 810 820 830

Cry1Ac KCAHSHHfSLDIDVGCTDLNEDLGVWVIFKIKtQDGHARLGNLEFLEEKPLVGEALARV
830 840 850 860 870 880

gi|197 KCAHSHHfSLDIDVGCTDLNEDLGVWVIFKIKtQDGHARLGNLEFLEEKPLVGEALARV
840 850 860 870 880 890

Cry1Ac KRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNiAMiHAADKRVHSi
890 900 910 920 930 940

gi|197 KRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNiAMiHAADKRVHSi
900 910 920 930 940 950

Cry1Ac REAYLPELSVIPGVNAIfEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVE
950 960 970 980 990 1000

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gi|197 REAYLEPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVVDVE
      960      970      980      990      1000     1010
Cry1Ac EQNNQRSVLVPEWEAEVSEVVRVCPGRGYLLRVYTAYKEGYGEGCVTIIHEIENNTDELK
      1010     1020     1030     1040     1050     1060
gi|197 EQNNHRSVLVPEWEAEVSEVVRVCPGRGYLLRVYTAYKEGYGEGCVTIIHEIENNTDELK
      1020     1030     1040     1050     1060     1070
Cry1Ac SMCVEEYIPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
      1070     1080     1090     1100     1110     1120
gi|197 SMCVEEYIPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
      1080     1090     1100     1110     1120     1130
Cry1Ac TDGRENPCFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
      1130     1140     1150     1160     1170     1180
gi|197 TDGRENPCFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
      1140     1150     1160     1170     1180     1190

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Cry1Ac EE
      ::
gi|197 EE

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>>gi|19700907|emb|CAD29024.1| unnamed protein product [s (1193 aa)
      in1n: 6357 in1l: 3146 opt: 3336 Z-score: 3923.8 bits: 738.0 E(): 1.2e-209
      Smith-Waterman score: 6884; 87.646% identity (92.738% similar) in 1198 aa overlap
      (5-1182:1-1193)

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      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
gi|197 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNLYQIYAESFRE
      70      80      90     100     110     120
gi|197 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90     100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|197 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190     200     210     220     230     240
gi|197 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSI RSPHL
      250     260     270     280     290     300

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gi|197 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSI RSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLQG
      310     320     330     340     350     360
gi|197 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLQG
      300     310     320     330     340     350
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
      370     380     390     400     410     420
gi|197 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPPQ
      360     370     380     390     400     410
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
      430     440     450     460     470     480
gi|197 NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
      490     500     510     520     530
gi|197 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS----LQVNSINSPITQ-RYRLRFRYAS
      480     490     500     510     520     530
Cry1Ac VTIPIHLNVNWNSSII----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
      540     550     560     570     580     590
gi|197 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTD FSNPFSFRANPDII
      540     550     560     570     580     590
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      600     610     620     630     640
gi|197 GISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT D
      600     610     620     630     640     650
Cry1Ac VTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
      650     660     670     680     690     700
gi|197 VTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRG
      660     670     680     690     700     710
Cry1Ac WGGSTGITIQGGDDVFKENYVTLQGTDFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQ
      710     720     730     740     750     760
gi|197 WRGSTDITIQGGDDVFKENYVTLQGTDFDECYPTYLYQKIDESKCLKAYTRYQLRGYIEDSQ
      720     730     740     750     760     770
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGE
      770     780     790     800     810     820
gi|197 DLEIYLIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGE
      780     790     800     810     820     830
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSI RSPHL
      830     840     850     860     870     880

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Cry1Ac KCAHSHHFSLDIDVGCSDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|197 KCAHSHHFSLDIDVGCSDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
      840      850      860      870      880      890
      890      900      910      920      930      940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSI
gi|197 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAIHAADKRVHSI
      900      910      920      930      940      950
      950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNVKGVHDVDE
gi|197 REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNVKGVHDVDE
      960      970      980      990      1000      1010
      1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSLVLPVPEWEAEVSVQEVVRCVPCGRGYLLRVTAAYKEGYGEGCVTIIHEIENNTDELKF
gi|197 EQNNHRSVLVPEWEAEVSVQEVVRCVPCGRGYLLRVTAAYKEGYGEGCVTIIHEIENNTDELKF
      1020      1030      1040      1050      1060      1070
      1070      1080      1090      1100      1110      1120
Cry1Ac SNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVVEEKSY
gi|197 SNCVEEEVYPNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAY
      1080      1090      1100      1110      1120      1130
      1130      1140      1150      1160      1170      1180
Cry1Ac TDGRENPCFNRGYRDTPLPVGYVTKLEYFPETDKVWVIEIGETEGTFIVDSVELLLM
gi|197 TDGRDNPCESNRGYDGTPLPAGYVTKLEYFPETDKVWVIEIGETEGTFIVDSVELLLM
      1140      1150      1160      1170      1180      1190

Cry1Ac EE
gi|197 EE

>>gi|19700909|emb|CAD29025.1| unnamed protein product [s (668 aa)
  initn: 3528 initl: 3139 opt: 3306 Z-score: 3892.1 bits: 731.3 E(): 7.1e-208
Smith-Waterman score: 3543; 82.912% identity (89.599% similar) in 673 aa overlap
(5-661:1-668)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|197 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|197 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110
      130      140      150      160      170      180

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|197 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|197 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDDGSRGSAQIEGSIKRSRPHL
gi|197 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDDGSRGSAQIEGSIKRSRPHL
      240      250      260      270      280      290
      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|197 MDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350
      370      380      390      400      410      420
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPO
gi|197 GVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPO
      360      370      380      390      400      410
      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSTIQIPA
gi|197 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATLNTIDPFRANQIPL
      420      430      440      450      460      470
      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|197 VKGFRVWGTSTVITGPGFTGGDILRRNTFGDFVS----LQVNINSBITQ-RYRLRFRYAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
gi|197 SRDARVIVLTGAATGVGGQSVNMPLQKTMEIGENLTSRTFRYTDFFSNPFRANPDII
      540      550      560      570      580      590
      600      610      620      630      640
Cry1Ac GVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|197 GISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIQLKTD
      600      610      620      630      640      650
      650      660      670      680      690      700
Cry1Ac VTDYHIDQVSNLVVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|197 VTDYHIDQVSNLVVDCLS
      660

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>>gi|19700903|emb|CAD29022.1| unnamed protein product [s (631 aa)
initn: 3332 init1: 3139 opt: 3304 Z-score: 3890.1 bits: 730.9 E(): 9.2e-208
Smith-Waterman score: 3347; 82.704% identity (89.308% similar) in 636 aa overlap
(5-624:1-631)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|197 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
gi|197 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
60 70 80 90 100 110 120
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|197 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170 180
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|197 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230 240
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
gi|197 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290 300
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|197 MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350 360
Cry1Ac GYVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
gi|197 GYVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
360 370 380 390 400 410 420
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA
gi|197 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA
420 430 440 450 460 470 480
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|197 VKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIITQ-RYRLRFRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTPIHLLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV
gi|197 SRDARVIVLTGAASTGVGGQVSVNMLQKTM EIGENLTSRTFRYDFSNPFSFRANPDI I
540 550 560 570 580 590
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|197 GISEQPLFGAGSISGGELYIDKIEIILLADATFEAESDLER
600 610 620 630
Cry1Ac VTDYHIDQVSNLVVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
>>gi|40189707|gb|AAR76447.1| Sequence 30 from patent US (1193 aa)
initn: 6267 init1: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)
10 20 30 40 50 60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|401 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
gi|401 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
60 70 80 90 100 110 120
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|401 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170 180
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|401 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230 240
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
gi|401 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290 300
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|401 MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350 360
Cry1Ac GYVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
gi|401 GYVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP S AVYRKS G T V D S L D E I P P Q
360 370 380 390 400 410 420
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA
gi|401 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRS AEFNNIIASDSITQIPA
420 430 440 450 460 470 480
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIITQ-RYRLRFRYAS
480 490 500 510 520 530

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gi|401 GVVRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDSLDEIPPO
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      .....

gi|401 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATLTNTIDPERINQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....

gi|401 VKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIQ-RYRLRFRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV
      .....

gi|401 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDFSNPFSFRANPDII
      540      550      560      570      580      590

      600      610      620      630      640
Cry1Ac GVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      .....

gi|401 GISEQPLFGAGS ISSGELYDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
      600      610      620      630      640      650

      650      660      670      680      690      700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
      .....

gi|401 VTDYHIDQVSNLVCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRG
      660      670      680      690      700      710

      710      720      730      740      750      760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
      .....

gi|401 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
      720      730      740      750      760      770

      770      780      790      800      810      820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      .....

gi|401 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      780      790      800      810      820      830

      830      840      850      860      870      880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARV
      .....

gi|401 KCAHSHHFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARV
      840      850      860      870      880      890

      890      900      910      920      930      940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSI
      .....

gi|401 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAAMIHAADKRVHRI
      900      910      920      930      940      950

      950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVDE

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      .....
gi|401 REAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVDE
      960      970      980      990      1000      1010

      1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSVLVPEWEAEVSEVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKF
      .....

gi|401 EQNNHRSVLVPEWEAEVSEVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIEDNTDELKF
      1020      1030      1040      1050      1060      1070

      1070      1080      1090      1100      1110      1120
Cry1Ac SNCVEEIIYPNNIVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
      .....

gi|401 SNCVEEIVPNNIVTVCNNYTGTEQEEYEGTYTSRNQGYDEAYGNPSPVPADYASVYEEKSY
      1080      1090      1100      1110      1120      1130

      1130      1140      1150      1160      1170      1180
Cry1Ac TDGRRNCPCEFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
      .....

gi|401 TDGRRNCPCESNRGYDYTPLPAGVYTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
      1140      1150      1160      1170      1180      1190

Cry1Ac EE
      ::
gi|401 EE

>>gi|31688819|gb|AAP60984.1| Sequence 30 from patent US (1193 aa)
      initn: 6267 init1: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
      Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
      (5-1182:1-1193)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....

gi|316 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      .....

gi|316 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....

gi|316 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      .....

gi|316 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      180      190      200      210      220      230

      250      260      270      280      290      300
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPNVLENFDGSRGSAQIEGSIRSPHL

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gi|316 240 250 260 270 280 290
Cry1Ac 310 320 330 340 350 360
gi|316 300 310 320 330 340 350
Cry1Ac 370 380 390 400 410 420
gi|316 360 370 380 390 400 410
Cry1Ac 430 440 450 460 470 480
gi|316 420 430 440 450 460 470
Cry1Ac 490 500 510 520 530
gi|316 480 490 500 510 520 530
Cry1Ac 540 550 560 570 580 590
gi|316 540 550 560 570 580 590
Cry1Ac 600 610 620 630 640
gi|316 600 610 620 630 640
Cry1Ac 650 660 670 680 690 700
gi|316 660 670 680 690 700 710
Cry1Ac 710 720 730 740 750 760
gi|316 720 730 740 750 760 770
Cry1Ac 770 780 790 800 810 820
gi|316 780 790 800 810 820 830
Cry1Ac 830 840 850 860 870 880

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Cry1Ac KCAHSHHFLDIDVCGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALRV
gi|316 KCAHSHHFTLDIDVCGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLLGEALRV
Cry1Ac 890 900 910 920 930 940
gi|316 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTNIAMIHAADKRVHRSI
Cry1Ac 950 960 970 980 990 1000
gi|316 REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNV IKNGDFNNGLCWNVKGVHDVDE
Cry1Ac 1010 1020 1030 1040 1050 1060
gi|316 EQNNQRSVLVPVEWAEVSEQEVRVCPGRGYILRV TAYKEGYEGGCVTIHEIENNTDELKPF
Cry1Ac 1070 1080 1090 1100 1110 1120
gi|316 SNCVEEIIYPNNTVT CNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
Cry1Ac 1130 1140 1150 1160 1170 1180
gi|316 TDGRRNCPCEFNRGRDY TPLPVGYVTKLEYFPETDKVWIEIGETEGT FIVDSVELLLM
Cry1Ac 1140 1150 1160 1170 1180 1190
gi|316 TDGRRNCPESNRGYD YTPLPAGYVTKDLEYFPETDKVWIEIGETEGT FIVDSVELLLM
Cry1Ac EE
gi|316 EE
>>gi|47257346|gb|AAT23509.1| Sequence 30 from patent US (1193 aa)
initn: 6267 init1: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)
Cry1Ac 10 20 30 40 50 60
gi|472 CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGF
Cry1Ac 70 80 90 100 110 120
gi|472 VLGVDV I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E
Cry1Ac 130 140 150 160 170 180
gi|472 VLGVDV I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|472 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
gi|472 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
gi|472 TLTVLDIVSLFFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|472 MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

370 380 390 400 410 420
Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDLEIIPPQ
gi|472 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSSAVYRKSQVSDLEIIPPQ
360 370 380 390 400 410

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNLIASDSITQIPA
gi|472 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNLIASDSITQIPA
420 430 440 450 460 470

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|472 VKGFRVWGGTSTVITGPGFTGGDILRRNTFGDFVS----LQVNINSPIIQ-RYRLRFYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VPIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV
gi|472 SRDARVIVLVTGAASTGVGGQVSVNMPLOKQTMIEIGENLTSRTFRYTDVDFSNPFRANPDI
540 550 560 570 580 590

600 610 620 630 640
Cry1Ac GVRN---F---SGTAG-VIIDRFEPVITATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|472 GISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
600 610 620 630 640 650

650 660 670 680 690 700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|472 VTDYHIDQVSNLVDCSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD
660 670 680 690 700 710

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710 720 730 740 750 760
Cry1Ac WGGSTGITIQQGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQ
gi|472 WRGSTDITIQGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYTRYELRGYIEDSQ
720 730 740 750 760 770

770 780 790 800 810 820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDE
gi|472 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDE
780 790 800 810 820 830

830 840 850 860 870 880
Cry1Ac KCAHSHHFLSLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|472 KCAHSHHFLDIDVCGTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
840 850 860 870 880 890

890 900 910 920 930 940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSI
gi|472 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAIHAADKRVHRI
900 910 920 930 940 950

950 960 970 980 990 1000
Cry1Ac REAYLPELSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVE
gi|472 REAYLPELSVIPGVNAAIPEELEGRIFTAYSLYDARNVIKNGDFNGLSCWNVKGVHDVE
960 970 980 990 1000 1010

1010 1020 1030 1040 1050 1060
Cry1Ac EQNNQRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKF
gi|472 EQNNHRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKF
1020 1030 1040 1050 1060 1070

1070 1080 1090 1100 1110 1120
Cry1Ac SNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|472 SNCVEEIVPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNNSVPADYASVYEEKSY
1080 1090 1100 1110 1120 1130

1130 1140 1150 1160 1170 1180
Cry1Ac TDGRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|472 TDGRENPCESNRGYDTPPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
1140 1150 1160 1170 1180 1190

Cry1Ac EE
::
gi|472 EE

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>>gi|112061965|gb|ABH98783.1| Sequence 30 from patent US (1193 aa)
initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

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Regulatory Product Characterization Team

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|112 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE  
gi|112 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL

Cry1Ac TLTVDLIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDFGSAQGIERSIRSPHL  
gi|112 TLTVDLIVALFPNYDSRRYPPIRTVSQLTREIYTNVLENFDFGSAQGIERSIRSPHL

Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
gi|112 MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

Cry1Ac GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ  
gi|112 GVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|112 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEATLTNTIPDERINQIPL

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
gi|112 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIIQ-RYRLRFYAS

Cry1Ac VPIHLNVWNGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV  
gi|112 SRDARVIVLTGAASTGVGGQVSVNMLPQKTMIEIGENLTSRTPRYTDFSNPFSFRANPDI

Cry1Ac GVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN  
gi|112 GISEQPLFGAGSISSELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT

Cry1Ac VTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG  
gi|112 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGR

Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQ  
gi|112 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYTRYELRGYIEDSQ

Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE  
gi|112 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE

Cry1Ac KCAHSHHFFSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV  
gi|112 KCAHSHHFFTLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV

Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSI  
gi|112 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNAMIHAADKRVHRI

Cry1Ac REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVE  
gi|112 REAYLPELSVIPGVNAAI FEELEGRIFTAYSLYDARNVIKNGDFNNGLSCWNVKGVHDVE

Cry1Ac EQNNQRSVLVPEWEAEVSVQEVVCPGRGYILRVTA YKEGYGECVTIHEIENNTDELK  
gi|112 EQNNHRSVLVPEWEAEVSVQEVVCPGRGYILRVTA YKEGYGECVTIHEIEDNTDELK

Cry1Ac SNCVEEIIYPNNTVTNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY  
gi|112 SNCVEEIVPNNTVTNNYTGTEYEGYTSRNQGYDEAYGNPSPVPADYASVYEEKSY

Cry1Ac TDGRRNPCEFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM  
gi|112 TDGRRNPCESNRYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM

Regulatory Product Characterization Team

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1140      1150      1160      1170      1180      1190
Cry1Ac EE
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gi|112 EE

>>gi|29718514|gb|AAP01238.1| Sequence 30 from patent US (1193 aa)
  initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
:::
gi|297 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
:::
gi|297 VLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
:::
gi|297 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
:::
gi|297 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIERSIRSPHL
:::
gi|297 TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVENFDGSGFRGSAQGIERSIRSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
:::
gi|297 MDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300     310     320     330     340     350
Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQ
:::
gi|297 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQ
      360     370     380     390     400     410
Cry1Ac NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
:::
gi|297 NNVVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAATLNTIDPERINQIPL

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420      430      440      450      460      470
      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
:::
gi|297 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIITQ-RYRLRFYRAS
      480      490      500      510      520      530
      540      550      560      570      580      590
Cry1Ac VTPIHLNVNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
:::
gi|297 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDFSNPFSFRANPDII
      540      550      560      570      580      590
      600      610      620      630      640
Cry1Ac GVRN---F---SGTAG-VI IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
:::
gi|297 GISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
      600      610      620      630      640      650
      650      660      670      680      690      700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
:::
gi|297 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD
      660      670      680      690      700      710
      710      720      730      740      750      760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLPGTDEFCYPTYLYQKIDESKLLKAFTRYQLRGLYEDSQ
:::
gi|297 WRGSTDITIQGGDDVFKENYVTLPGTDEFCYPTYLYQKIDESKLLKAYTRYELRGLYEDSQ
      720      730      740      750      760      770
      770      780      790      800      810      820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGE
:::
gi|297 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRDGE
      780      790      800      810      820      830
      830      840      850      860      870      880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARV
:::
gi|297 KCAHSHHFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARV
      840      850      860      870      880      890
      890      900      910      920      930      940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSI
:::
gi|297 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRVHRI
      900      910      920      930      940      950
      950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVE
:::
gi|297 REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVE
      960      970      980      990      1000      1010
      1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSVLVVPEWEAEVSEQEVRVCPGRGYILRVTA YKEGYEGCVTIHEIENNTDELKF
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gi|297 EQNNHRSVLVPIEWEAEVSVQEVVRCVPCGRGYILRVYTAYKEGYEGCVTIIHEIEDNTDELKPF
1020 1030 1040 1050 1060 1070

Cry1Ac SNCVEEIIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
1070 1080 1090 1100 1110 1120

gi|297 SNCVEEIVPNNVTVCNNYTGQEEYEGTYTSRNQGYDEAYGNNPSVPADYASVYEEKSY
1080 1090 1100 1110 1120 1130

Cry1Ac TDGRENPCFNRGYRDYTPPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
1130 1140 1150 1160 1170 1180

gi|297 TDGRENPCSNRGYGDYTPPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
1140 1150 1160 1170 1180 1190

Cry1Ac EE
::

gi|297 EE

>>gi|77376721|gb|ABA70268.1| Sequence 30 from patent US (1193 aa)
initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50 60

gi|773 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|773 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|773 WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
190 200 210 220 230 240

gi|773 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPVENFDGSRGSAQGIERSIRSPHL
250 260 270 280 290 300

gi|773 TLTVLDIVALFPNYSRRYPPIRTVSQLTREIYTNPVENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360

gi|773 MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360

gi|773 MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
370 380 390 400 410 420

gi|773 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
430 440 450 460 470 480

gi|773 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSATLNTIDPERINQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKGFRVWGGTSVITGPGFTGGDILRRNTPGDFVS---LQVNSINSPITQ-RYRLRFRYAS
480 490 500 510 520 530

Cry1Ac VTPIHNLVNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
540 550 560 570 580 590

gi|773 SRDARVIVLTGAASTGVGGQVSVNMPLOKTMIEIGENLTSRTFRYDFSNPFSFRANPDI
540 550 560 570 580 590

Cry1Ac GVRN---F---SGTAG-VIIDRFEPVITATLEAEYNLERAQKAVNALFTSTNQLGLKTN
600 610 620 630 640

gi|773 GISEQLFAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
600 610 620 630 640 650

Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
650 660 670 680 690 700

gi|773 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD
660 670 680 690 700 710

Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
710 720 730 740 750 760

gi|773 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
720 730 740 750 760 770

Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
770 780 790 800 810 820

gi|773 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
780 790 800 810 820 830

Cry1Ac KCAHSHHFLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEKPLVGEALARV
830 840 850 860 870 880

gi|773 KCAHSHHFTLIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEKPLVGEALARV
840 850 860 870 880 890

Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSI
890 900 910 920 930 940

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gi|773 KRAEKKWRDKREKLEQLTNI VYKEAKESVDALFVNSQVDRLQVDNIAAMIHAADKRVRHI
      900      910      920      930      940      950
Cry1Ac REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVE
      950      960      970      980      990     1000
gi|773 REAYLPELSVIPGVNAAI FEELEGRIFTAYSLYDARNVIKNGDFNNGLLCWNVKGHVDE
      960      970      980      990     1000     1010
Cry1Ac EQNNQRSVLVPEWEAEVSVQEVRCVPCGRGYLLRVTA YKEGYGEGCVTTHEIENNTDELK
      1010     1020     1030     1040     1050     1060
gi|773 EQNNHRSVLVIPWEAEVSVQEVRCVPCGRGYLLRVTA YKEGYGEGCVTTHEIEDNTDELK
      1020     1030     1040     1050     1060     1070
Cry1Ac SNCVEEEIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEKSY
      1070     1080     1090     1100     1110     1120
gi|773 SNCVEEVEYVNNVTVCNNYTGTEQEEYEGTYTSRNGQYDEAYGNNPSVPADYASVYEKSY
      1080     1090     1100     1110     1120     1130
Cry1Ac TDGRRNPECFNRGYRDTPLPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLM
      1130     1140     1150     1160     1170     1180
gi|773 TDGRRNPECFNRGYRDTPLPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLM
      1140     1150     1160     1170     1180     1190
Cry1Ac EE
      ::
gi|773 EE

>>gi|20221576|gb|AAE87149.1| Sequence 30 from patent US (1193 aa)
  initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
gi|202 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      70      80      90     100     110     120
gi|202 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      60      70      80      90     100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130     140     150     160     170     180
gi|202 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      190     200     210     220     230     240

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gi|202 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      180     190     200     210     220     230
Cry1Ac TLTVLIDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
      250     260     270     280     290     300
gi|202 TLTVLIDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHL
      240     250     260     270     280     290
Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIV AQLGQ
      310     320     330     340     350     360
gi|202 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIV AQLGQ
      300     310     320     330     340     350
Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDSLDEIPPO
      370     380     390     400     410     420
gi|202 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDSLDEIPPO
      360     370     380     390     400     410
Cry1Ac NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      430     440     450     460     470     480
gi|202 NNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEATLNTIDPERINQIPL
      420     430     440     450     460     470
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      490     500     510     520     530
gi|202 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNNISPITQ-RYRLRFRYAS
      480     490     500     510     520     530
Cry1Ac VTPIHNLVNWGNSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
      540     550     560     570     580     590
gi|202 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTDFSNPNPFRANPDII
      540     550     560     570     580     590
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      600     610     620     630     640
gi|202 GISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
      600     610     620     630     640     650
Cry1Ac VTDYHIDQVSNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDQSNFKDINRQPERG
      650     660     670     680     690     700
gi|202 VTDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD
      660     670     680     690     700     710
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQ
      710     720     730     740     750     760
gi|202 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYTYELRGYIEDSQ
      720     730     740     750     760     770
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      770     780     790     800     810     820

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Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|202 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
780 790 800 810 820 830

Cry1Ac KCAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|202 KCAHSHHFTLTDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
840 850 860 870 880 890

Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSI
gi|202 KRAEKKWRDKREKLQLETNIVYKEAKESVDALFVNSQYDRLQVDTNIAAMIHAADKRVHRI
900 910 920 930 940 950

Cry1Ac REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVDE
gi|202 REAYLPELSVIPGVNAAIFEELEGRIFTAYSLYDARNVIKNGDFNNGLSCWNVKGVHDVDE
960 970 980 990 1000 1010

Cry1Ac EQNNQRSVLVPEWEAEVSQEVVRCVCPGRGYLLRVTAAYKEGYGEGCVTTHIEIENNTDELKCF
gi|202 EQNNHRSVLVPEWEAEVSQEVVRCVCPGRGYLLRVTAAYKEGYGEGCVTTHIEIEDNTDELKCF
1020 1030 1040 1050 1060 1070

Cry1Ac SNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|202 SNCVEEEVYPNNTVTCNNYTGTEEEYEGYTSRNQGYDEAYGNNPSVPADYASVYEEKSY
1080 1090 1100 1110 1120 1130

Cry1Ac TDGRRNPCEFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|202 TDGRRNPCESNRGYGDYTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
1140 1150 1160 1170 1180 1190

Cry1Ac EE
gi|202 EE

>>gi|12824342|gb|AAE49248.1| Sequence 30 from patent US (1193 aa)
initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|128 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60
70 80 90 100 110 120

Cry1Ac VLGLVDIIWGIWIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|128 VLGLVDIIWGIWIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|128 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|128 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
gi|128 TLTVLDIVALFPNYDSRRYPVRTVSQLTREIYTNPVLENFDGSRGSAQGIERSIRSPHL
240 250 260 270 280 290

Cry1Ac MDILNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|128 MDILNSITITYTDAHRGYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300 310 320 330 340 350

Cry1Ac GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|128 GYVRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|128 NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEATLNTIDPERINQIPL
420 430 440 450 460 470

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS----LQVNIINSPIQ-RYRLRFRYAS
480 490 500 510 520 530

Cry1Ac VTIPIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
gi|128 SRDARVIVLTGAASTGVGGQVSVNMLPQKTMEIGENLTSRTFRYTFDFSNPFFRANPDII
540 550 560 570 580 590

Cry1Ac GVRN---F---SGTAG-VI IDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|128 GISEQPLFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
600 610 620 630 640 650

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650      660      670      680      690      700
Cry1Ac VTDYHIDQVSNLVTVLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|128 VTDYHIDQVSNLVLDCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQPDGRG
660      670      680      690      700      710

710      720      730      740      750      760
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
gi|128 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
720      730      740      750      760      770

770      780      790      800      810      820
Cry1Ac DLEIYSIRYNAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|128 DLEIYLIRYNAKHEIVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
780      790      800      810      820      830

830      840      850      860      870      880
Cry1Ac KCAHSHHFSLDIDVGCDDLNEGLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
gi|128 KCAHSHHFSLDIDVGCDDLNEGLVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
840      850      860      870      880      890

890      900      910      920      930      940
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSI
gi|128 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAIHAADKRVRHI
900      910      920      930      940      950

950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVDE
gi|128 REAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVDE
960      970      980      990      1000      1010

1010     1020     1030     1040     1050     1060
Cry1Ac EQNNQRSVLVPEWEAEVSVQEVVCPGRGYILLRVTAIYKEGYGEGCVTTHIEIENNTDELKF
gi|128 EQNNHRSVLVPEWEAEVSVQEVVCPGRGYILLRVTAIYKEGYGEGCVTTHIEIEDNTDELKF
1020     1030     1040     1050     1060     1070

1070     1080     1090     1100     1110     1120
Cry1Ac SNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSY
gi|128 SNCVEEIVYPNNTVTCNNYTGQEEYEGTYTSRNGYDEAYGNNPSVPADYASVYEEKSY
1080     1090     1100     1110     1120     1130

1130     1140     1150     1160     1170     1180
Cry1Ac TDGRENPCFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|128 TDGRENPCFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLM
1140     1150     1160     1170     1180     1190

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Cry1Ac EE
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gi|128 EE

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>>gi|16242913|gb|AAE80143.1| Sequence 30 from patent US (1193 aa)
  initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|162 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
gi|162 VLGLVDIIWGIWIFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|162 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
gi|162 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWIRYNQFREL
180     190     200     210     220     230

250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHL
gi|162 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHL
240     250     260     270     280     290

310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|162 MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
300     310     320     330     340     350

370     380     390     400     410     420
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQGTVDLSDEIPPO
gi|162 GVYRTLSSITLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQGTVDLSDEIPPO
360     370     380     390     400     410

430     440     450     460     470     480
Cry1Ac NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|162 NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
420     430     440     450     460     470

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|162 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNSINSPITQ-RYRLRFRVRYAS
480     490     500     510     520     530

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540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV
      . . . . . : . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 SRDARVIVLVTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTDFSNPF SFRANPDI I
      540      550      560      570      580      590

540      550      560      570      580      590
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 GISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKTD
      600      610      620      630      640      650

540      550      560      570      580      590
Cry1Ac VTDYHIDQVSNLVTLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 VTDYHIDQVSNLVDCLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPPDRG
      660      670      680      690      700      710

540      550      560      570      580      590
Cry1Ac WGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
      720      730      740      750      760      770

540      550      560      570      580      590
Cry1Ac DLEIYSIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
      780      790      800      810      820      830

540      550      560      570      580      590
Cry1Ac KCAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 KCAHSHHFTLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARV
      840      850      860      870      880      890

540      550      560      570      580      590
Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMIHAAKRVHRI
      900      910      920      930      940      950

540      550      560      570      580      590
Cry1Ac REAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLLCWNVKGHV DVE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 REAYLPELSVIPGVNAAFEELEGRIFTAYS LYDARNVIKNGDFNNGLLCWNVKGHV DVE
      960      970      980      990      1000

540      550      560      570      580      590
Cry1Ac EQNNQRSVLVVPWEAEVSEVVRVCPGRGYILRVTA YKEGYEGCVT IHEIENNTDELKF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 EQNNHRSVLVIPWEAEVSEVVRVCPGRGYILRVTA YKEGYEGCVT IHEIEDNTDELKF
      1020      1030      1040      1050      1060      1070

540      550      560      570      580      590
Cry1Ac SNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 SNCVEEEVYPNNTVTCNNYTGTEYEGTYTSRNRQGYDEAYGNNSVPADYASVYEEKSY

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1080      1090      1100      1110      1120      1130
Cry1Ac TDGRRNCPCEFNRYGDRYDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 TDGRRNCPCESNRGYDYPPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
      1140      1150      1160      1170      1180      1190

1080      1090      1100      1110      1120      1130
Cry1Ac EE
      . .
gi|162 EE

>>gi|15126308|gb|AAE73544.1| Sequence 30 from patent US (1193 aa)
      initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
      Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
      (5-1182:1-1193)

1080      1090      1100      1110      1120      1130
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50      60

1080      1090      1100      1110      1120      1130
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      60      70      80      90      100      110

1080      1090      1100      1110      1120      1130
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      120      130      140      150      160      170

1080      1090      1100      1110      1120      1130
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
      180      190      200      210      220      230

1080      1090      1100      1110      1120      1130
Cry1Ac TLTVLDIVSLFPNYDSRYPVRTVSQLTREIYTNPVLENF DGSFRGSAQGIERSIRSPHL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 TLTVLDIVALFPNYDSRYPVRTVSQLTREIYTNPVLENF DGSFRGSAQGIERSIRSPHL
      240      250      260      270      280      290

1080      1090      1100      1110      1120      1130
Cry1Ac MDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 MDILNSITIIYTDHARGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      300      310      320      330      340      350

1080      1090      1100      1110      1120      1130
Cry1Ac GVYRTLSSLTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|151 GVYRTLSSLTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQ

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360      370      380      390      400      410
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|151  NNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSATLNTIDPERINQIPL
420      430      440      450      460      470
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|151  VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIQ-RYRLRFYAS
480      490      500      510      520      530
Cry1Ac  VPIHLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
gi|151  SRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTRYDFSNPFSFRANPDII
540      550      560      570      580      590
Cry1Ac  GVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|151  GISEQPLFGAGSISSGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT
600      610      620      630      640
Cry1Ac  VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|151  VTDYHIDQVSNLVDLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPD
650      660      670      680      690      700
Cry1Ac  WGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
gi|151  WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQ
710      720      730      740      750      760
Cry1Ac  DLEIYSIRYNAKHETVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
gi|151  DLEIYLIRYNAKHEIVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGE
770      780      790      800      810      820
Cry1Ac  KCAHSHHFSLDIDVGCDDLNLNEDLGWVWVIFKIKTQDGHARLGNLFELEKPLVGEALARV
gi|151  KCAHSHHFTLIDVGCDDLNLNEDLGWVWVIFKIKTQDGHARLGNLFELEKPLLGEALARV
830      840      850      860      870      880
Cry1Ac  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSI
gi|151  KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAIHAADKRVHRI
890      900      910      920      930      940
Cry1Ac  REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVE
gi|151  REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVE
950      960      970      980      990      1000

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gi|151  REAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVE
960      970      980      990      1000      1010
Cry1Ac  EQNNQRSVLVVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKF
gi|151  EQNNHRSVLVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIEDNTDELKF
1010      1020      1030      1040      1050      1060
Cry1Ac  SNCVEEIIYPNNITVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPPADYASVYEEKSY
gi|151  SNCVEEIVYPNNITVTCNNYTGTEQEEYEGTYTSRNGYDEAYGNNSVPADYASVYEEKSY
1070      1080      1090      1100      1110      1120
Cry1Ac  TDGRRENPCFENRGYRDYTPLPVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|151  TDGRRENPCESNRGYDYPPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVELLLM
1130      1140      1150      1160      1170      1180
Cry1Ac  EE
gi|151  EE
1180      1190
Cry1Ac  EE
gi|151  EE

>>gi|83329856|gb|ABC06985.1| Sequence 30 from patent US (1193 aa)
initn: 6267 initl: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)
10      20      30      40      50      60
Cry1Ac  CMQAMNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|833  MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
70      80      90      100      110      120
Cry1Ac  VLGLVDIIVGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
gi|833  VLGLVDIIVGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
gi|833  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVYQAAANLHLSVLRDVS
190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
gi|833  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWVRYNQFRREL
250      260      270      280      290      300
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL

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gi|833 TLTVLDIVALFPNYDSRRYPVRTVSQTLTREIYTNPVLENFDGFSFRGSAQGIERSIRSPHL
      240      250      260      270      280      290

      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVaQLGQ
      .....
gi|833 MDILNSITIIYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVaQLGQ
      300      310      320      330      340      350

      370      380      390      400      410      420
Cry1Ac GvyrtLSSTlyRRPFNIGINNqQLSVLDGTEfAYGTSSNLPSAVYRKSgTVDSLDEIppQ
      .....
gi|833 GvyrtLSSTlyRRPFNIGINNqQLSVLDGTEfAYGTSSNLPSAVYRKSgTVDSLDEIppQ
      360      370      380      390      400      410

      430      440      450      460      470      480
Cry1Ac NNNVpPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPa
      .....
gi|833 NNNVpPRQGFShRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFLTNTIDPERINQIPL
      420      430      440      450      460      470

      490      500      510      520      530
Cry1Ac VKGNfLfnG-SVIsGPGFTGGDLVRLNssGNNIQRGyIEVPIHfPSTSTRYRVRVRYAS
      .....
gi|833 VKGFRVWGGTSVITGPGFTGGDILRRNTFGDFVS----LQVnINSPITQ-RYRLRFRYAS
      480      490      500      510      520      530

      540      550      560      570      580      590
Cry1Ac VtPIHLNvNwGnSSi----FSntVPATATSL--DNLQSSDFGyFESANaFTSSLG-NIV
      .....
gi|833 SRDARVILVtGAAStGVGGQVSVNMPLQKtMEIGENLTSRtFRYtDFSNPFsFRANPDII
      540      550      560      570      580      590

      600      610      620      630      640
Cry1Ac GVRN---F---SGTAG-VIIdRFfIPVtATLEAEyNLERaQKAVNALfTStNQLGLKtN
      .....
gi|833 GISeQPLfGAGSISSGELYIDKIEIILADATFEAESDLERaQKAVNALfTSSNqIGLkTD
      600      610      620      630      640      650

      650      660      670      680      690      700
Cry1Ac VtDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPerg
      .....
gi|833 VtDYHIDQVSNLVdCLSDfCLDEKRElSEKVKHAKRLSDERNLLQDPNfRGINRQPDRG
      660      670      680      690      700      710

      710      720      730      740      750      760
Cry1Ac WGGStGITIQGGDDVfKenyVtLSGtFDEcYPTyLQKIDeSKLKAfTRYQLRgyIEDsQ
      .....
gi|833 WRGStDIITIQGGDDVfKenyVtLPgtVDEcYPTyLQKIDeSKLKAfTRYELRgyIEDsQ
      720      730      740      750      760      770

      770      780      790      800      810      820
Cry1Ac DLeyISIRyNAKHETVNVPGtGSLWPLSAQSPiGKCGEPNRCAPhLEWNPDLDCSCRdGe
      .....
gi|833 DLeyILIRyNAKHETVNVPGtGSLWPLSAQSPiGKCGEPNRCAPhLEWNPDLDCSCRdGe
      780      790      800      810      820      830

      830      840      850      860      870      880
Cry1Ac KCAHSHHFSLDIDVGCTDLNEDLGvVvIFKIKtQDGHARLGNLFLEEKPLVGEALARV

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      .....
gi|833 KCAHSHHFSLDIDVGCTDLNEDLGvVvIFKIKtQDGHARLGNLFLEEKPLVGEALARV
      840      850      860      870      880      890

      890      900      910      920      930      940
Cry1Ac KRAEKWRDKREKLEWETNIvYKEAKESVDALFVNSQYDQLQADtNIAMIHAADKRvHSI
      .....
gi|833 KRAEKWRDKREKLEWETNIvYKEAKESVDALFVNSQYDRLQVDTNIAMIHAADKRvHRI
      900      910      920      930      940      950

      950      960      970      980      990      1000
Cry1Ac REAYLPELSVIPGVNAaIFEELEGRIFTAFSLYDARNvIKNGDFNNGLSCWNVKGhVDVDe
      .....
gi|833 REAYLPELSVIPGVNAaIFEELEGRIFTAYSlyDARNvIKNGDFNNGLLcWNVKGhVDVDe
      960      970      980      990      1000      1010

      1010      1020      1030      1040      1050      1060
Cry1Ac EQnQRsvLVVpEWEAeVsqEVRVcPGRGYILRvtAYKEGyGEGCVtIHEIEntDDELKf
      .....
gi|833 EQnNHRsvLVVpEWEAeVsqEVRVcPGRGYILRvtAYKEGyGEGCVtIHEIEntDDELKf
      1020      1030      1040      1050      1060      1070

      1070      1080      1090      1100      1110      1120
Cry1Ac SncVEEiYpNntVtCNDYtVnQEEYGGAYtSRNRgyNEA---PSVPADYASvYEEKsY
      .....
gi|833 SncVEEiYpNntVtCnNYtGTQEEYEGTYtSRNQYDEAYGNnPSVPADYASvYEEKsY
      1080      1090      1100      1110      1120      1130

      1130      1140      1150      1160      1170      1180
Cry1Ac tDGRRENpCEfNRgyRDYtPLpVgYvTKELEyFPETDKVWIEIGETEGtFIVDSvELLLM
      .....
gi|833 tDGRRENpCESNRgyDYtPLpAGYvTKDLEyFPETDKVWIEIGETEGtFIVDSvELLLM
      1140      1150      1160      1170      1180      1190

Cry1Ac EE
::
gi|833 EE

>>gi|162500743|gb|ABY14167.1| Sequence 30 from patent US (1193 aa)
initn: 6267 init1: 3108 opt: 3301 Z-score: 3882.5 bits: 730.4 E(): 2.5e-207
Smith-Waterman score: 6814; 86.561% identity (92.321% similar) in 1198 aa overlap
(5-1182:1-1193)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYtPIDISLSLTQFLlSEfVPGAGf
      .....
gi|162 MDNPNINeCIPYNCLSNPEVEVLGGERIETGYtPIDISLSLTQFLlSEfVPGAGf
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESfRE
      .....
gi|162 VLGLVDIIWGIgFgPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESfRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLlSVYVQAANLHLSVLrDVS

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Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|539 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF

10 20 30 40 50

70 80 90 100 110 120

Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE  
 gi|539 VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE

60 70 80 90 100 110

130 140 150 160 170 180

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|539 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

120 130 140 150 160 170

190 200 210 220 230 240

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
 gi|539 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

180 190 200 210 220 230

250 260 270 280 290 300

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQQLTREIYTNVLENFDGSRFGSAQIEGSIIRSPHL  
 gi|539 TLTVLDIVSLFPNYSRTPYPIRTVSQQLTREIYTNVLENFDGSRFGSAQIEGSIIRSPHL

240 250 260 270 280 290

310 320 330 340 350 360

Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ  
 gi|539 MDILNSITIIYTDHRGEYWSGHQIMASVGFSGPEFTFPLYGTMGNAAPQRIVAQLGQ

300 310 320 330 340 350

370 380 390 400 410 420

Cry1Ac GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ  
 gi|539 GVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTVDLDEIPPQ

360 370 380 390 400 410

430 440 450 460 470 480

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 gi|539 NNNVPPRQGFSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

420 430 440 450 460 470

490 500 510 520 530

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS  
 gi|539 VKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIIQ-RYRLRFYAS

480 490 500 510 520 530

540 550 560 570 580 590

Cry1Ac VTIPIHLNVWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFSTSSLG-NIV  
 gi|539 SRDARVIVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTFDSNPPSFRANPDII

540 550 560 570 580 590

600 610 620 630 640

Cry1Ac GVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN  
 gi|539 GISEQLPFGAGSISGGELYIDKIEIILADATFEAESDLERAQKAVNALFTSSNQIGLKT

600 610 620 630 640 650

650 660 670 680 690 700

Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERG  
 gi|539 VTDYHIDQVSNLVDCLSDEFCLDEKRESEKVKHAKRLSDERNLLQDPNFRGINRQPRG

660 670 680 690 700 710

710 720 730 740 750 760

Cry1Ac WGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQ  
 gi|539 WRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLLKAYTRYELRGYIEDSQ

720 730 740 750 760 770

770 780 790 800 810 820

Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDE  
 gi|539 DLEIYLIRYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDE

780 790 800 810 820 830

830 840 850 860 870 880

Cry1Ac KCAHSHHFLSDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV  
 gi|539 KCAHSHHFTLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARV

840 850 860 870 880 890

890 900 910 920 930 940

Cry1Ac KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSI  
 gi|539 KRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQVDTNIAMHAADKRVHRI

900 910 920 930 940 950

950 960 970 980 990 1000

Cry1Ac REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVE  
 gi|539 REAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVE

960 970 980 990 1000 1010

1010 1020 1030 1040 1050 1060

Cry1Ac EQNNQRSVLVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELK  
 gi|539 EQNNHRSVLVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIEDNTDELK

1020 1030 1040 1050 1060 1070

1070 1080 1090 1100 1110 1120

Cry1Ac SNCVEEIIYPNNTVTNNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEKSY  
 gi|539 SNCVEEVYPNNTVTNNTYTGTEYEGYTSRNRQGYDEAYGNNSVPADYASVYEKSY

1080 1090 1100 1110 1120 1130

1130 1140 1150 1160 1170 1180

Cry1Ac TDGRRNRCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVLELLM  
 gi|539 TDGRRNRCESNRYGDTPLPAGYVTKDLEYFPETDKVWIEIGETEGTFIVDSVLELLM

1140 1150 1160 1170 1180 1190

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Cry1Ac EE
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gi|539 EE

>>gi|1831476|gb|AAB45930.1| Sequence 12 from patent US 5 (1190 aa)
initn: 4543 initl: 1388 opt: 3286 Z-score: 3864.8 bits: 727.1 E(): 2.4e-206
Smith-Waterman score: 4811; 64.410% identity (78.282% similar) in 1211 aa overlap
(5-1182:1-1190)

Sequence alignment for Cry1Ac EE (1-60) vs gi|183 (1-60), Cry1Ac (61-120) vs gi|183 (61-120), Cry1Ac (121-180) vs gi|183 (121-180), Cry1Ac (181-240) vs gi|183 (181-240), Cry1Ac (241-300) vs gi|183 (241-300), Cry1Ac (301-360) vs gi|183 (301-360), Cry1Ac (361-420) vs gi|183 (361-420), Cry1Ac (421-480) vs gi|183 (421-480).

Sequence alignment for Cry1Ac (470-520) vs gi|183 (470-520), Cry1Ac (530-580) vs gi|183 (530-580), Cry1Ac (590-630) vs gi|183 (590-630), Cry1Ac (640-690) vs gi|183 (640-690), Cry1Ac (700-750) vs gi|183 (700-750), Cry1Ac (760-810) vs gi|183 (760-810), Cry1Ac (820-870) vs gi|183 (820-870), Cry1Ac (880-930) vs gi|183 (880-930), Cry1Ac (940-990) vs gi|183 (940-990), Cry1Ac (1000-1050) vs gi|183 (1000-1050).

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1000      1010      1020      1030      1040      1050
Cry1Ac 1060 1070 1080 1090 1100
IHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSV
gi|183 IHEIENNTDELKFSNXVEEIVPNNTVTCNDYTAXQEEYXGXYSXNRGYDXXYXSNXSV
1060 1070 1080 1090 1100 1110

1110 1120 1130 1140 1150 1160
Cry1Ac PADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLELYFPETDKVWIEIGETE
gi|183 PADYASXYEEKAYTDGRRDNPCESNRGYGDYTPLPAGYVTKXLEYFPETDKVWIEIGETE
1120 1130 1140 1150 1160 1170

1170 1180
Cry1Ac GTFIVDSVELLLMEE
gi|183 GTFIVDSVELLLMEE
1180 1190

>>gi|37993013|gb|AAR06667.1| hybrid Cry1Ab-Cry1Ca protei (640 aa)
initn: 3352 initl: 3113 opt: 3278 Z-score: 3859.4 bits: 725.2 E(): 4.8e-206
Smith-Waterman score: 3367; 82.171% identity (88.992% similar) in 645 aa overlap
(5-633:1-640)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|379 MANNPNINECIPYNCLSNPEVELLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|379 VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|379 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|379 VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
180 190 200 210 220 230

250 260 270 280 290 300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHL
gi|379 TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHL
240 250 260 270 280 290

310 320 330 340 350 360
Cry1Ac MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|379 MDILNSITIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

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300      310      320      330      340      350
Cry1Ac 370 380 390 400 410 420
GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
gi|379 GVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIPPQ
360 370 380 390 400 410

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|379 NNNVPPRQGFSHRLSHVSMFRSGFSNSRVRIIRAPMFSWIHRSAEATNTIDPERINQIPL
420 430 440 450 460 470

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|379 VKGFRVWGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPTIQ-RYRLRFRYAS
480 490 500 510 520 530

540 550 560 570 580 590
Cry1Ac VTIHILNVNWNSSII----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIV
gi|379 SRDARVIVLTGAASTGVGGQVSVNMLPQKTMIEIGENLTSRTFRYTDFFSNPFSFRANPDI
540 550 560 570 580 590

600 610 620 630 640
Cry1Ac GVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|379 GISEQLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALL
600 610 620 630 640

650 660 670 680 690 700
Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG

>>gi|34429674|gb|AAQ72335.1| Sequence 2 from patent US 5 (593 aa)
initn: 2823 initl: 2623 opt: 3222 Z-score: 3793.8 bits: 713.0 E(): 2.1e-202
Smith-Waterman score: 3222; 83.806% identity (91.486% similar) in 599 aa overlap
(33-627:1-593)

10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL
gi|344 IETGYTPIDISLSLTQFLLSEFVPGAGFVL
10 20 30

70 80 90 100 110 120
Cry1Ac GLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWE
gi|344 GLVDIIWGFGPSQWDAFL-QIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWE
40 50 60 70 80

130 140 150 160 170 180
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVF
gi|344 ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVF
90 100 110 120 130 140

190 200 210 220 230 240

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Cry1Ac GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT
gi|344 GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT
150 160 170 180 190 200

250 260 270 280 290 300
Cry1Ac TVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHLM
gi|344 TVLDIVALFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKSPHLM
210 220 230 240 250 260

310 320 330 340 350 360
Cry1Ac ILNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
gi|344 ILNSITIIYTDHRGFYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
270 280 290 300 310 320

370 380 390 400 410 420
Cry1Ac YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPQNN
gi|344 YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSCTVDSLDEIPPQNN
330 340 350 360 370 380

430 440 450 460 470 480
Cry1Ac NVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
gi|344 NVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIPSSQITQIPLTK
390 400 410 420 430 440

490 500 510 520 530 540
Cry1Ac GNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVYASVT
gi|344 STNLGSGTSSVVKGPGFTGGDILRRTPGQISTLRVNITAPL----SQRYRVRIRYASTT
450 460 470 480 490 500

550 560 570 580 590
Cry1Ac PIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNFGS
gi|344 NLQFHTSIHGRPIQGNFSATMSSGSLQSGSFRVTGPTTFPNFNGSSVFTLSAHVFNL
510 520 530 540 550 560

600 610 620 630 640 650
Cry1Ac TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
gi|344 GNEVYIDRIEFVPAKVTFEAEYDLERAQK
570 580 590

>>gi|62548840|gb|AAx86871.1| delta-endotoxin Cry1-A32 [B (769 aa)
initn: 2937 initl: 1300 opt: 3176 Z-score: 3737.9 bits: 703.0 E(): 2.8e-199
Smith-Waterman score: 3248; 67.812% identity (81.425% similar) in 786 aa overlap
(23-797:1-769)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|625 PEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30

70 80 90 100 110 120

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Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|625 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
40 50 60 70 80 90

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|625 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
100 110 120 130 140 150

190 200 210 220 230
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS---RDWIRYNQFR
gi|625 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLDRL--PRTGGLRNWARFNQFR
160 170 180 190 200 210

240 250 260 270 280 290
Cry1Ac RELTLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIK-IR
gi|625 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREYVITDYPVINITDYRVGSPFENIENSAIR
220 230 240 250 260 270

300 310 320 330 340 350
Cry1Ac SPHLMIDLNSITIIYTDHRGEYYSWGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|625 SPHLMDFLNNLTIDTDLIRGVHYWAGHRVTSHTFG--SSQVITTPQYGITANAEPRRTIAP
280 290 300 310 320 330

360 370 380 390 400 410
Cry1Ac QLGGQV---YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSCTVDS
gi|625 STFPGNLNLYRTLSNPFRRSENI-TPTLGINVVQGVGFI---QPNAEVLRYRSCTVDS
340 350 360 370 380 390

420 430 440 450 460 470
Cry1Ac LDEIPPQNNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|625 LNELPIDGEN--SLVGYSHRSLSHVTLTRSLYNTNITSL---PTFWTHHSATNTNTINPD
400 410 420 430 440

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|625 IITQIPLVKGFRLLGGTTSVIKGGFTGGDILRRNTIGEFVS---LQVNINSPITQ-RYR
450 460 470 480 490 500

540 550 560 570 580 590
Cry1Ac VRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLG-NIV
gi|625 LRFYASSRDARITVAIGQIRVDMTLEKTMEIGESLTSRTFSYTNFNSNPFRRANPDII
510 520 530 540 550 560

600 610 620 630 640
Cry1Ac GVRNFGSTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|625 RIAEELPIRGGELYIDKIELILADATFEEYDLERAQKAVNALFTSTNQLGLKTDVTDYH
570 580 590 600 610 620

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650      660      670      680      690      700
Cry1Ac IDQVSNLVLYLSEDFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|625 IDQVSNLVECLSEDFCLDKKRELSEKVKHAKRLSDERNLLQDPNFRGINRQPDGRWGST
630      640      650      660      670      680

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710      720      730      740      750      760
Cry1Ac GITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
gi|625 DITIQQGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAYTRYELRGYIEDSQDLEIY
690      700      710      720      730      740

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770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH
gi|625 LIRYNAKHETVNVPGTGSWPLSAQSPI
750      760

```

>>gi|10053905|gb|AAE30812.1| Sequence 2 from patent US 5 (452 aa)  
 initn: 3084 init1: 3084 opt: 3084 Z-score: 3632.8 bits: 682.8 E(): 2e-193  
 Smith-Waterman score: 3084; 99.779% identity (99.779% similar) in 452 aa overlap  
 (731-1182:1-452)

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710      720      730      740      750      760
Cry1Ac PERGWGGSTGITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYI
gi|100      FDECYPTYLYQKIDESKLFKAFTRYQLRGYI
10      20      30

```

```

770      780      790      800      810      820
Cry1Ac EDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC
gi|100 EDSQDLEIYLIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSC
40      50      60      70      80      90

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830      840      850      860      870      880
Cry1Ac RDGEKCAHSHHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEA
gi|100 RDGEKCAHSHHFSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEA
100      110      120      130      140      150

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890      900      910      920      930      940
Cry1Ac LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKR
gi|100 LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKR
160      170      180      190      200      210

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950      960      970      980      990      1000
Cry1Ac VHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGH
gi|100 VHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGH
220      230      240      250      260      270

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1010     1020     1030     1040     1050     1060
Cry1Ac VDVEEQNNQRSLVVPWEAEVSVQEVVPCGRGYILRVYAYKEGYEGECVTTIHEIENNTD
gi|100 VDVEEQNNQRSLVVPWEAEVSVQEVVPCGRGYILRVYAYKEGYEGECVTTIHEIENNTD
280     290     300     310     320     330

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1070     1080     1090     1100     1110     1120
Cry1Ac ELKFNSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSY
gi|100 ELKFNSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSY
340     350     360     370     380     390

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1130     1140     1150     1160     1170     1180
Cry1Ac TDGRRNRCPEFNRGRYDTPPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
gi|100 TDGRRNRCPEFNRGRYDTPPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLM
400     410     420     430     440     450

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```

Cry1Ac EE
      ::
gi|100 EE

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>>gi|34422134|gb|AAQ68245.1| Sequence 6 from patent US 5 (1129 aa)  
 initn: 5519 init1: 2569 opt: 2997 Z-score: 3524.2 bits: 664.0 E(): 2.2e-187  
 Smith-Waterman score: 5931; 76.574% identity (86.986% similar) in 1191 aa overlap  
 (2-1182:1-1129)

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10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|344 MEIMNNQ--NQCVYPNCLNDPTIEILEGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10      20      30      40      50

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70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAEAFRE
gi|344 VLGLIDLWGFVGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQIYAEAFRE
60      70      80      90      100     110

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130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|344 WEADPTNPALTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVS
120     130     140     150     160     170

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190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
gi|344 VFGQRWGFDAATINSRYNDLTRLIGTYTDYAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
180     190     200     210     220     230

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250     260     270     280     290     300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSRPHL
gi|344 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGMAQRIEQNIRQPHL
240     250     260     270     280     290

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310     320     330     340     350     360
Cry1Ac MDILNSITITYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPPVQQRIVAQLGQ
gi|344 MDLLNSITITYTDVHRGFNYWSGHQITASPVGFAGPEFTFPRYGTMGNAAPPV-LISTTGL
300     310     320     330     340     350

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          370      380      390      400      410
Cry1Ac  GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT--SSNLPSAVYRKSSTVDSLDEIP
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  GIFRTLSSPLYRRIILGSGPNNQNLFLVLDGTEFSFASLTADLPSTIYRQRGTVDSDLVIP
          360      370      380      390      400      410

          420      430      440      450      460      470
Cry1Ac  PQNNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  PQDNSVPARAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFSWRHRSAEFNSLIPSSQITQI
          420      430      440      450      460      470

          480      490      500      510      520      530
Cry1Ac  PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  PLTKSINLGSSTSVVKGPGFTGGDILRRTSPGQISTLRVTTITAPL----SQRYRVRIRY
          480      490      500      510      520

          540      550      560      570      580      590
Cry1Ac  ASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  ASTTNLQFHTSIDGRPINQGNFSATMSSGGNLQSGSFRTAGFTTFFNFNSNGSSIPTLSAH
          530      540      550      560      570      580

          600      610      620      630      640      650
Cry1Ac  NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  VFNNSGNEVYIDRIEFVPAEVTFAEYDLERAQEAVALFTSSNQLGLKTNVTDYHIDQVS
          590      600      610      620      630      640

          660      670      680      690      700      710
Cry1Ac  NLVTVLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  NL-----GSTDITIQ
          650

          720      730      740      750      760      770
Cry1Ac  GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  GGDDVFKENYVTLPGTFNNECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRYN
          660      670      680      690      700      710

          780      790      800      810      820      830
Cry1Ac  AKHETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHHFS
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  TKHETVNVPGTGSGLWPLSVENPIGKCGEPNRCAPQLEWNPDLDCSCRDEKCAHSHSHHFS
          720      730      740      750      760      770

          840      850      860      870      880      890
Cry1Ac  LDIDVGCTDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  LDIDIGCTDLNENLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
          780      790      800      810      820      830

          900      910      920      930      940      950
Cry1Ac  REKLEWETNIVVKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIRIAYLPELSV
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  REKLVETNIVVKEAKESVDALFVNSQYDRLQADTDIAMIHAADKRVHRIIAYLPELSV
          840      850      860      870      880      890

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          960      970      980      990      1000      1010
Cry1Ac  IPGVNAEIFEELRIFTAFLSYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSVLV
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  IPGVNAGIFEELRIFTAYSLYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNHRSVLV
          900      910      920      930      940      950

          1020      1030      1040      1050      1060      1070
Cry1Ac  VPEWEAEVQEVRCVPCGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEIVP
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  VPEWEAEVQEVRCVPCGRGYILRVTAKEGYGEGCVTIHEIEDNTDELKFSNCVVEEVYP
          960      970      980      990      1000      1010

          1080      1090      1100      1110      1120      1130
Cry1Ac  NNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  NNTVTCNDYTVNQEEYGGAYTSRNRGYGESYESNSNIPAEYAPVYEE-AYIDGRKENPC
          1020      1030      1040      1050      1060      1070

          1140      1150      1160      1170      1180
Cry1Ac  FNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|344  SNRGYDYPPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
          1080      1090      1100      1110      1120

>>gi|1171233|gb|AAA86265.1| CryIA(a) (620 aa)
  initn: 2496 init1: 2301 opt: 2993 Z-score: 3523.4 bits: 663.0 E(): 2.5e-187
Smith-Waterman score: 2993; 74.363% identity (87.102% similar) in 628 aa overlap
(5-626:1-620)

          10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|117  MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
          10      20      30      40      50

          70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|117  VLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

          130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVS
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|117  WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

          190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWRIRYNQFRREL
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|117  VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSRDWRIRYNQFRREL
          180      190      200      210      220      230

          250      260      270      280      290      300
Cry1Ac  TLTVLDDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKIRSPHL
:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|117  TLTVLDDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGMAQRIEQNIRQPHL
          240      250      260      270      280      290

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          310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
          300      310      320      330      340      350

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          370      380      390      400      410
Cry1Ac GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDEIP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSDLVIP
          360      370      380      390      400      410

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          420      430      440      450      460      470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
          420      430      440      450      460      470

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          480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 PLTKSTNLGSGTSSVVKGPFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRY
          480      490      500      510      520

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          540      550      560      570      580      590
Cry1Ac ASVTPIHLNVNMGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIV---GVR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTGFTTFFNFNSNGSSVFTLSAH
          530      540      550      560      570      580

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          600      610      620      630      640      650
Cry1Ac NFSGTAAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|117 VFNSGNEVYIDRIEFVPAEVTFAEYDLERAQ
          590      600      610      620

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          660      670      680      690      700      710
Cry1Ac NLVTTYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWGGSTGITIQ

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>>gi|112025965|gb|ABH87582.1| Sequence 8 from patent US (609 aa)  
 initn: 2441 initl: 2308 opt: 2942 Z-score: 3463.4 bits: 651.9 E(): 5.5e-184  
 Smith-Waterman score: 2942; 74.392% identity (86.872% similar) in 617 aa overlap  
 (5-615:1-609)

```

          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
          10      20      30      40      50

```

```

          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNAQAI SRLEGLSNLYQIYAESFRE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNAQAI SRLEGLSNLYQIYAESFRE
          60      70      80      90      100      110

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          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

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          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
          120      130      140      150      160      170

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          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYQFRREL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVGPDSDRDWIRYQFRREL
          180      190      200      210      220      230

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          250      260      270      280      290      300
Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKSPHPL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSAQIEGSIKSPHPL
          240      250      260      270      280      290

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          310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
          300      310      320      330      340      350

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          370      380      390      400      410
Cry1Ac GVRTLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDEIP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSDLVIP
          360      370      380      390      400      410

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          420      430      440      450      460      470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI
          420      430      440      450      460      470

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          480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 PLTKSTNLGSGTSSVVKGPFTGGDILRRTSPGQISTLRVNITAPL-----SQRYRVRIRY
          480      490      500      510      520

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          540      550      560      570      580      590
Cry1Ac ASVTPIHLNVNMGNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIV---GVR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTGFTTFFNFNSNGSSVFTLSAH
          530      540      550      560      570      580

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          600      610      620      630      640      650
Cry1Ac NFSGTAAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 VFNSGNEVYIDRIEFVPAEVT
          590      600

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>>gi|112025964|gb|ABH87581.1| Sequence 7 from patent US (609 aa)  
 initn: 2435 initl: 2302 opt: 2936 Z-score: 3456.3 bits: 650.6 E(): 1.4e-183  
 Smith-Waterman score: 2936; 74.230% identity (86.710% similar) in 617 aa overlap  
 (5-615:1-609)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

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gi|112      .....
            MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
              10      20      30      40      50

Cry1Ac     70      80      90      100     110     120
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|112     60      70      80      90      100     110
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE

Cry1Ac     130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112     120     130     140     150     160     170
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac     190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112     180     190     200     210     220     230
VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac     250     260     270     280     290     300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGLEGSIRSPHL
gi|112     240     250     260     270     280     290
TLTVLDIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSRGMAQRIEQNIRQPHL

Cry1Ac     310     320     330     340     350     360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112     300     310     320     330     340     350
MDILNRITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL

Cry1Ac     370     380     390     400     410
GVYRTLSSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPNAVYRKSQTVDSLDEIP
gi|112     360     370     380     390     400     410
GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSDLVIP

Cry1Ac     420     430     440     450     460     470
PQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
gi|112     420     430     440     450     460     470
PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRPTFSWQHRSAEFNNIIPSSQITQI

Cry1Ac     480     490     500     510     520     530
PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRY
gi|112     480     490     500     510     520
PLTKSTNLGSGTSVVKGPGFTGGDLRRTSPGQISTLRVNITAPL----SQRYRVRIRY

Cry1Ac     540     550     560     570     580     590
ASVTPPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|112     530     540     550     560     570     580
ASTTNLQFHTSIDGRPINQNFSAISMSSGSLQSGSFRVTGFTTFFNFNSNGSVFTLSAH

Cry1Ac     600     610     620     630     640     650

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Cry1Ac     NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
            :.. : ..... :
gi|112     VFNSGNEVIDRIEFVPAEVT
            590      600

>>gi|112025963|gb|ABH87580.1| Sequence 6 from patent US (609 aa)
initn: 2434 initl: 2301 opt: 2935 Z-score: 3455.1 bits: 650.3 E(): 1.6e-183
Smith-Waterman score: 2935; 74.230% identity (86.872% similar) in 617 aa overlap
(5-615:1-609)

Cry1Ac     10      20      30      40      50      60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|112     MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
            10      20      30      40      50

Cry1Ac     70      80      90      100     110     120
VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|112     VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFRE
            60      70      80      90      100     110

Cry1Ac     130     140     150     160     170     180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112     WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
            120     130     140     150     160     170

Cry1Ac     190     200     210     220     230     240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112     VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL
            180     190     200     210     220     230

Cry1Ac     250     260     270     280     290     300
TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGLEGSIRSPHL
gi|112     TLTVLDIVSLFPNYDSRRYPIRTVSQLTREIYTNPVLENFDGSRGMAQRIEQNIRQPHL
            240     250     260     270     280     290

Cry1Ac     310     320     330     340     350     360
MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112     MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
            300     310     320     330     340     350

Cry1Ac     370     380     390     400     410
GVYRTLSSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPNAVYRKSQTVDSLDEIP
gi|112     GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSDLVIP
            360     370     380     390     400     410

Cry1Ac     420     430     440     450     460     470
PQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
gi|112     MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
            300     310     320     330     340     350

Cry1Ac     370     380     390     400     410
GVYRTLSSSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPNAVYRKSQTVDSLDEIP
gi|112     GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTTLNLPSTIYRQRGTVDSDLVIP
            360     370     380     390     400     410

Cry1Ac     420     430     440     450     460     470
PQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
gi|112     PQDNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRPTFSWQHRSAEFNNIIPSSQITQI
            420     430     440     450     460     470

Cry1Ac     480     490     500     510     520     530

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Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|112 PLTKSTNLGSGT SVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRY

Cry1Ac ASVTPPIHLNVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|112 ASTTNLQFHSTIDGRPINQGNFSATMSSGSLQSGSFRVTGFTTTPFNFSNGSSVFTLSAH

Cry1Ac NFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|112 VFNSGNEVYIDRIEFVPAEVT

>>gi|112025962|gb|ABH87579.1| Sequence 5 from patent US (609 aa)
initn: 2434 initl: 2301 opt: 2935 Z-score: 3455.1 bits: 650.3 E(): 1.6e-183
Smith-Waterman score: 2935; 74.230% identity (86.872% similar) in 617 aa overlap
(5-615:1-609)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|112 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|112 VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL

Cry1Ac TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGFSFRGMAQRIEQNIRQPHL
gi|112 TLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGFSFRGMAQRIEQNIRQPHL

Cry1Ac MDILNSITTYTDAHRGEYYSWGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|112 MDILNSITTYTDAHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL

370 380 390 400 410

Cry1Ac GVYRTLSSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SSNLPSAVYRKSGTVDSLDEIP
gi|112 GIFRTLSSPLRYRIILGSGPNQQLFVLDGTEFSFASLTTNLPSTIYRQGTVDLSDVIP

Cry1Ac PQNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|112 PQDNSVPPRAGFHRSHVMTLSQ--AAGAVYTLRAPTFWQHRSAEFNIIIPSSQITQI

Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|112 PLTKSTNLGSGT SVVKGPFTGGDILRRTSPGQISTLRVNITAPL----SQRYRVRIRY

Cry1Ac ASVTPPIHLNVNWGSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVR
gi|112 ASTTNLQFHSTIDGRPINQGNFSATMSSGSLQSGSFRVTGFTTTPFNFSNGSSVFTLSAH

Cry1Ac NFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|112 VFNSGNEVYIDRIEFVPAEVT

>>gi|112025960|gb|ABH87577.1| Sequence 3 from patent US (609 aa)
initn: 2425 initl: 2292 opt: 2926 Z-score: 3444.5 bits: 648.4 E(): 6.1e-183
Smith-Waterman score: 2926; 74.068% identity (86.710% similar) in 617 aa overlap
(5-615:1-609)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|112 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|112 VLGLVDIIWGFQPSQWDAFPVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFRE

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRREL

250 260 270 280 290 300

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Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIKSPHL
gi|112 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGMAQRIEQNIRQPHL
      240      250      260      270      280      290
Cry1Ac      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
      300      310      320      330      340      350
Cry1Ac      370      380      390      400      410
Cry1Ac GVYRTLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSQGTVDLDEIP
gi|112 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQRTVDSLDVIP
      360      370      380      390      400      410
Cry1Ac      420      430      440      450      460      470
Cry1Ac PQNNVPPRQGFSHRSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|112 PQDNSVPPRAGFSHRSHVMTLSQ--AAGAVYTLRAPTFSWQHRSAEFNIIIPSSQITQI
      420      430      440      450      460      470
Cry1Ac      480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY
gi|112 PLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRY
      480      490      500      510      520
Cry1Ac      540      550      560      570      580      590
Cry1Ac ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR
gi|112 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTTFNFSNGSSVFTLSAH
      530      540      550      560      570      580
Cry1Ac      600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|112 VFNSGNEVYIDRIEFVPAEVT
      590      600
>>gi|112025961|gb|ABH87578.1| Sequence 4 from patent US (609 aa)
  initn: 2425 initl: 2292 opt: 2926 Z-score: 3444.5 bits: 648.4 E(): 6.1e-183
Smith-Waterman score: 2926; 74.068% identity (86.710% similar) in 617 aa overlap
(5-615:1-609)
Cry1Ac      10      20      30      40      50      60
Cry1Ac CMQAMNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|112 MDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      10      20      30      40      50
Cry1Ac      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFRE
gi|112 VLGLVDIIWGFQPSQWDAFPVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFRE
      60      70      80      90      100     110
Cry1Ac      130     140     150     160     170     180

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|112 WEADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVS
      120      130      140      150      160      170
Cry1Ac      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
gi|112 VFGQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERWVWGPDSRDWIRYNQFRREL
      180      190      200      210      220      230
Cry1Ac      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQGIIEGSIKSPHL
gi|112 TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGMAQRIEQNIRQPHL
      240      250      260      270      280      290
Cry1Ac      310      320      330      340      350      360
Cry1Ac MDILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|112 MDILNSITIIYTDVHRGFNYWSGHQITASPVGFSGPEFAFPLFGNAGNAAPPV-LVSLTGL
      300      310      320      330      340      350
Cry1Ac      370      380      390      400      410
Cry1Ac GVYRTLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYRKSQGTVDLDEIP
gi|112 GIFRTLSSPLYRRIILGSGPNNQELFVLDGTEFSFASLTNLPSTIYRQRTVDSLDVIP
      360      370      380      390      400      410
Cry1Ac      420      430      440      450      460      470
Cry1Ac PQNNVPPRQGFSHRSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|112 PQDNSVPPRAGFSHRSHVMTLSQ--AAGAVYTLRAPTFSWQHRSAEFNIIIPSSQITQI
      420      430      440      450      460      470
Cry1Ac      480      490      500      510      520      530
Cry1Ac PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY
gi|112 PLTKSTNLGSGTSVVKGPFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRIRY
      480      490      500      510      520
Cry1Ac      540      550      560      570      580      590
Cry1Ac ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIV--GVR
gi|112 ASTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRTVGFPTTFNFSNGSSVFTLSAH
      530      540      550      560      570      580
Cry1Ac      600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|112 VFNSGNEVYIDRIEFVPAEVT
      590      600
>>gi|34429673|gb|AAQ72334.1| Sequence 1 from patent US 5 (593 aa)
  initn: 2304 initl: 2103 opt: 2801 Z-score: 3297.2 bits: 621.1 E(): 9.8e-175
Smith-Waterman score: 2801; 73.544% identity (86.522% similar) in 601 aa overlap
(33-627:1-593)
Cry1Ac      10      20      30      40      50      60

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Cry1Ac QAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVL
gi|344 IETGYTPIDISLSLTQFLLESEFVPGAGFVL
          10          20          30

          70          80          90          100          110          120
Cry1Ac GLVDIIWGIWGFPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFREWE
gi|344 GLVDIIWGIWGFPSQWDAFPVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFREWE
          40          50          60          70          80          90

          130          140          150          160          170          180
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
gi|344 ADPTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
          100          110          120          130          140          150

          190          200          210          220          230          240
Cry1Ac QQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT
gi|344 QQRWGFDAATINSRYNDLTRLIGNYTDYAVRWYNTGLERVWGPDSRDWIRYNQFRRELT
          160          170          180          190          200          210

          250          260          270          280          290          300
Cry1Ac TVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRPHLMD
gi|344 TVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSGFRGSAQRIEQNIRPHLMD
          220          230          240          250          260          270

          310          320          330          340          350          360
Cry1Ac ILNSITIIYTDHAHRGEYIYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
gi|344 ILNSITIIYTDVHRGENYIYWSGHQITASPVGFGSGPEFAPPLFGNAGNAAPPV-LVSLTGLGI
          280          290          300          310          320

          370          380          390          400          410          420
Cry1Ac YRTLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPsAVYRKSQTVDSLDEIPPQ
gi|344 FRTLSSPLYRRIILGSGPNNQELFVLDGTEFASLTTNLPSTIYRQRGTVDSLDVIPPQ
          330          340          350          360          370          380

          430          440          450          460          470          480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|344 DNSVPPRAGFSHRLSHVTMLSQ--AAGAVYTLRAPTFWSQHRSAEFNNIIIPSSQITQIPL
          390          400          410          420          430          440

          490          500          510          520          530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|344 TKSTNLGSGTSSVVKGPGFTGGDILRRTSPGQISTLRVNIITAPL----SQRYRVRVRYAS
          450          460          470          480          490          500

          540          550          560          570          580          590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIV---GVRNF
gi|344 TTNLQFHTSIDGRPINQGNFSATMSSGNSLQSGSFRTVGFSTTPFNFSNGSSVFTLSAHVF
          510          520          530          540          550          560

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          600          610          620          630          640          650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|344 NSGNEVYIDRIEFVPAEVTFEAEYDLERAQK
          570          580          590

          660          670          680          690          700          710
Cry1Ac VTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGG

>>gi|77364098|gb|ABA65394.1| Sequence 2 from patent US 6 (823 aa)
  initn: 2633 init1: 1290 opt: 2711 Z-score: 3188.9 bits: 601.5 E(): 1.1e-168
  Smith-Waterman score: 2982; 57.194% identity (77.051% similar) in 841 aa overlap
  (5-820:1-823)

          10          20          30          40          50          60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
gi|773 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
          10          20          30          40          50

          70          80          90          100          110          120
Cry1Ac VLGLVDIIWGIWGFPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|773 LVGLIDFVWGVIGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNINIEYEAFFKE
          60          70          80          90          100          110

          130          140          150          160          170          180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|773 WEEDPNPATRTRVIDRFRILDGLLDRDIPSPFRISGFVPLLSVYAQAANLHLLAILRDSV
          120          130          140          150          160          170

          190          200          210          220          230          240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|773 IPGERWGLTTINVNENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL
          180          190          200          210          220          230

          250          260          270          280          290
Cry1Ac TLTVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSGFRGSAQG-----IEGS-
gi|773 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREYTDPLI-NFNPQLQSVLQPTFNVMESSA
          240          250          260          270          280          290

          300          310          320          330          340          350
Cry1Ac IRSPHLMIDLNSITIIYTDHAHR-GE-YYWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQ
gi|773 IRNPHLFDILNLTIFTDWFSVGRNFYWGGRHVISSLIG--GGNITSPYIGREANQEPPR
          300          310          320          330          340          350

          360          370          380          390          400          410
Cry1Ac RIVAQLGQGVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV
gi|773 SFT--FNGPVFRTLSIPTLRL-LQQPCQRHFNLRGGEGVEFSTPTN--SFTYRGRGTVD
          360          370          380          390          400

          420          430          440          450          460          470
Cry1Ac SLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNNIIA

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gi|773 SLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTNTID
410 420 430 440 450 460

Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
480 490 500 510 520 530

gi|773 PERINQIPLVKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNINSPITQ-R
470 480 490 500 510

Cry1Ac YRVRVRYASVTPIHLLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAF
540 550 560 570 580

gi|773 YRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMP LQKMEIGENLTSRTFFRYTDFSNPF
520 530 540 550 560 570

Cry1Ac TSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTS
590 600 610 620 630

gi|773 SFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTS
580 590 600 610 620 630

Cry1Ac TNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFK
640 650 660 670 680 690

gi|773 SNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR
640 650 660 670 680 690

Cry1Ac DINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQ
700 710 720 730 740 750

gi|773 GINRQPDGRWGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKCLKAYTRYE
700 710 720 730 740 750

Cry1Ac LRGYIEDSQDLEIYLIYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPD
760 770 780 790 800 810

gi|773 LRGYIEDSQDLEIYLIYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPD
760 770 780 790 800 810

Cry1Ac LDCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLLEEK
820 830 840 850 860 870

gi|773 LDCSC
820

>>gi|17918194|gb|AAE85628.1| Sequence 2 from patent US 6 (823 aa)
initn: 2633 initl: 1290 opt: 2711 Z-score: 3188.9 bits: 601.5 E(): 1.1e-168
Smith-Waterman score: 2982; 57.194% identity (77.051% similar) in 841 aa overlap
(5-820:1-823)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50 60

gi|179 MEEN-NQNCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESPFE
70 80 90 100 110 120

.....

gi|179 LVGLIDFVWGVIGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|179 WEEDPNNPATRTRVIDRFRILDGLLERDIPSFRI SGFEVPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|179 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDL
180 190 200 210 220 230

Cry1Ac TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-
250 260 270 280 290

gi|179 TLTVLVDIAAFFPNYDNRRIPIQFVQGLTREVTYDPLI-NFNPQLQSVLAQLPTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHLMIDILNSITIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
300 310 320 330 340 350

gi|179 IRNPHLFDILNLTIFTDWFSVGRNFYWGGRVVISLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLQGQVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV
360 370 380 390 400 410

gi|179 SFT--FNGPVFRTLSIPTLRL-LQQPCQRHHFNLRGGEVGFSTPTN--SFTYRGRGTVD
360 370 380 390 400

Cry1Ac SLDEIPPQNNVPPRQGFSHRSLHVSMTF-RSGFSNSSVSIIRAPMFSWIHRSAEFNIIA
420 430 440 450 460 470

gi|179 SLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTNTID
410 420 430 440 450 460

Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
480 490 500 510 520 530

gi|179 PERINQIPLVKGFRVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNINSPITQ-R
470 480 490 500 510

Cry1Ac YRVRVRYASVTPIHLLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAF
540 550 560 570 580

gi|179 YRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMP LQKMEIGENLTSRTFFRYTDFSNPF
520 530 540 550 560 570

Cry1Ac TSSLG-NIVGVRN---F---SGTAG-VIIDRFEPVPTATLEAEYNLERAQKAVNALFTS
590 600 610 620 630

gi|179 SFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFTS
580 590 600 610 620 630

Cry1Ac TNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFK
640 650 660 670 680 690

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initn: 2633 init1: 1290 opt: 2711 Z-score: 3188.9 bits: 601.5 E(): 1.1e-168
Smith-Waterman score: 2982; 57.194% identity (77.051% similar) in 841 aa overlap
(5-820:1-823)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|400 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
Cry1Ac VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|400 LVGLIDFVWGIWVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|400 WEEDPNPATRTRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLAALRDSV
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|400 IFGERWGLTTINVENYENRILRHIDEYADHCANTYNRGLNLPKSTYQDWITYNLRRLDL
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQG-----IEGS-
gi|400 TLTVLDIAAFFPNYDNRYPVQVGLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA
Cry1Ac IRSPHLMIDILNSITTYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ
gi|400 IRNPHLFDILNLLTIFTDFWVSGRNFYWGGRHVISSLIG--GGNITSPIYGREANQEPFR
Cry1Ac RIVAQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV
gi|400 SFT--FNGPVFRTLSTIPTLRL-LQQPCQRHHFNLRGGEGVEFSTPTN--SFTYRGRGTVD
Cry1Ac SLDEIPPNQNNVPPRQGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIA
gi|400 SLTELPPEDNSVPPREGYSHRLCHATFVQRSGTPTPLTTGVV---FSWTHR SATLTNTID
Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
gi|400 PERINQIPLVKGRVWGGT SVITGPGFTGGDILRRNTFGDFVSS---LQVNNISPITQ-R
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|426 WEEDPNPATRTRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLAALRDSV

Cry1Ac YRVRVRYASVTPHILNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAF
gi|400 YRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMLPQKTIMEIGENLTSRTFFRYTDFSNPF
Cry1Ac TSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTS
gi|400 SFRANPDIIGISEQLPFGAGSISGELYIDKIEIILLADATFEAESDLERAQKAVNALFTS
Cry1Ac TNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFK
gi|400 SNQIGLKTVDYHIDQVSNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFR
Cry1Ac DINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQ
gi|400 GINRQPDGRGWRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKATRYE
Cry1Ac LRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNP
gi|400 LRGYIEDSQDLEIYLIAYNAKHEIVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNP
Cry1Ac LDCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKP
gi|400 LDCSC
820
>>gi|42690552|gb|AAS32607.1| Sequence 2 from patent US 6 (823 aa)
initn: 2633 init1: 1290 opt: 2711 Z-score: 3188.9 bits: 601.5 E(): 1.1e-168
Smith-Waterman score: 2982; 57.194% identity (77.051% similar) in 841 aa overlap
(5-820:1-823)
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|426 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
Cry1Ac VLGLVDIHWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|426 LVGLIDFVWGIWVPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNNFNIIYVEAFKE
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|426 WEEDPNPATRTRVIDRFRILDGLLERDIPSPFRISGFVPLLSVYAQAANLHLAALRDSV

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Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|426 IPGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL  
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQTLTREIYTNPVLNFDGSGFRGSAQG-----IEGS-  
gi|426 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPTFNVMESSA  
240 250 260 270 280 290

Cry1Ac IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ  
gi|426 IRNPHLFDILNLLTIFTDFWFSVGRNFYWGHRVVISLIG--GGNITSPYIGREANQPEPR  
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVTD  
gi|426 SFT--FNGPVFRTLSIPTLRL-LQQPCQRHHFNLRGEGVEFSTPTN--SFTYRGRGTVD  
360 370 380 390 400

Cry1Ac SLDEIPPNQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNIIIA  
gi|426 SLTELPPEDNSVPPREGYSHRSLCHATFVQRSQTPFLTTGVV---FSWTHRSATLNTNID  
410 420 430 440 450 460

Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR  
gi|426 PERINQIPLVKGFVRVWGGTSTVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIQ-R  
470 480 490 500 510

Cry1Ac YRVRVRYASVTPIHLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAF  
gi|426 YRLRFRYASSRDARVIVLTGAASTGVGGQVSVNMPLQKTMIEGENLTSRTFRYTDVSNPF  
520 530 540 550 560 570

Cry1Ac TSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFSTS  
gi|426 SFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFEAESDLERAQKAVNALFSTS  
580 590 600 610 620 630

Cry1Ac TNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFK  
gi|426 SNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR  
640 650 660 670 680 690

Cry1Ac DINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQ  
gi|426 GINRQPRDGRWGSTGITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYE  
700 710 720 730 740 750

Cry1Ac LRGYIEDSQDLEIYSIRYNAKHETVNPVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPD  
gi|426 LRGYIEDSQDLEIYLIAYNAKHEIVNPVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPD  
760 770 780 790 800 810

Cry1Ac LDCSCRDGEKCAHSHHFLSDIDVGCCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKP  
gi|426 LDCSC  
820

>>gi|490199|emb|CAA00882.1| lepidoptera larvicidal prote (823 aa)  
initn: 2633 init1: 1290 opt: 2709 Z-score: 3186.6 bits: 601.1 E(): 1.4e-168  
Smith-Waterman score: 2982; 57.194% identity (77.051% similar) in 841 aa overlap  
(5-820:1-823)

Cry1Ac CMQAMDNPNININECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
gi|490 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF  
10 20 30 40 50 60

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGSLNLYQIYAESFRE  
gi|490 LVGLIDFVWIGIFGPSQWDAFLVQIEQLINERIAEAFARNAAIANLEGLGNNFNIIYVEAFKE  
70 80 90 100 110 120

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|490 WEEDPNPATRTRVDRFRILDGLLDRDIPSPRISGFVPLLSVYVQAANLHLLAIRDVS  
130 140 150 160 170 180

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|490 IPGERWGLTTINVNENYNRLIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRRDL  
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQTLTREIYTNPVLNFDGSGFRGSAQG-----IEGS-  
gi|490 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPTFNVMESSA  
240 250 260 270 280 290

Cry1Ac IRSPHLMIDLNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ  
gi|490 IRNPHLFDILNLLTIFTDFWFSVGRNFYWGHRVVISLIG--GGNITSPYIGREANQPEPR  
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVTD  
gi|490 SFT--FNGPVFRTLSIPTLRL-LQQPCQRHHFNLRGEGVEFSTPTN--SFTYRGRGTVD  
360 370 380 390 400

Regulatory Product Characterization Team

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          420      430      440      450      460      470
Cry1Ac SLDEIPPNQNNVPPRQGFSHRSLSHVSMF-RSGFSNSSSVSIIRAPMFSWIHRSAEFNNIIIA
gi|490 SLTELPPEDNSVPPREGYSHRLCHATFVQSRGTFPLTTGVV----FSWTHRSATLNTNTID
          410      420      430      440      450      460

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          480      490      500      510      520      530
Cry1Ac SDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
gi|490 PERINQIPLVKGFVWGGTSTVITGPGFTGGDILRRNTFGDFVS----LQVNNINSPITQ-R
          470      480      490      500      510

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          540      550      560      570      580
Cry1Ac YRVRVRYASVTPIHNLNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESANAF
gi|490 YRLRFYASSRDARVIVLTGAASTGVGGQVSVXMPLOKMEIGENLTSRTFRYTDFTSNPF
          520      530      540      550      560      570

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          590      600      610      620      630
Cry1Ac TSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTS
gi|490 SFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFEAESDLERAQKAVNALFTS
          580      590      600      610      620      630

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          640      650      660      670      680      690
Cry1Ac TNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFK
gi|490 SNQIGLKTVDVTDYHIDQVSNLVDCLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFR
          640      650      660      670      680      690

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          700      710      720      730      740      750
Cry1Ac DINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQ
gi|490 GINRQPDGRWGRGSTDITIQGGDDVFKENYVTLPGTVDECYPTYLYQKIDESKLFKAYTRYE
          700      710      720      730      740      750

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          760      770      780      790      800      810
Cry1Ac LRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPD
gi|490 LRGYIEDSQDLEIYLAIYNAKHEIVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPD
          760      770      780      790      800      810

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          820      830      840      850      860      870
Cry1Ac LDCSCRDEKCAHSHHFLSLDIDVGCTDLNEDLGWVVFKIKIQDGHARLGNLEFLEEKP
gi|490 LDCSC
          820

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>>gi|33765729|gb|AAQ52380.1| Sequence 38 from patent US (1228 aa)  
 initn: 3679 init1: 1836 opt: 2710 Z-score: 3185.2 bits: 601.4 E(): 1.7e-168  
 Smith-Waterman score: 4293; 56.818% identity (77.029% similar) in 1232 aa overlap  
 (5-1182:27-1228)

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          10      20      30
Cry1Ac CMQAMDNPN--INE--CIPYNCLSNPEVEVLGGERIE
gi|337 MTSNRKNEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVQ
          10      20      30      40      50

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          40      50      60      70      80      90
Cry1Ac TGYPIDISLSLTQFLLSEFVPG-AGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIE
gi|337 TG---INIAGRILGLVLPVFAQIASFYSLVGLWLP-RGRDQWEIFLEHVEQLINQOIT
          60      70      80      90      100      110

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          100      110      120      130      140      150
Cry1Ac EFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFA
gi|337 ENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFA
          120      130      140      150      160      170

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          160      170      180      190      200      210
Cry1Ac VQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVR
gi|337 IRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVBE
          180      190      200      210      220      230

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          220      230      240      250      260      270
Cry1Ac WYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYT
gi|337 WYNTGLNSLRGTNAASWVRYNQFRDLTLGVLDLVALFPYSDTRTYPIINTSAQLTREVYT
          240      250      260      270      280      290

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          280      290      300      310
Cry1Ac NPVLE-----NFDGSRGSAQGI EGS-IRSPHLMIDLNSITIYT----DAHRGEYY
gi|337 DAIGATGVNMMASMNWYNNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRSATRHMTY
          300      310      320      330      340      350

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          320      330      340      350      360      370
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRILSST-----LYRR
gi|337 WRGHTIQSRPIG-GG--LNTSTHGSTNTSINPVRL-SFFSRDVSYTESYAGVLLWGIYLE
          360      370      380      390      400

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          380      390      400      410      420      430
Cry1Ac PFNIGINNQLSVLDGTE-FAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGF
gi|337 PIH-GVPTVRFNFRNPQNTFERGTANY--SQPYESPGLQLKDSSETLPPETTERPNYESY
          410      420      430      440      450      460

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          440      450      460      470      480
Cry1Ac SHRLSHVSMFRSGFSNSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-
gi|337 SHRLSHIGLI---SQSRVHV---PVYSWTHRSADRNTISSDSITQIPLVKSFLNLSGT
          470      480      490      500      510

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          490      500      510      520      530      540
Cry1Ac SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRVRVRYASVTPIHNLVN
gi|337 SVVSGPGFTGGDIIRTNVNGS-----VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVT
          520      530      540      550      560      570

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          550      560      570      580      590      600
Cry1Ac WGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFSGTAGVIIDR
gi|337 VGGSTTFDQGFPTMSANESLTSQSFRAEFPPVGISASGSGTAGISISNAGRQTFHFDK
          580      590      600      610      620      630

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490      490      500      510      520      530      540
Cry1Ac  SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST--RYRVRVRYASVTPIHLNVN
gi|135  SVVSGPGFTGGDIIRTNVNGS-----VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVT
520      530      540      550      560      570
Cry1Ac  WGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFSGTAGVIIDR
gi|135  VGGSTTFDQGFSTMSANESLTSQSFRFAEFPVGLISASGSQTAGISISNAGRQTFHFDK
580      590      600      610      620      630
Cry1Ac  FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCL
gi|135  IEFIPITATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSEDFCL
640      650      660      670      680      690
Cry1Ac  DEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----ERGWGGS
gi|135  DEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIEHQSEHGWWGS
700      710      720      730      740      750
Cry1Ac  TGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEI
gi|135  ENITIQEGNDVFKENYVTLPGTFNFCYPTYLYQKIGSELKAYTRYQLRGYIEDSQDLEI
760      770      780      790      800      810
Cry1Ac  YSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
gi|135  YLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFEWNPDLDCSCRDGKCAH
820      830      840      850      860      870
Cry1Ac  HSHHFSLDIDVGTCTDLNEDLGWVVFVKIKTQEGHARLGNLEFIEEKPLVGEALARVKRAE
gi|135  HSHHFSLDIDIGCTDLHENLGWVVFVKIKTQEGHARLGNLEFIEEKPLVGEALSrvkRAE
880      890      900      910      920      930
Cry1Ac  KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNMIHAADKRVHSIREAY
gi|135  KKWRDKREKLQLETRVYTEAKEAVDALFVDSQYNRLQADTNIGMIHAADKLVHRIREAY
940      950      960      970      980      990
Cry1Ac  LPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNN
gi|135  LSELVSVIPGVNAEIFEELGRITAFSLYDARNVVKNGDFNNGLACWNVKGVHDVQ-QSH
1000     1010     1020     1030     1040     1050
Cry1Ac  QRSVLVPEWEAEVSVQAVRVCPRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCV
gi|135  QRSVLVPEWEAEVSVQAVRVCPRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCV

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gi|135  HRSVLVPEWEAEVSVQAVRVCPRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFKNCE
1060     1070     1080     1090     1100     1110
Cry1Ac  EEEIYNNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSVA----DYASVYEEKSYTDGR
gi|135  EEEVYPTDTGTCDYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKPTYEEETVTDVR
1120     1130     1140     1150     1160     1170
Cry1Ac  RENPCFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|135  RDNHCYEYDRGVVNYPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSIELLLMEE
1180     1190     1200     1210     1220
>>gi|112088054|gb|ABI06961.1| Sequence 38 from patent US (1228 aa)
initn: 3679 initl: 1836 opt: 2710 Z-score: 3185.2 bits: 601.4 E(): 1.7e-168
Smith-Waterman score: 4293; 56.818% identity (77.029% similar) in 1232 aa overlap
(5-1182:27-1228)
Cry1Ac  CMQAMDNNPN--INE--CIPYNCLSNPEVEVLGGERIE
10      20      30
gi|112  LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVQ
10      20      30      40      50
Cry1Ac  TGYPIDISLSLTLQFLLEFVPG-AGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIE
gi|112  TG---INIAGRILGLVGVFPFAGQIASFYSLVGLWLP-RGRDQWEIFLHVQLINQOIT
60      70      80      90      100     110
Cry1Ac  EFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFA
gi|112  ENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIALELDPLNAMPLFA
120     130     140     150     160     170
Cry1Ac  VQNYQVPLLSVYVQAANLHLSVLRDVSFVQRFQWGFDAATINSRYNDLTRLIGNYTDHAVR
gi|112  IRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSYCVVE
180     190     200     210     220     230
Cry1Ac  WYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTYPIRTVSQTLREIYT
gi|112  WYNTGLNSLRGTNAASWVRYNQFRRLDTLGLVLDLVALFSPYDTRTYPIINTSAQLREVYV
240     250     260     270     280     290
Cry1Ac  NPVLE-----NFDGSRGSAQGIEGS-IRSPHMLDILNSITITYT----DAHRGEYY
gi|112  DAIGATGVNMMASMNWYNNAPSFAIETAVIRSPHLLDFLEQLTIFSTSSRWASATRHMTY
300     310     320     330     340     350
Cry1Ac  WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-----LYRR
320     330     340     350     360     370

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Regulatory Product Characterization Team

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gi|112 WRGHTIQSRPIG-GG--LNTSTHGSTNTSINPURL-SFFSRDVYWTESYAGVLLWGIYLE
      360      370      380      390      400
      380      390      400      410      420      430
Cry1Ac PFNIGINNQQLSVLDGTE-FAYGTSSNLPsAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 PIH-GVPTVRFNFRNPQNTFERGTANY--SQPYESPGLQLKDSSETLPPETTERPNYESY
      410      420      430      440      450      460
      440      450      460      470      480
Cry1Ac SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-
      . . . . . : : . . . : : : : : : : : : : : : : : : : : : : :
gi|112 SHRLSHIGLI----SQSRVHV--PVYSWTHRSADRTNTISSDSITQIPLVKSFNLNSGT
      470      480      490      500      510
      490      500      510      520      530      540
Cry1Ac SVISGPGFTGGDLVRLNSSGNINQRGYIEVPIHPSTST-RYRVRVRYASVTPIHILNVN
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 SVVSGPGFTGGDIIRTNVNGS-----VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVT
      520      530      540      550      560      570
      550      560      570      580      590      600
Cry1Ac WGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFSGTAGVIIDR
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 VGGSTTFDQGFPTMSANESLTSQSFRFAEFPVGISASGSQTAGISISNNAQRQTFHFDDK
      580      590      600      610      620      630
      610      620      630      640      650      660
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDEFCL
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 IEFIPITATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVLACLSDEFCL
      640      650      660      670      680      690
      670      680      690      700
Cry1Ac DEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----ERGWGGS
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 DEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGS
      700      710      720      730      740      750
      710      720      730      740      750      760
Cry1Ac TGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 ENITIQEGNDVFKENYVTLPGTFNFCYPTYLYQKIGESSELKAYTRYQLRGYIEDSQDLEI
      760      770      780      790      800      810
      770      780      790      800      810      820
Cry1Ac YSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAH
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 YLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNRCAPHFWNPDLDCSCRDGEKCAH
      820      830      840      850      860      870
      830      840      850      860      870      880
Cry1Ac HSHHFSLDIDVCGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 HSHHFSLDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPLLGEALSrvkRAE
      880      890      900      910      920      930
      890      900      910      920      930      940
Cry1Ac KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAY

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      940      950      960      970      980      990
gi|112 KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAY
      950      960      970      980      990      1000
Cry1Ac LPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNN
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 LSELSVIPGVNAEIFFEELEGRITAITSLYDARNVVKNGDFNNGLACWNVKGVHDVQ-QSH
      1000      1010      1020      1030      1040      1050
      1010      1020      1030      1040      1050      1060
Cry1Ac QRSVLVPEWEAEVSVQVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNVC
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 HRSVLVIPWEAEVSVQVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFKNCE
      1060      1070      1080      1090      1100      1110
      1070      1080      1090      1100      1110      1120
Cry1Ac EEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRYNEAPSVA---DYASVYEEKSYTDGR
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 EEEVYPTDTGTCDNYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKPTYEEETVTDVR
      1120      1130      1140      1150      1160      1170
      1130      1140      1150      1160      1170      1180
Cry1Ac RENPCFNRGRDYTPLPVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|112 RDNHCYDRGVVNYPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1180      1190      1200      1210      1220
      >>gi|125172653|gb|ABN37586.1| Sequence 2 from patent US (1228 aa)
      initn: 3670 init1: 1836 opt: 2699 Z-score: 3172.2 bits: 599.0 E(): 9e-168
      Smith-Waterman score: 4282; 56.772% identity (76.886% similar) in 1233 aa overlap
      (5-1182:27-1228)
      10      20      30
Cry1Ac CMQAMDNPN--INE--CIPYNCLSNPEVEVLGGERIE
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|125 LTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVQ
      10      20      30      40      50
      40      50      60      70      80      90
Cry1Ac TGYTPIDISLSLTQFLLEFVPG-AGFVLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIE
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|125 TG---INIAGRILGLVGVPPFAQIASFYSLVGLWLP-RGRDQWEIFLEHVEQLINQKIT
      60      70      80      90      100      110
      100      110      120      130      140      150
Cry1Ac EFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFA
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|125 ENARNALARLQGLGDSFRAYQOSLEDWLENRDDARTRSVLYTQYIALELDFLNAMPLFA
      120      130      140      150      160      170
      160      170      180      190      200      210
Cry1Ac VQNYQVPLLSVYVQAANLHLSVLRDVSFVQGWGDAATINSRYNDLTRLIGNYTDHAVR
      . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|125 IRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVQTRDYSYCVCE
      180      190      200      210      220      230
      220      230      240      250      260      270
Cry1Ac WYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTPYPIRTVSQLTREIYT

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      .....
gi|125 WYNTGLNSLRGTNAASWVRYNQFRDLTLGVLDLVALFPYSYDTRYPINTSAQLTREYVT
      240      250      260      270      280      290
Cry1Ac NPVLE-----NFDGSGFRGSAQGI EGS-IRSPHMLDILNSITIYT-----DAHRGEYY
      280      290      300      310
gi|125 DAIGATGVNMASMNWYNNNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRWSATRHMTY
      300      310      320      330      340      350
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLST-----LYRR
      320      330      340      350      360      370
gi|125 WRGHTIQSRPIG-GG--LNTSTHGSTNTSINPVL--SFFSRDVYWTESYAGVLLWGIYLE
      360      370      380      390      400
Cry1Ac PFNIGINQQQLSVLDGTE-FAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      380      390      400      410      420      430
gi|125 PIH-GVPTVRFNFRNPQNTFERGTANY--SQPYESPGLQLKDSSETLPPETTERPNYESY
      410      420      430      440      450      460
Cry1Ac SHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-
      440      450      460      470      480
gi|125 SHRLSHIGLI----SQSRVHV---PVYSWTHRSADRTNTISSDSITQIPLVKSFNLSNGT
      470      480      490      500      510
Cry1Ac SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTST-RYRVRVRYASVTPIHILNVN
      490      500      510      520      530      540
gi|125 SVVSGPGFTGGDIIRTNVNGS-----VLSMGLNFNNTSLQRYRVRVRYAASQTMVLRVT
      520      530      540      550      560      570
Cry1Ac WGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFSGTAGVIIDR
      550      560      570      580      590      600
gi|125 VGGSTTFDQGFSPSTMSANESLTSQSFRFAEFPVGISASGSQTAGISISNAGRQTFHFDK
      580      590      600      610      620      630
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCL
      610      620      630      640      650      660
gi|125 IEFIPITATFAEAYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDEFCL
      640      650      660      670      680      690
Cry1Ac DEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----ERGWGGS
      670      680      690      700
gi|125 DEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNTSIEHQSEHGWWGS
      700      710      720      730      740      750
Cry1Ac TGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
      710      720      730      740      750      760
gi|125 ENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESLKAAYTRYQLRGYIEDSQDLEI
      760      770      780      790      800      810
Cry1Ac
      770      780      790      800      810      820

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Cry1Ac YSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH
      .....
gi|125 YLIRYNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFEWNPDLDCSCRDGKCAH
      820      830      840      850      860      870
Cry1Ac HSHHFSLDIDVGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE
      830      840      850      860      870      880
gi|125 HSHHFSLDIDIGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPLLGEALSVRKRAE
      880      890      900      910      920      930
Cry1Ac KKRWDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAY
      890      900      910      920      930      940
gi|125 KKRWDKREKLQLETKRVTYEAKEAVDALFVDSQYNRLQADTNIAMIHAADKLVHRIREAY
      940      950      960      970      980      990
Cry1Ac LPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNN
      950      960      970      980      990      1000
gi|125 LSELVSVIPGVNAEIFFEELEGRITAFSLYDARNVVKNGDFNNGLSCWNVKGVHDVQ--QSH
      1000      1010      1020      1030      1040      1050
Cry1Ac QRSVLVVPWEAEVSVQEVRCVPCGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCV
      1010      1020      1030      1040      1050      1060
gi|125 HRSVLVVPWEAEVSVQAVRVCVPCGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFKNCE
      1060      1070      1080      1090      1100      1110
Cry1Ac EEEIYPNNIVTNCNDYTVNQEEYGGAY-TSRNRGYNEAPSVPA----DYASVVEEKSYTDG
      1070      1080      1090      1100      1110      1120
gi|125 EEEVYPTDTGTCNDYTAHQ---GTAVCNRSNAGYEDAYEVDVTTASVNYKPTYEETVTDV
      1120      1130      1140      1150      1160
Cry1Ac RRENPCFNRRGYRDTYPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1130      1140      1150      1160      1170      1180
gi|125 RRDNHCEYDRGVVNYPLPAGYMTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1170      1180      1190      1200      1210      1220
>>gi|15143039|emb|CAC50778.1| unnamed protein product [B (1228 aa)
      initn: 3670 init1: 1836 opt: 2699 Z-score: 3172.2 bits: 599.0 E(): 9e-168
      Smith-Waterman score: 4282; 56.772% identity (76.886% similar) in 1233 aa overlap
      (5-1182:27-1228)
Cry1Ac
      10      20      30
gi|151 MTSNRKNENEIINALSIPAVSNHSTQMDLSPDARIEDSLCIAEGNNINP---LVSASTVQ
      10      20      30      40      50
Cry1Ac
      40      50      60      70      80      90
gi|151 TG---INIAGRILGVLGVPFAGQIASFYSFLVGLWP-RGRDQWEI FLBEHVEQLINQKIT
      60      70      80      90      100      110
Cry1Ac
      100      110      120      130      140      150

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Regulatory Product Characterization Team

Cry1Ac EFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFA  
gi|151 ENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLVYQYIALELDFLNAMPLFA  
120 130 140 150 160 170

Cry1Ac VQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVR  
gi|151 IRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVEQTRDYSDYCV  
180 190 200 210 220 230

Cry1Ac WYNTGLERVWGPDSRDWRIRYNQFRELTTLTVLDIVSLFNPYDSRTYPIRTVQSOLTREIYT  
gi|151 WYNTGLNSLRGTNAASWVRYNQFRDLTLGVLDLVALFSPYDTRTYPIINTSAQLTREVVT  
240 250 260 270 280 290

Cry1Ac NPVLE-----NFDGSFRGSAQGIEGS-IRSPHLMIDLNSITIYT-----DAHRGEYY  
gi|151 DAIGATGVNMAASMWNYNAPSFSAIETAVIRSPHLLDFLEQLTIFSTSSRSWSATRHTMY  
300 310 320 330 340 350

Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLSST-----LYRR  
gi|151 WRGHTIQSRPIG-GG--LNTSTHGSTNTSINPVRL-SFSDRVYWTESYAGVLLWGIYLE  
360 370 380 390 400

Cry1Ac PFNIGINNQQLSVLDGTE-FAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGF  
gi|151 PIH-GVPTVRVFNFRNPQNTFERGTANY--SQPYESPLQLKDSSETLPPETTERPNYESY  
410 420 430 440 450 460

Cry1Ac SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-  
gi|151 SHRLSHIGLI----SQSRVHV---PVYSWTHRSADRTFTISSDSITQIPLVKSNFLNSGT  
470 480 490 500 510

Cry1Ac SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTST-RYRVRVRYASVTPPIHLNWN  
gi|151 SVVSGPGFTGGDIIRTNVNGS-----VLSMGLNFNNTSLQRYRVRYAASQTMVLRVT  
520 530 540 550 560 570

Cry1Ac WGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFGTAGVVIDR  
gi|151 VGGSTTFDQGFPTMSANESLTSQSFRFAEFPVGISASGSQTAGISISNNAQRQTFHFDDK  
580 590 600 610 620 630

Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCL  
gi|151 IEFIPITATFEAEYDLERAQEAVALNFTNTNPRRLKTDVTDYHIDQVSNLVACLSDDEFCL  
640 650 660 670 680 690

Cry1Ac 670 680 690 700  
DEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----ERGWGGS  
gi|151 DEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIHEQSEHGWWGS  
700 710 720 730 740 750

Cry1Ac 710 720 730 740 750 760  
TGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEI  
gi|151 ENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESSELKAYTRYQLRGYIEDSDLEI  
760 770 780 790 800 810

Cry1Ac 770 780 790 800 810 820  
YSIRYNAKHETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAH  
gi|151 YLIRYNAKHETLDVPGTESVWPLSVESPIGRCEPNCAPHFEWNPDLDCSCRDGKCAH  
820 830 840 850 860 870

Cry1Ac 830 840 850 860 870 880  
HSHHFLSLDIDVGCCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAE  
gi|151 HSHHFLSLDIDIGCTDLHENLGWVVFVKIKTQEGHARLGNLEFIEEKPLLGEALSrvkRAE  
880 890 900 910 920 930

Cry1Ac 890 900 910 920 930 940  
KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAY  
gi|151 KKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYNRLQADTNIAMIHAADKLVHRIREAY  
940 950 960 970 980 990

Cry1Ac 950 960 970 980 990 1000  
LPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQVWVGHVDVVEEQNN  
gi|151 LSELSVIPGVNABIFEELEGRITAITAISLYDARNVVKNGDFNNGLACVWVGHVDVQ-QSH  
1000 1010 1020 1030 1040 1050

Cry1Ac 1010 1020 1030 1040 1050 1060  
QRSVLVVPWEAEVVSQEVVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCV  
gi|151 HRSVLVIPWEAEVVSQAVRVCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFKNCE  
1060 1070 1080 1090 1100 1110

Cry1Ac 1070 1080 1090 1100 1110 1120  
EEEIYPNNIVTCDYTVNQEEYGGAY-TSRNRGYNEAPSVA----DYASVYEEKSYTDG  
gi|151 EEEVYPTDGTGTCNDYTAHQ---GTAVCNRSRAGYEDAYEVDTTASVNYKPTVEEETVTDV  
1120 1130 1140 1150 1160

Cry1Ac 1130 1140 1150 1160 1170 1180  
RRENPCFNRYRDYTPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|151 RRDNHCEYDRGVVNYPLPAGYMTKLEYFPETDKVWIEIGETEGKFIVDSVELLMEE  
1170 1180 1190 1200 1210 1220

>>gi|37729016|gb|AA039720.1| insecticidal crystal protei (1235 aa)  
initn: 3654 initl: 1822 opt: 2696 Z-score: 3168.6 bits: 598.4 E(): 1.4e-167  
Smith-Waterman score: 4232; 56.281% identity (76.998% similar) in 1226 aa overlap  
(18-1182:35-1235)

Regulatory Product Characterization Team

Cry1Ac 10 20 30 40  
 CMQAMDNPNINECIPYNCLSNPEVE---VLGGERIE--TGYPID  
 gi|377 RKNENEIIDASFPVAVSNESVTISKEYAQTNLQNNISIEDGLCIAEGEYIDPFVFASTVQ  
 10 20 30 40 50 60

Cry1Ac 50 60 70 80 90  
 ISLSLTQPLLSEF-VPGAGFVLGLVDIIWGFGPS---QWDAFLVQIEQLINQRIEFPAR  
 gi|377 TGISIAGRILGLVGFVAGQLASFYSFIVGELWPKGRDQWEIFMEHVEQLVRQQITANAR  
 70 80 90 100 110 120

Cry1Ac 100 110 120 130 140 150  
 NQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNY  
 gi|377 NTALARLQGLGDSFRAYQQSLEDWLENRNDARTRSVLYTQYIALELDFLNAMPLFAIREQ  
 130 140 150 160 170 180

Cry1Ac 160 170 180 190 200 210  
 QVPLLSVYVQAANLHLSVLRDVSFVQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNT  
 gi|377 EVPLLMVYAQAANLHLLLRDASLYGREFGLTSQEIQRYYERQVTRTDYSDHCQVQWYNT  
 190 200 210 220 230 240

Cry1Ac 220 230 240 250 260 270  
 GLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL  
 gi|377 GLNNLRGTNAESWVRYNQFRDLTLGVLDLVALFSPYDTRTPYINTSAQLTREVYTDIAIG  
 250 260 270 280 290 300

Cry1Ac 280 290 300 310 320  
 E-----NFDGSGFRGSAQGI EGS-IRSPHLM DILNSIT IYTD AHRGEY-----YWSGH  
 gi|377 ATGVNMMASMNWYNNAPSFSAIETAVIRSPHLLDFLEQLKIFSASSRSWNRHMTYWRGH  
 310 320 330 340 350 360

Cry1Ac 330 340 350 360 370  
 QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA-QL-GQGVYRTLSST-----LYRRPF  
 gi|377 TIQSRPI--RGALIT----STHGNTNTSINPVTFQFPSRDVYRTESYAGVLLWGIYLEPI  
 370 380 390 400 410

Cry1Ac 380 390 400 410 420 430  
 NIGINNQQLSVLDGTE-FAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSSH  
 gi|377 H-GVPTVRFNFRNPQNTFERGTANY--SQPYESPGLQLKDSETEPLPETTERPNYESYSH  
 420 430 440 450 460 470

Cry1Ac 440 450 460 470 480 490  
 RLSHVSMPFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLPFG-SV  
 gi|377 RLSHIGIILQTRLN-----VPVYSWTHRSADRNTNTISSDSITQIPLVKSFNLSGTSV  
 480 490 500 510 520

Cry1Ac 500 510 520 530 540 550  
 ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRVRVRYASVTPIHLLNVNNG  
 gi|377 VSGPGFTGGDIIRTNVNGS-VLSMG----LNFNNTSLQRYRVRVRYAASQTMVLRVTVG  
 530 540 550 560 570 580

Cry1Ac 560 570 580 590 600  
 NSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFSGTAGVIIDRFE  
 gi|377 GSTTFDQGFSPSTMSANESLTSQSFRFAEFPVVGISASGSQTAGISISNNAQRQTFHFDKIE  
 590 600 610 620 630 640

Cry1Ac 610 620 630 640 650 660  
 FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE  
 gi|377 FIPITATFEAEYDLERAQEAVALFTNTNPRRLKTVTDYHIDEVSNLVAELSDDEFCLDE  
 650 660 670 680 690 700

Cry1Ac 670 680 690 700 710  
 KRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----ERGWGSGTG  
 gi|377 KRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSIEHQSEHWGWSSEN  
 710 720 730 740 750 760

Cry1Ac 720 730 740 750 760 770  
 ITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYS  
 gi|377 ITIQEGNDVFKENYVTLPGTYNECYPTYLYQKIGSESELKAYTRYQLRGYIEDSQDLEIYL  
 770 780 790 800 810 820

Cry1Ac 780 790 800 810 820 830  
 IRYNAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHHS  
 gi|377 IRYNAKHETLDVPGTESVWPLSVESPIRRCGEPNRCAPHFEWNPDLDCSCRDEKCAHHS  
 830 840 850 860 870 880

Cry1Ac 840 850 860 870 880 890  
 HHFSLDIDVGCIDLHNLGVVVFVKIKTQDGHARLGNLEFIEEKPLVGEALARVKRAEKK  
 gi|377 HHFSLDIDVGCIDLHNLGVVVFVKIKTQEGHARLGNLEFIEEKPLLGEALSrvkRAEKK  
 890 900 910 920 930 940

Cry1Ac 900 910 920 930 940 950  
 WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLP  
 gi|377 WRDKREKLQLETKRKYTEAKEAVDALFVDSQYDRLQADTNIIGMIHAADKLVHRIREAYLS  
 950 960 970 980 990 1000

Cry1Ac 960 970 980 990 1000 1010  
 ELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVVEEQNNQR  
 gi|377 ELSVIPGVNAEIFEELGRITAIISLYDARNVVKNGDFNNGLACWNVKGHVDVQ-QSHHR  
 1010 1020 1030 1040 1050 1060

Cry1Ac 1020 1030 1040 1050 1060 1070  
 SVLVVPEWEAEVSEQEVRVCPGRGYILLRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVVEE  
 gi|377 SVLVVPEWEAEVSEQAVRVCPRGYILLRVTAAYKEGYGEGCVTIIHEIENNTDELKFKNCEEE  
 1070 1080 1090 1100 1110 1120

Cry1Ac 1080 1090 1100 1110 1120  
 EIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVA----DYASVYEEKSYTDGRRE  
 gi|377 EVYPTDTGTCDNYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKPTYEBEETDVRDRD



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gi|337 VKGHVDVQ-QSHHRSVLVPEWAEVSVQAVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIE
1050 1060 1070 1080 1090

Cry1Ac 1060 1070 1080 1090 1100 1110
NNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAY-TSRNRGYNEAPSVA----DY

gi|337 NNTDELKFKNCEEEVYPTDTGTCNDYTAHQ---GTAVCNRSRAGYEDAYEVDTTASVNY
1100 1110 1120 1130 1140 1150

Cry1Ac 1120 1130 1140 1150 1160 1170
ASVYEEKSYTDGRRENPCFNRGRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFI

gi|337 KPTYEEETYTDVRRDNHCYDRGYVNYPPVPAGYMTKELEYFPETDKVWIEIGETEGKFI
1160 1170 1180 1190 1200 1210

Cry1Ac 1180
VDSVELLLMEE

gi|337 VDSVELLLMEE
1220

>>gi|112088065|gb|ABI06968.1| Sequence 63 from patent US (1227 aa)
initn: 3106 initl: 1825 opt: 2681 Z-score: 3151.0 bits: 595.1 E(): 1.4e-166
Smith-Waterman score: 4192; 57.494% identity (77.307% similar) in 1181 aa overlap
(55-1182:72-1227)

Cry1Ac 30 40 50 60 70 80
VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWIGIFGP---SQWDAFL

gi|112 AEGNNIDPFVSASTVQTGINIAGRILGVLGVFAGQIASFYSLVGLWPRGRDPWEIFL
50 60 70 80 90 100

Cry1Ac 90 100 110 120 130 140
VQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM

gi|112 EHVEHLIRQQVTENTRDTALARLQGLGNSFRAYQQSLEDWLENRDDRTRSVLYTQYIAL
110 120 130 140 150 160

Cry1Ac 150 160 170 180 190 200
NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLT

gi|112 ELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQV
170 180 190 200 210 220

Cry1Ac 210 220 230 240 250 260
RLIGNYTDHAVRWYNTGLERWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI

gi|112 EKTREYSYCARWYNTGLNLRGTNAESWLRYNQFRRLDTLGVLDLVALFPSYDTRVYPM
230 240 250 260 270 280

Cry1Ac 270 280 290 300 310
RTVSQLTREIYTNPVLE-NFDGSRG-----SAQIEGS-IRSPHLMIDLNSITITY

gi|112 NTSAQLTREIYTDPIGRTNAPSGFASTNWFNNAPSFAIAEAAVIRPPHLLDFPEQLTTF
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL-GQGYYR

gi|112 SVLSRWSNTQYMNMYVWGHRLRESRTI--RGLSLSTWTHGNTNTSINP---VTLQFTSRDVYR
350 360 370 380 390

Cry1Ac 370 380 390 400 410
TLS---STLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQT--VDSLDEIP

gi|112 TEFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTYIGYTVGTQLFDSETELP
400 410 420 430 440 450

Cry1Ac 420 430 440 450 460 470
PQNNNVPPRQGFSHRSLHVSFMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI

gi|112 PETTERPNYESYSHRSLNIRLI-SG-----NTLRAPVYSWTHRSADRNTISSDSITQI
460 470 480 490 500

Cry1Ac 480 490 500 510 520 530
PAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRVRVR

gi|112 PLVKSFNLNSGTSVVSQPGFTGGDIIRTNVNGS-VLSMG----LNFNNTSLQRYRVRVR
510 520 530 540 550 560

Cry1Ac 540 550 560 570 580 590
YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVR--

gi|112 YAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAEFPVGISAGSQTAGISIS
570 580 590 600 610 620

Cry1Ac 600 610 620 630 640 650
NFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS

gi|112 NNAGRQTFHFDFKIEFIPITATFEAEYDLERAQAVNALFTNTNPRRLKTVGTDYHIDEVS
630 640 650 660 670 680

Cry1Ac 660 670 680 690 700
NLVYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQP-----

gi|112 NLVACLSEDEFCLDEKRELESEKVKYAKRLSDERNLLQDPNFTSINKQPDFNSNNEQSNFTS
690 700 710 720 730 740

Cry1Ac 710 720 730 740 750
-----ERGGWGSGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLFKAFTRYQL

gi|112 IHEQSEHGWWGSENITIQEGNDVFKENYVTLVPGTFNECYPTYLYQKIGEAELKAYTRYQL
750 760 770 780 790 800

Cry1Ac 760 770 780 790 800 810
RGYIEDSQLEIYSIRYNAKHETVNVVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL

gi|112 SGYIEDSQLEIYLIRYNAKHETLDVPGTESVWPLSVESPIGRCGEPNRCAPHLEWNPDL
810 820 830 840 850 860

Cry1Ac 820 830 840 850 860 870
DCSCRDGKCAHSHHSLDIDVGCIDLHENLGVVVFVKIKTQDGHARLGNLEFLEEKPL

gi|112 DCSCRDGKCAHSHHSLDIDVGCIDLHENLGVVVFVKIKTQEGHARLGNLEFLEEKPL
870 880 890 900 910 920

Cry1Ac 880 890 900 910 920 930
VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHA

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gi|112 LGEALSRVKRAEKWKREKLEKLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHA
      930      940      950      960      970      980
Cry1Ac 940      950      960      970      980      990
ADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWN
gi|112 ADKLVHRIREAYLSELSVIPGVNAEIFELEGRITAIISLYDARNVVKNGDFNGLACWN
      990      1000     1010     1020     1030     1040
Cry1Ac 1000     1010     1020     1030     1040     1050
VKGHVDVEEQNNQRSVLVVPEWEAEVSEQEVRVCPGRGYILRVTAKEGYGEGCVTIHEIE
gi|112 VKGHVDVQ-QSHHRSVLVIPWEAEVSAQAVRVCPCGRGYILRVTAKEGYGEGCVTIHEIE
      1050     1060     1070     1080     1090
Cry1Ac 1060     1070     1080     1090     1100     1110
NNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAY-TSRNRGYNEAPSVPA----DY
gi|112 NNTDELKFKNCEEEVYPTDTGTTCNDYTAHQ---GTAVCNRSRNAGYEDAYEVDTTASVNY
      1100     1110     1120     1130     1140     1150
Cry1Ac 1120     1130     1140     1150     1160     1170
ASVYEEKSYTDGRRNCPCEFNRGRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFI
gi|112 KPTYEEETDVRDRNHCEYDRGYVNYPPVPAGYMTKELEYFPETDKVWIEIGETEGKFI
      1160     1170     1180     1190     1200     1210
Cry1Ac 1180
VDSVELLLMEE
gi|112 VDSVELLLMEE
      1220
>>gi|3410671|gb|AAC31093.1|I90731 Sequence 8 from patent (1227 aa)
  in1n: 3106 init1: 1819 opt: 2680 Z-score: 3149.8 bits: 594.9 E(): 1.6e-166
Smith-Waterman score: 4190; 57.337% identity (77.354% similar) in 1179 aa overlap
(55-1182:72-1227)
Cry1Ac 30      40      50      60      70      80
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIGIFGP---SQWDAFL
gi|341 AEGNNIDPFVFASTVQTGINIAGRILGLVGVFAGQIASFYSLVGLWLRGRDPWEIFL
      50      60      70      80      90     100
Cry1Ac 90      100     110     120     130     140
VQIEQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|341 EHVEQLIRQQVNTENTRDALARLQGLGNSFRAYQQSLEDWLENRDARTRSVLYTQYIAL
      110     120     130     140     150     160
Cry1Ac 150     160     170     180     190     200
NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLT
gi|341 ELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYERQV
      170     180     190     200     210     220
Cry1Ac 210     220     230     240     250     260
RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI

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gi|341 EKTREYSDYCARWYNTGLNLRGTNAESWLRYNQFRRLDTLGLVLDLVALFPDYTRVYPM
      230     240     250     260     270     280
Cry1Ac 270     280     290     300     310
RTVSQTLTREIYTNPVLE-NFDGSRFG-----SAQGIEGS-IRSPHMLDILNSITIIY
gi|341 NTSAQLTREIYTDPIGRNTAPSGFASTNWFNANNAPSFSAIEAAVIRPPHLLDFPEQLTIF
      290     300     310     320     330     340
Cry1Ac 320     330     340     350     360
TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
gi|341 SVLSRWSNTQYMNWVWGHRLSRTIRGS---LSTSTHGNT-NTSINPVTLQFTSRDVIYRT
      350     360     370     380     390
Cry1Ac 370     380     390     400     410
LS---STLYRRFPFNIGINNQQSLVDGTEFAYGTSSNLPSAVYRKSQT--VDSLDEIIPP
gi|341 ESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTIGYTGVTGQLFDSSETLEPP
      400     410     420     430     440     450
Cry1Ac 420     430     440     450     460     470
QNNNVPPRQGFSSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIP
gi|341 ETTERPNYESYSHRSLNIRLI-SG-----NTRAPVYSWTHRSADRINTISSDSITQIP
      460     470     480     490     500
Cry1Ac 480     490     500     510     520     530
AVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRVRVRY
gi|341 LVKSFNLNSGTSVSVSGPGFTGGDIIRTNVNGS-VLSMG----LNFNNTSLQRYRVRVRY
      510     520     530     540     550     560
Cry1Ac 540     550     560     570     580     590
ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVR--N
gi|341 AASQTMVLRVTVGGSTTFDQGFSTMSANESLTSQSFRAEFPVGISASGSQTAGISISN
      570     580     590     600     610     620
Cry1Ac 600     610     620     630     640     650
FSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
gi|341 NAGRQTFHFDFKIEFIPITATFEAEYDLERAQEAVALNFNTNPRRLKTVTDYHIDEVSN
      630     640     650     660     670     680
Cry1Ac 660     670     680     690     700
LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----
gi|341 LVACLSDDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTSI
      690     700     710     720     730     740
Cry1Ac 710     720     730     740     750
---ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLR
gi|341 HEQSEHGWSSENITIQEGNDVFKENYVILPGTFNECYPTYLYQKIGEAELKAYTRYQLS
      750     760     770     780     790     800
Cry1Ac 760     770     780     790     800

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Cry1Ac GYIEDSQDLEIYSIRYNNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|341 GYIEDSQDLEIYLIRYNNAKHETLDVPGTESVWPLSVESPIGRGCEPNRCAPHFEWNPDL
810 820 830 840 850 860

Cry1Ac CSCRDGEKCAHSHHFLSDIDVGCIDLHNLGVVWVFKIKTQDGHARLGNLEFLEEKPLV
gi|341 CSCRDGEKCAHSHHFLSDIDVGCIDLHNLGVVWVFKIKTQEGHARLGNLEFIEEKPLL
870 880 890 900 910 920

Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
gi|341 GEALSrvKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHAA
930 940 950 960 970 980

Cry1Ac DKRVHSIREAYLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWCWNV
gi|341 DKLVHRIREAYLSELSVIPGVNAEIFEELGRITAITSLYDARNVVKNGDFNNGLACWNV
990 1000 1010 1020 1030 1040

Cry1Ac KGHVDVVEEQNNQSRVSLVPEWEAEVSVQEVVRCVCPGRGYILRVTAAYKEGYEGCVTIHEIEN
gi|341 KGHVDVQ-QSHHRSVLVPEWEAEVSVQAVRVCVCPGRGYILRVTAAYKEGYEGCVTIHEIEN
1050 1060 1070 1080 1090 1100

Cry1Ac NTDELKFNCEVEEYYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVA---DYAS
gi|341 NTDELKFNCEVEEYYPNNTVTCNDYTAHQGT--AACNSRNAGYEDAEVDTTASVNYKP
1110 1120 1130 1140 1150

Cry1Ac VYEEKSYTDGRENPCFNRGYRDTPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVD
gi|341 TYEEETVTVRRDNHCEYDRGYVNYPPVAGYMTKELEYFPETDKVWIEIGETEGTFIVD
1160 1170 1180 1190 1200 1210

Cry1Ac SVLELLMEE
gi|341 SVLELLMEE
1220

>>gi|3360519|gb|AAC32850.1| Cry1Be1 delta-endotoxin [Bac (1227 aa)
initn: 3106 initl: 1819 opt: 2680 Z-score: 3149.8 bits: 594.9 E(): 1.6e-166
Smith-Waterman score: 4190; 57.337% identity (77.354% similar) in 1179 aa overlap
(55-1182:72-1227)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIGIFGP---SQWDAFL
gi|336 AEGNNIDPFVSASTVQTGINIAGRILGVLGVPPAQIASFYSFLVGEIWRGRDPWEIFL
50 60 70 80 90 100
90 100 110 120 130 140

Cry1Ac VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|336 EHVEQLIRQVQVTEVTRDALTALARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIAL
110 120 130 140 150 160

Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWFDAATINSRYNDLT
gi|336 ELDFLNLAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQV
170 180 190 200 210 220

Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPI
gi|336 EKTREYSDYCARWYNTGLNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSYDTRVYPM
230 240 250 260 270 280

Cry1Ac RTVSQTLTREIYTNPVLE-NFDGSRFG-----SAQGIEGS-IRSPHMLDILNSITIIY
gi|336 NTSAQTLTREIYTDPIGRNTAPSGFASTNWFNNAPSFSIAEAAVIRPPHLLDFPEQLTIF
290 300 310 320 330 340

Cry1Ac TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAPQQRIVAQLGQVYRT
gi|336 SVLSRWSNTQYMYVWGHRLSRTIRGS---LSTSTHGNT-NTSINPVTLQFTSRDVIYRT
350 360 370 380 390

Cry1Ac LS---STLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQT--VDSLDEIIP
gi|336 ESFAGINILLTTPVNV-GVPWARFNWRNPLNSLRG--SLLYTIGYTGVTQLFSETLELPP
400 410 420 430 440 450

Cry1Ac QNNNVPPRQGFHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNI IASDSITQIP
gi|336 ETTERPNYESYSHRLSNIRLI-SG-----NTLRAPVYSWTHRSADRTNTISSDSITQIP
460 470 480 490 500

Cry1Ac AVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNGYIEVPIHFPSTST-RYRVRVRY
gi|336 LVKSPNLSGTSVVSPPGFTGGDIIRTNVNGS-VLSMG----LNFNNTSLQRYRVRVRY
510 520 530 540 550 560

Cry1Ac ASVTPHILNVNWNSSIFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--N
gi|336 AASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAEFPVGISASGSQTAGISISN
570 580 590 600 610 620

Cry1Ac FSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
gi|336 NAGRQTFHFDPKIEFIPITATFEAEYDLERAQEAVALNFNTNPRRLKTVTDYHIDEVSN
630 640 650 660 670 680



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540      550      560      570      580      590
Cry1Ac SVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDF---GYFESANAFSTSSLGNIVGVNR
gi|474 STTDLQFFTRINGTTVNIIGNFRTMNRGDNLEYSFRTAGFSTPFNFLNAQSTFTLGAQS
      570      580      590      600      610      620

600      610      620      630      640      650
Cry1Ac FSGTAGVIIDRFEFIPVTATLEAEYNLEAQAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
gi|474 FSNQE-VYIDRVEFVPAEVTFAEAYDLERAQAQKAVNALFTSTNPRRLKTDVTDYHIDQVSN
      630      640      650      660      670      680

660      670      680      690
Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQD-----SNFKDI
gi|474 MVACLSDDEFCLDEKRELFEKVKYAKRLSDERNLLQDPNFTFISGQLSFASIDGQSNFPSI
      690      700      710      720      730      740

700      710      720      730      740      750
Cry1Ac NRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLR
gi|474 NELSEHGWWGSANVTIQEGNDVFKENYVTLPGTFNECYPNLYQKIGESSELKAYTRYQLR
      750      760      770      780      790      800

760      770      780      790      800      810
Cry1Ac GYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|474 GYIEDSQDLEIYLIRYNAKHETLDVPGTDSLWPLSVESPIGRCGEPNRCAPHFEWNPDL
      810      820      830      840      850      860

820      830      840      850      860      870
Cry1Ac CSCRDGEKCAHSHHSLDIDVGCSDLNEDLGVVVFVKIKTQDGHARLGNLEFLEEKPLV
gi|474 CSCRDGERCAHSHHSLDIDVGCSDLHENLGVVVFVKIKTQEGYARLGNLEFIEEKPLI
      870      880      890      900      910      920

880      890      900      910      920      930
Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
gi|474 GEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
      930      940      950      960      970      980

940      950      960      970      980      990
Cry1Ac DKRVHSIREAYLPELSPVPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWNV
gi|474 DKLVHRIREAYLSELSPVPGVNAEIFEELGRIITAMSLYDARNVVKNGDFNNGLTCWNV
      990      1000      1010      1020      1030      1040

1000     1010     1020     1030     1040     1050
Cry1Ac KGHVDVEEQNNQSRVLPVPEWAEVSVQEVVCPGRGYILRVTAAYKEGYGEGCVTIHEIEN
gi|474 KGHVDVQ-QSHHRSDLVIPWEAEVSVQAVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIEN
      1050     1060     1070     1080     1090     1100

1060     1070     1080     1090     1100     1110
Cry1Ac NTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVA----DYAS
gi|474 NTDELKFKNCEEEVYPTDTGTCNDYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKP

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1110     1120     1130     1140     1150     1160
Cry1Ac VYEEKSYTDGRRNPECFNRRGYRDTPLPVGYVTKLEYFPETDKVVWIEIGETEGTFIVD
gi|474 TYEETTYTDVRRDNHCEYDRGVVNYPPVPAGYVTKLEYFPETDVTVWIEIGETEGKFIVD
      1170     1180     1190     1200     1210     1220

1180
Cry1Ac SVLELLMEE
gi|474 SVLELLMEE

>>gi|2096163|gb|AAB54995.1| Sequence 4 from patent US 56 (1229 aa)
initn: 3225 init1: 1824 opt: 2667 Z-score: 3134.4 bits: 592.0 E(): 1.1e-165
Smith-Waterman score: 4202; 57.082% identity (77.523% similar) in 1179 aa overlap
(55-1182:72-1229)

30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFGPS--QWDAFL
gi|209 AEVNNIDPFVFASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGLWPSGRDPWEIFL
      50      60      70      80      90      100

90      100     110     120     130     140
Cry1Ac VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|209 EHVEQLIRQVVTENTRTAIARLEGLGRGYSYQQALETWLDNRDARSRSIILERYVAL
      110     120     130     140     150     160

150     160     170     180     190     200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRQWGFDAATINSRYNDLT
gi|209 ELDITTAIPLFRIRNEEVPLLMVYAQAANLHLLLRDASLFGSEWGMASDVSQYQEQI
      170     180     190     200     210     220

210     220     230     240     250     260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPI
gi|209 RYTEEYSNHCVQWYNTGLNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPSYDTRTYPI
      230     240     250     260     270     280

270     280     290     300     310     320
Cry1Ac RTVSQLTREIYTNPVLE-NFDGSRFG-----SAQGIEGSI-RSPHLMIDLNSITTY
gi|209 NTSAQLTREIYTDPIGRTNAPSGFASTNWFNNAPSFSAIEAEIFRPPHLLDFPEQLTIY
      290     300     310     320     330     340

320     330     340     350     360
Cry1Ac TDAHRGEY----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQORIVAQLGQGVYRT
gi|209 SASSRWSSTQHMNYVWGHRLNFRPIGGT---LNTSTQGLTNTSINPVTLQFTSRDVYRT
      350     360     370     380     390

370     380     390     400     410
Cry1Ac LSST----LYRRPFNIGINNQQSLVDGTEFAYGTSSNLPASAVYRKSQT--VDSLDEIIPP
gi|209 ESNAGTNILFTTPVN-GVPWARFNFINPQNI-YERGATTYSQPYQGVGVLQFLDSETELPP

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400      410      420      430      440      450
Cry1Ac QNNVPPRQGFHSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIP
      . . . . .
gi|209 ETTERPNEYESYSHRLSHIGLI---IGNT----LRAPVYSWTHRSADRNTNTIGPNRITQIP
      460      470      480      490      500

480      490      500      510      520      530
Cry1Ac AVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA
      . . . . .
gi|209 LVKALNLHSGVTVVGGPGFTGGDILRRNTNTGTFGDIRLNINVPL-----SQRYRVRIRYA
      510      520      530      540      550      560

540      550      560      570      580      590
Cry1Ac SVTPIHLLNWNWGNSSIFSNTVPATATSLDNLQSSDF---GYFESANAFTSSLGNIVGVRN
      . . . . .
gi|209 STTDLQFFTRINGTTVNIIGNFSRTMNRGDNLEYRSFRTAGFSTPFNFLNAQSTFTLGAQS
      570      580      590      600      610      620

600      610      620      630      640      650
Cry1Ac FSGTAGVVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSN
      . . . . .
gi|209 FSNQE-VYIDRVEFVPAEVTFEAEYDLERAQKAVNALFTSTNPRRKTDVTDYHIDQVSN
      630      640      650      660      670      680

660      670      680      690
Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQD-----SNFKDI
      . . . . .
gi|209 MVACLSDEFCLDEKRELFEKVKYAKRLSDERNLLQDPNFTFISGQLSFASIDGQSNFPSI
      690      700      710      720      730      740

700      710      720      730      740      750
Cry1Ac NRQPERGGWGSGTITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLR
      . . . . .
gi|209 NELSEHGWWGSANVTIQEGNDVFKENYVTLPGTFNECYPNYLYQKIGSELKAYTRYQLR
      750      760      770      780      790      800

760      770      780      790      800      810
Cry1Ac GYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
      . . . . .
gi|209 GYIEDSQDLEIYLIRYNAKHETLDVPGTDSLWPLSVESPIGRCGEPNRCAPHFEWNPDL
      810      820      830      840      850      860

820      830      840      850      860      870
Cry1Ac CSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLV
      . . . . .
gi|209 CSCRDGERCAHSHHFTLDIDVGCTDLHENLGVWVIFKIKTQEGYARLGNLEFIEEKPLI
      870      880      890      900      910      920

880      890      900      910      920      930
Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
      . . . . .
gi|209 GEALSRVKRAEKKWRDKREKLQLETKRVTYEAKEAVDALFVDSQYDQLQADTNIAMIHAA
      930      940      950      960      970      980

940      950      960      970      980      990
Cry1Ac DKRVHSIREAYLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWNV
      . . . . .

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gi|209 DKLVHRIREAYLSELPVPGVNAEIFEELGHIITAMSLYDARNVVKNGDFNNGLTCWNV
      990      1000      1010      1020      1030      1040

1000      1010      1020      1030      1040      1050
Cry1Ac KGHVDVEEQNNQRSVLVPEWEAEVSVQEVRCVPCGRGYILRVTAAYKEGEGCVTIHEIEN
      . . . . .
gi|209 KGHVDVQ-QSHHRSDLVIPEWEAEVSVQAVRVCVPCGRGYILRVTAAYKEGEGCVTIHEIEN
      1050      1060      1070      1080      1090      1100

1060      1070      1080      1090      1100      1110
Cry1Ac NTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPA---DYAS
      . . . . .
gi|209 NTDELKFKNCEEEVYPTDTGTCNDYTAHQGT--AACSRNAGYEDAYEVDTTASVNYKP
      1110      1120      1130      1140      1150      1160

1120      1130      1140      1150      1160      1170
Cry1Ac VYEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVD
      . . . . .
gi|209 TYEETTYDVRDRNHCEYDRGVYVNPVPAGYVTKLEYFPETDVTWIEIGETEGKFIVD
      1170      1180      1190      1200      1210      1220

1180
Cry1Ac SVELLMLME
      . . . . .
gi|209 SVELLMLME

>>gi|3006692|gb|AAC09534.1|I70557 Sequence 4 from patent (1229 aa)
      initn: 3225 initl: 1824 opt: 2667 Z-score: 3134.4 bits: 592.0 E(): 1.1e-165
      Smith-Waterman score: 4202; 57.082% identity (77.523% similar) in 1179 aa overlap
      (55-1182:72-1229)

30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIWIWIFGPS--QWDAFL
      . . . . .
gi|300 AEVNNIDPFVFASTVQTGINIAGRILGLVGVVFAQQLASFYSLVGLWPSGRDPWEIFL
      50      60      70      80      90      100

90      100      110      120      130      140
Cry1Ac VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
      . . . . .
gi|300 EHVEQLIRQQVTRNTAARLEGLGRGYRSYQQALETWLDNRNDARSRSIILERYVAL
      110      120      130      140      150      160

150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLT
      . . . . .
gi|300 ELDITTAIPLFRIRNEEVPLLMVYAQAANLHLLLRDASLFGSEWGMASSDVNYQEQEI
      170      180      190      200      210      220

210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPPNYDSRTYPI
      . . . . .
gi|300 RYTEEYSNHCVQWYNTGLNLRGTNAESWLRYNQFRDLTLGVLDLVALFPPSYDTRTYPI
      230      240      250      260      270      280

270      280      290      300      310
Cry1Ac RTVSQLTRIIYTNPLE-NFDGSFRG-----SAQIEGSI-RSPHMLDILNSITY
      . . . . .

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gi|472 LGEALSRVKRAEKKWRDKREKLQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHA
900 910 920 930 940 950

Cry1Ac 940 950 960 970 980 990
ADKRVHSIREAYLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNGLSCWN

gi|472 ADKLVHRIREAYLSELSPVPGVNAEIFEELGHIITAIISLYDARNVVKNGDFNGLTWCWN
960 970 980 990 1000 1010

Cry1Ac 1000 1010 1020 1030 1040 1050
VKGHVDVEEQNNQSRVSVLVPWEAEVSVQEVVPCGRGYILRVTAAYKEGYGEGCVTIHEIE

gi|472 VKGHVDVQ-QSHHRSDLVPEWEAEVSVQAVRVCPGCGYILRVTAAYKEGYGEGCVTIHEIE
1020 1030 1040 1050 1060 1070

Cry1Ac 1060 1070 1080 1090 1100 1110
NNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRNGYNEAPSVA----D

gi|472 NNTDELKFKNREEEVEYPTDGTCTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
1080 1090 1100 1110 1120 1130

Cry1Ac 1120 1130 1140 1150 1160 1170
YASVYEEKSYTDGRENPECFNNGYRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTF

gi|472 YKPTYEEETDVRDRNHCEYDRGYVNYPPVPAGYVTKLELYFPETDVTWIEIGETEGKF
1140 1150 1160 1170 1180 1190

Cry1Ac 1180
IVDSVELLLMEE

gi|472 IVDSVELLLMEE
1200

>>gi|21713534|emb|CAD38220.1| unnamed protein product [s (1207 aa)
initn: 3624 initl: 1837 opt: 2661 Z-score: 3127.5 bits: 590.7 E(): 2.8e-165
Smith-Waterman score: 4169; 57.107% identity (77.496% similar) in 1182 aa overlap
(55-1182:46-1207)

Cry1Ac 30 40 50 60 70 80
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQWDAF

gi|217 AEGNNIDPFVVSASTVQTGINIAGRILGVLGVFPAGQLASFYSFLVWELWP-RGRDQWEIF
20 30 40 50 60 70

Cry1Ac 90 100 110 120 130 140
LVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNIPALREEMRIQFND

gi|217 LEHVEQLINQITENARNALTARLQGLGDSFRAYQOSLEDWLENRDDARTRSVLYTQYIA
80 90 100 110 120 130

Cry1Ac 150 160 170 180 190 200
MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDL

gi|217 LELDFLNAMPLFAIRNQEVPLLMVYAQANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
140 150 160 170 180 190

Cry1Ac 210 220 230 240 250 260
TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYP

gi|217 VERTRDYSYCVWEYNTGLNSLRGTNAASWVRYNQFRDLTLGLVLDLVALFPSYDTRTYP
200 210 220 230 240 250

Cry1Ac 270 280 290 300 310
IRTVSOLTRREIYTNPVLE-----NFDGSRFRGSAQGIIEGS-IRSPHMLDILNSITIIYT

gi|217 INTSAQLTREVYTDIAGTGVNMAASMNWYNNNAPSFAIEAAAIRSPHLLDFLEQLTIFFS
260 270 280 290 300 310

Cry1Ac 320 330 340 350 360
DAHRGEY-----YWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTL

gi|217 ASSRWSNTRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
320 330 340 350 360 370

Cry1Ac 370 380 390 400 410
SST-----LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV--DSLDEIP

gi|217 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLGLQKDSSETELP
380 390 400 410 420

Cry1Ac 420 430 440 450 460 470
PQNNVPPRQGFHSHLRSVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI

gi|217 PETTERPNYESYSHRLSHIGILQ-----SRVNVVYVSWTHRSADRNTTIGPNRITQI
430 440 450 460 470 480

Cry1Ac 480 490 500 510 520 530
PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY

gi|217 PMVKASELPQGTIVVRGPGFTGGDILRRNTTGG---FGPIRVTVNGPLTQ-RYRIGFRY
490 500 510 520 530

Cry1Ac 540 550 560 570 580 590
ASVTPIHNLVNVWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFN-SSLGNIV--GVR

gi|217 ASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAPFTTPTFTQIQDIIRTSIQ
540 550 560 570 580 590

Cry1Ac 600 610 620 630 640 650
NFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS

gi|217 GLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
600 610 620 630 640 650

Cry1Ac 660 670 680 690 700
NLVTYLSDFECLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQP-----

gi|217 NLVACLSDFECLDEKRELESEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
660 670 680 690 700 710

Cry1Ac 710 720 730 740 750
-----ERWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFATRYQL

gi|217 IHEQSEHGWSGENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESEKAYTRYQL
720 730 740 750 760 770

Cry1Ac 760 770 780 790 800 810
RGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHEWNPDL



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Cry1Ac  NLVVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP-----
      . . . . .
gi |128  NLVACLSEDFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
      660      670      680      690      700      710

      710      720      730      740      750
Cry1Ac  -----ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQL
      . . . . .
gi |128  IHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGSELKAYTRYQL
      720      730      740      750      760      770

      760      770      780      790      800      810
Cry1Ac  RGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL
      . . . . .
gi |128  RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDL
      780      790      800      810      820      830

      820      830      840      850      860      870
Cry1Ac  DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVWVFKIKTQDGHARLGNLEFLEEKPL
      . . . . .
gi |128  DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGWVWVFKIKTQEGHARLGNLEFIEEKPL
      840      850      860      870      880      890

      880      890      900      910      920      930
Cry1Ac  VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHA
      . . . . .
gi |128  LGEALSrvKRAEKKWRDKREKLQLETKRvYTEAKEAVDALFVDSQYDRLQADTNIGMIHA
      900      910      920      930      940      950

      940      950      960      970      980      990
Cry1Ac  ADKRVHSIREAYLPELSVIPGVNAEIFEELGRIPTAFSLYDARNVIKNGDFNNGLSWCWN
      . . . . .
gi |128  ADKLVHRIREAYLSELVPIPGVNAEIFEELGHIITAIISLYDARNVVKNGDFNNGLTWCWN
      960      970      980      990      1000     1010

      1000     1010     1020     1030     1040     1050
Cry1Ac  VKGHVDVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTIHEIE
      . . . . .
gi |128  VKGHVDVQ-QSHHRSDLVIPWEAEVSVQAVRVCPGCGYILRVTAAYKEGYGEGCVTIHEIE
      1020     1030     1040     1050     1060     1070

      1060     1070     1080     1090     1100     1110
Cry1Ac  NNTDELKFSNcVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVPA----D
      . . . . .
gi |128  NNTDELKfKNREEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYVDVTTASVN
      1080     1090     1100     1110     1120     1130

      1120     1130     1140     1150     1160     1170
Cry1Ac  YASVYEEKSYTDGRRNPCEFNrgYrdYtPLVgYvTKeLeyFPeTdkVwIeIgeTegTF
      . . . . .
gi |128  YKPTYEEETyTDVRRDNHCEYDRGYvNYPpVpAgYvTKeLeyFPeTdTvwIeIgeTegKF
      1140     1150     1160     1170     1180     1190

      1180
Cry1Ac  IVDSVELLLMEE
      . . . . .
gi |128  IVDSVELLLMEE
      1200

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>>gi|2095428|gb|AAB57610.1|I42023 Sequence 7 from patent (1207 aa)
      initn: 3624 init1: 1837 opt: 2661 Z-score: 3127.5 bits: 590.7 E(): 2.8e-165
      Smith-Waterman score: 4169; 57.107% identity (77.496% similar) in 1182 aa overlap
      (55-1182:46-1207)

      30      40      50      60      70      80
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIGIFGPSQWDAF
      . . . . .
gi |209  AEGNNIDPFVSASTVQTGINIAGRILGLVGLVFPAGQLASFYSFLVGLWLP-RGRDQWEIF
      20      30      40      50      60      70

      90      100     110     120     130     140
Cry1Ac  LVQIEQLINQRIIEFARNQAIISREGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
      . . . . .
gi |209  LEHVEQLINQQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIA
      80      90      100     110     120     130

      150     160     170     180     190     200
Cry1Ac  MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDL
      . . . . .
gi |209  LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRERQ
      140     150     160     170     180     190

      210     220     230     240     250     260
Cry1Ac  TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTYTP
      . . . . .
gi |209  VERTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNQFRRLDTLGLVLDLVALFPYSYDTRTYTP
      200     210     220     230     240     250

      270     280     290     300     310
Cry1Ac  IRTVSQLTREIYTNPVLE-----NFDGSFRGSAQGIEGS-IRSPHMLDILNSITIYT
      . . . . .
gi |209  INTSAQLTREVYTDAGATGVNMASMNWYNNNAPSFAIEAAAIRPHLLDFLEQLTIFPS
      260     270     280     290     300     310

      320     330     340     350     360
Cry1Ac  DAHRGEY-----YWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTL
      . . . . .
gi |209  ASSRWSNTRHMTYWRGHTIQSRPIG--GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
      320     330     340     350     360     370

      370     380     390     400     410
Cry1Ac  SST-----LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVTV--DSLDEIP
      . . . . .
gi |209  SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLQLKDSSETELP
      380     390     400     410     420

      420     430     440     450     460     470
Cry1Ac  PQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQI
      . . . . .
gi |209  PETTERPNYESYSHRSLSHIGIILQ-----SRVNVVSVWTHRSADRNTTIGPNRITQI
      430     440     450     460     470     480

      480     490     500     510     520     530
Cry1Ac  PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY
      . . . . .
gi |209  PMVKASELPQGTTVVVRGPGFTGGDLVRLNTTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      490     500     510     520     530

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540      550      560      570      580      590
Cry1Ac ASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
gi|209 ASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQ
540      550      560      570      580      590

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|209 GLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
600      610      620      630      640      650

660      670      680      690      700
Cry1Ac NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----
gi|209 NLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
660      670      680      690      700      710

710      720      730      740      750
Cry1Ac -----ERGWGSGTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAFTRYQL
gi|209 IHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGSELKAYTRYQL
720      730      740      750      760      770

760      770      780      790      800      810
Cry1Ac RGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|209 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCEPNCAPHFEWNPDL
780      790      800      810      820      830

820      830      840      850      860      870
Cry1Ac DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPL
gi|209 DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGVVWVIFKIKTQEGHARLGNLEFLEEKPL
840      850      860      870      880      890

880      890      900      910      920      930
Cry1Ac VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHA
gi|209 LGEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIGMIHA
900      910      920      930      940      950

940      950      960      970      980      990
Cry1Ac ADKRVHSIREAYLPELSVIPGVNAAIFFEELEGRIPTAFSLYDARNVIKNGDFNGLSCWN
gi|209 ADKLVHRIREAYLSELVPIPGVNAEIFEELEGHIIITAFSLYDARNVVKNGDFNGLTWCWN
960      970      980      990      1000      1010

1000     1010     1020     1030     1040     1050
Cry1Ac VKGHVDVEEQNQRSVLVPEWEAEVSVQEVVCPGRGYILRVVTAYKEGYGEGCVTIHEIE
gi|209 VKGHVDVQ-QSHHRSDLVPIPEWEAEVSAVRVCPGCGYILRVVTAYKEGYGEGCVTIHEIE
1020     1030     1040     1050     1060     1070

1060     1070     1080     1090     1100     1110
Cry1Ac NNTDELKFSNCVEEIEYPNNTVTCTNDYTVNQEYEG--GAYTSRNRGYNEAPSVA----D
gi|209 NNTDELKFKNREEEVYPTDTGTCNDYTAHQGTAGCADACNSRNGAYEDAYEVDVTTASVN
1080     1090     1100     1110     1120     1130

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1120     1130     1140     1150     1160     1170
Cry1Ac YASVYEEKSYTDGRRENPCFEFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTF
gi|209 YKPTYEEETYTDDRNDNHCEYDRGVVNYPPVPAGYVTKELEYFPETDVTWIEIGETEGKF
1140     1150     1160     1170     1180     1190

1180
Cry1Ac IVDSVELLLMEE
gi|209 IVDSVELLLMEE
1200

>>gi|126566926|gb|ABO20894.1| insecticidal protein Cry1B (1228 aa)
initn: 3624 initl: 1837 opt: 2661 Z-score: 3127.4 bits: 590.7 E(): 2.8e-165
Smith-Waterman score: 4169; 57.107% identity (77.496% similar) in 1182 aa overlap
(55-1182:67-1228)

30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAG---FVLGLVDIIWGFPSQWDAF
gi|126 AEGNNIDPFVSASTVQTGINIAGRILGVLVGVPFAGQLASFYSFLVGELWP-RGRDQWEIF
40      50      60      70      80      90

90      100     110     120     130     140
Cry1Ac LVQIEQLINQRIEAFARNQAIISRLGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
gi|126 LEHVEQLINQQTENARNTALARLQGLGDSFRAYQQSLEDWLENRDARTRSVLYTQYIA
100     110     120     130     140     150

150     160     170     180     190     200
Cry1Ac MNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDL
gi|126 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
160     170     180     190     200     210

210     220     230     240     250     260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYP
gi|126 VERTRDYSDYCVWEYNTGLNSLRGTNAASWVRYNQFRRDLTLGVLDLVALFPPSYDTRTYP
220     230     240     250     260     270

270     280     290     300     310
Cry1Ac IRTVSQLTREIYTNPVE-----NFDGSFRGSAQGIEGS-IRSPHMLDILNSITIIYT
gi|126 INTSAQLTREVYTDAGATGVNMASMNWYNNNAPSFAIEAAAIRSPHLLDFLEQLTIFPS
280     290     300     310     320     330

320     330     340     350     360
Cry1Ac DAHRGEY----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTL
gi|126 ASSRWSNTRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
340     350     360     370     380     390

370     380     390     400     410
Cry1Ac SST-----LYRRFPNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV--DSLDEIP
gi|126 SYAGVLLWGIYLEPIH-GVPTVRFNFNTPQNISDRGTANY-SQPYESPGLQKDSSETELP
400     410     420     430     440

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420      430      440      450      460      470
Cry1Ac PQNNNVPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
gi|126 PETTERPNYESYSHRLSHIGIILQ-----SRVNVVYVSWTHRSADRTNTIGPNRITQI
450      460      470      480      490      500

480      490      500      510      520      530
Cry1Ac PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRVRY
gi|126 PMVKASELPQGGTTVVRGPGFTGGDILRRINTGG---FGPIRVTVNGPLTQ-RYRIGFRY
510      520      530      540      550

540      550      560      570      580      590
Cry1Ac ASVTPIHNLNVNMGNSIFSNVTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
gi|126 ASTVDFDFVSRGGTTVNNFRFLRMTNNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQ
560      570      580      590      600      610

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVS
gi|126 GLSGNGEYVIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
620      630      640      650      660      670

660      670      680      690      700
Cry1Ac NLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----
gi|126 NLVACLSDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
680      690      700      710      720      730

710      720      730      740      750
Cry1Ac -----ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLKAFTRYQL
gi|126 IHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQL
740      750      760      770      780      790

760      770      780      790      800      810
Cry1Ac RGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|126 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRGCEPNRCAPHFEWNPDL
800      810      820      830      840      850

820      830      840      850      860      870
Cry1Ac DCSCRDGEKCAHSHHFFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFIEEKPL
gi|126 DCSCRDGEKCAHSHHFFSLDIDVGCTDLHENLGVVVFVKIKTQEGHARLGNLEFIEEKPL
860      870      880      890      900      910

880      890      900      910      920      930
Cry1Ac VGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDALFVNSQYDQLQADTNAMIHA
gi|126 LGEALSRVKRAEKKWRDKREKLELQLETKRVYTEAKEAVDALFVDSQYDRLQADTNIGMIHA
920      930      940      950      960      970

940      950      960      970      980      990
Cry1Ac ADKRVSIREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWN
gi|126 ADKLVHRIREAYLSELVPIGVNAEIFEELEGHIIITAIISLYDARNVVKNGDFNNGLTCWN

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980      990      1000      1010      1020      1030
Cry1Ac VKGHVDVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILRVYAYKEGYEGECVTTIHEIE
gi|126 VKGHVDVQ-QSHHRSDLVIPEWEAEVSVQAVRVCPGCGYILRVYAYKEGYEGECVTTIHEIE
1040      1050      1060      1070      1080      1090

1060      1070      1080      1090      1100      1110
Cry1Ac NNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVA----D
gi|126 NNTDELKFKNREEEVYPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
1100      1110      1120      1130      1140      1150

1120      1130      1140      1150      1160      1170
Cry1Ac YASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTF
gi|126 YKPTYEEETDVRDNDHCEYDRGVVNYPPVPAGYVTKELEYFPETDTVWIEIGETEGKF
1160      1170      1180      1190      1200      1210

1180
Cry1Ac IVDSVELLLMEE
gi|126 IVDSVELLLMEE
1220

>>gi|1200002|emb|CAA65003.1| cry1Ba2 [Bacillus thuringie (1228 aa)
initn: 3625 initl: 1837 opt: 2661 Z-score: 3127.4 bits: 590.7 E(): 2.8e-165
Smith-Waterman score: 4170; 57.107% identity (77.580% similar) in 1182 aa overlap
(55-1182:67-1228)

30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF
gi|120 AEGNNIDPFVSASTVQTGINIAGRILGVLGVFPAGQLASFYSFLVGLWP-RGRDQWEIF
40      50      60      70      80      90

90      100      110      120      130      140
Cry1Ac LVQIEQLINQRIEFPARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
gi|120 LEHVEQLINQITENARNTALARLQGLGDSFRAYQSSLEDWLENRDDARTRSVLHTQYIA
100      110      120      130      140      150

150      160      170      180      190      200
Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDL
gi|120 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
160      170      180      190      200      210

210      220      230      240      250      260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYP
gi|120 VERTRDYSYCVWEYNTGLNSLRGTNAASWVRYNQFRDLTLGVLDLVALFSPYDTRTYP
220      230      240      250      260      270

270      280      290      300      310
Cry1Ac IRTVSQLTREIYTNPVLE-----NFDGSRGSAQGIEGS-IRSPHLMIDLNSITIYT
gi|120 INTSAQLTRREVYTDIAGTGVNMAASMNWYNNAPSFSALAEAAAIRSPHLLDFLEQLTIFS

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gi|580 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
      160      170      180      190      200      210
Cry1Ac 210      220      230      240      250      260
      TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYP
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 VERTRDYSYDVCWEYNTGLNSLRGTNAASWVRYNQFRDLTLGLVLDLVALFSPYDTRTYT
      220      230      240      250      260      270
Cry1Ac 270      280      290      300      310
      IRTVSQLTREIYTNPLE-----NFDGSGFRGSAQGLEGS-IRSPHMLDILNSITTYT
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 INTSAQLTREVYTDAGATGVNMMASMNWYNNAPSFSASEAAAIRSPHLLDFLEQLTIFS
      280      290      300      310      320      330
Cry1Ac 320      330      340      350      360
      DAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTL
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 ASSRWSNTRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
      340      350      360      370      380      390
Cry1Ac 370      380      390      400      410
      SST-----LYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQGTV--DSLDEIP
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLQLKDSSETELP
      400      410      420      430      440
Cry1Ac 420      430      440      450      460      470
      PQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 PETTERPNYESYSHRLSHGIIILQ-----SRVNVVYVSWTHRSADRNTTIGPNRITQI
      450      460      470      480      490      500
Cry1Ac 480      490      500      510      520      530
      PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGIEVPIHFPSTSTRYRVRY
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 PMVKASELPQGTTVVRGPGFTGGDILRRINTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      510      520      530      540      550
Cry1Ac 540      550      560      570      580      590
      ASVTPIHNLVNVWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT-SSLGNIV--GVR
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 ASTVDFDFVSRGGTIVNNFRFLRMTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQ
      560      570      580      590      600      610
Cry1Ac 600      610      620      630      640      650
      NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 GLSGNGEVIYDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
      620      630      640      650      660      670
Cry1Ac 660      670      680      690      700
      NLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP-----
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 NLVACLSDDEFCLDEKRELLEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
      680      690      700      710      720      730
Cry1Ac 710      720      730      740      750
      -----ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQL

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      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 IHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECPTLYLQKIGSESEKAYTRYQL
      740      750      760      770      780      790
Cry1Ac 760      770      780      790      800      810
      RGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDL
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFENWNPDL
      800      810      820      830      840      850
Cry1Ac 820      830      840      850      860      870
      DCSCRDGEKCAHSHHSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPL
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 DCSCRDGEKCAHSHHSLDIDVGCTDLHENLGVVWVFKIKTQEGHARLGNLEFIEEKPL
      860      870      880      890      900      910
Cry1Ac 880      890      900      910      920      930
      VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHA
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 LGEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHA
      920      930      940      950      960      970
Cry1Ac 940      950      960      970      980      990
      ADKRVHSIREAYLPELSPVIGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWCWN
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 ADKLVRHIREAYLSELVPIGVNAEIFEELGHIITAIISLYDARNVVKNGDFNNGLTCWN
      980      990      1000      1010      1020      1030
Cry1Ac 1000      1010      1020      1030      1040      1050
      VKGHVDVEEQNQSRVSLVPEWEAEVQEVVPCGRGYILRVYAYKEGYEGECVTIHEIE
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 VKGHVDVQ-QSHHRSDLVPEWEAEVQAVRVCPCGCGYILRVYAYKEGYEGECVTIHEIE
      1040      1050      1060      1070      1080      1090
Cry1Ac 1060      1070      1080      1090      1100      1110
      NNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVA---D
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 NNTDELKFKNREEEYVPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
      1100      1110      1120      1130      1140      1150
Cry1Ac 1120      1130      1140      1150      1160      1170
      YASVYEEKSYTDGRRENPCFNRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTF
      : : : : : : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|580 YKPTYEEETYTDVRRDNHCEYDRGVVNYPPVPAGYVTKLEYFPETDKVWIEIGETEGKF
      1160      1170      1180      1190      1200      1210
Cry1Ac 1180
      IVDSVELLLMEE
      : : : : : : : : : :
gi|580 IVDSVELLLMEE
      1220
>>gi|14486714|gb|AAK63251.1|AF368257_1 Cry1Ba [Bacillus (1228 aa)
      initn: 3624 initl: 1837 opt: 2661 Z-score: 3127.4 bits: 590.7 E(): 2.8e-165
      Smith-Waterman score: 4159; 57.022% identity (77.496% similar) in 1182 aa overlap
      (55-1182:67-1228)
      30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQLLSEFVEGAG---FVLGLVDIIGWIFGSPQWDAF

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:: : : : : : : : : :
gi|144 AEGNNIDPFVSASTVQTGINIAGRILGLVGVFAGQLASFYSFLVGLWLP-RGRDQWEIF
      40      50      60      70      80      90
Cry1Ac 90      100     110     120     130     140
LVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 LEHVEQLINQKITENARNNTALARLQGLGDSFRAYQOSLEDWLENRDDARTRSVLYTQYIA
      100     110     120     130     140     150
Cry1Ac 150     160     170     180     190     200
MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
      160     170     180     190     200     210
Cry1Ac 210     220     230     240     250     260
TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 VERTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNQFRDLTLGLVLDLVALFPSYDTRTYP
      220     230     240     250     260     270
Cry1Ac 270     280     290     300     310     320     330
IRTVSQLTREIYTNPVLE-----NFDGSGFRGSAQIEGS-IRSPHLMIDLNSITITYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 INTSAQLTREYVTDIAGATGVNMMASMNWYNNAPSFSAIEAAAIRSPHLLDFLEQLTIFS
      280     290     300     310     320     330
Cry1Ac 320     330     340     350     360
DAHRGEY----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 ASSRSWNRHMTYWRGRTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
      340     350     360     370     380     390
Cry1Ac 370     380     390     400     410
SST-----LYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPYSAVYRKSQGTV--DSLDEIP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLQLKDSSETLP
      400     410     420     430     440
Cry1Ac 420     430     440     450     460     470
PQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 PETERPNYESYSHRLSHIGIILQ-----SRVNVVYSWTHRSADRTNTIGPNRITQI
      450     460     470     480     490     500
Cry1Ac 480     490     500     510     520     530
PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 PMVKASELPQGTTVVRGPGFTGGDILRRINTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      510     520     530     540     550
Cry1Ac 540     550     560     570     580     590
ASVTPIHLLNVNMGNSSIFSNTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 ASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRATTPFTTQIQDIIRTSIQ
      560     570     580     590     600     610
Cry1Ac 600     610     620     630     640     650

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Cry1Ac NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 GLSGNGEVYIDKLEIIPVTATFEAEYDLERAQAVNALFTNTNPRRLKTDVTDYHIDQVS
      620     630     640     650     660     670
Cry1Ac 660     670     680     690     700
NLVTVLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQP-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 NLVACLSDDEFCLDEKRELESEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
      680     690     700     710     720     730
Cry1Ac 710     720     730     740     750
-----ERGWGGSTGITIQGGDDVFKENYVTLVSGTFDECYPTYLYQKIDESKLFKAFTRYQL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 IHEQSEHGWWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGESLKYTRYQL
      740     750     760     770     780     790
Cry1Ac 760     770     780     790     800     810
RGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDL
      800     810     820     830     840     850
Cry1Ac 820     830     840     850     860     870
DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGVVWVIFKIKTQEGHARLGNLEFLEEKPL
      860     870     880     890     900     910
Cry1Ac 880     890     900     910     920     930
VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 LGEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHA
      920     930     940     950     960     970
Cry1Ac 940     950     960     970     980     990
ADKRVHSIREAYLPELSVIPGVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 ADKLVHRIREAYLSELVPIPGVNAEIFEELEGGHITTAISLYDARNVVKNGDFNNGLTCWN
      980     990     1000    1010    1020    1030
Cry1Ac 1000    1010    1020    1030    1040    1050
VKGHVDVEEQNNQQRSLVVPWEAEVSVQVRRVCPGRGYLLRVITAYKEGYEGECVTTIHEIE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 VKGHVDVQ-QSHHRSDLVIPWEAEVSVQAVRVCPCGCGYLLRVITAYKEGYEGECVTTIHEIE
      1040    1050    1060    1070    1080    1090
Cry1Ac 1060    1070    1080    1090    1100    1110
NNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVA----D
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 NNTDELKFKNREEEVYPTDTGTCDNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
      1100    1110    1120    1130    1140    1150
Cry1Ac 1120    1130    1140    1150    1160    1170
YASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLEYFPETDKVWVIEIGETEGTF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|144 YKPTYEEETDVRDRNHCEYDRGVVNYPPVPAGYVTKLEYFPETDVTWVIEIGETEGKF
      1160    1170    1180    1190    1200    1210

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1180
Cry1Ac IVDSVELLMEE
: : : : :
gi|144 IVDSVELLMEE
1220

>>gi|13959051|gb|AAK51084.1|AF363025_1 delta-endotoxin C (1228 aa)
  initn: 3625 initl: 1837 opt: 2661 Z-score: 3127.4 bits: 590.7 E(): 2.8e-165
Smith-Waterman score: 4170; 57.107% identity (77.580% similar) in 1182 aa overlap
(55-1182:67-1228)

      30      40      50      60      70      80
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 AEGNNIDPFVFASTVQTGINIAGRILGLVGVFPAGQLASFYSLVWELWLP-RGRDQWEIF
      40      50      60      70      80      90

      90      100     110     120     130     140
Cry1Ac LVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADTPNAPALREEMRIQFND
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 LEHVEQLINQITENARNTALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLHTQYIA
      100     110     120     130     140     150

      150     160     170     180     190     200
Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQRWGFDAAATINSRYNDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
      160     170     180     190     200     210

      210     220     230     240     250     260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFRRELTTLTVLDIVSLFPNYSRTYP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 VERTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNQFRRLDTLGLVLDLVALFSPYDTRTYP
      220     230     240     250     260     270

      270     280     290     300     310
Cry1Ac IRTVSQTLREIYTNPVLE-----NFDGSFRGSAQGIEGS-IRSPHLMIDLNSITITYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 INTSAQLTREVYTDAIGATGVNMAAMNWNAPSFSAIEAAAIRSPHLLDFLEQLTIF'S
      280     290     300     310     320     330

      320     330     340     350     360
Cry1Ac DAHRGEY----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 ASSRWSNRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVRYTE
      340     350     360     370     380     390

      370     380     390     400     410
Cry1Ac SST-----LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYKSGTV--DSLDEIP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLQLKDSETELP
      400     410     420     430     440

      420     430     440     450     460     470
Cry1Ac PQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAPFNIIASDSITQI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 PETTERPNYESYSHRLSHIGIILQ-----SRVNVVYSWTHRSADRNTTIGPNRITQI
      450     460     470     480     490     500

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480      490      500      510      520      530
Cry1Ac PAVKGNFLFNFS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 PMVKASELPQGTTVVRGPGFTGGDILRRNTTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      510     520     530     540     550

      540     550     560     570     580     590
Cry1Ac ASVTPIHLLNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFT-SSLGNIV--GVR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 ASTVDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRAPFTTPTFTQIQDIIRTSIQ
      560     570     580     590     600     610

      600     610     620     630     640     650
Cry1Ac NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 GLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
      620     630     640     650     660     670

      660     670     680     690     700
Cry1Ac NLVTVLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQP-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 NLVACLSDDEFCLDEKRELEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
      680     690     700     710     720     730

      710     720     730     740     750
Cry1Ac -----ERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 IHEQSEHGHWGSENITIQEGNDVFKENYVTLPGTFNECYPTYLYQKIGSESKAYTRYQL
      740     750     760     770     780     790

      760     770     780     790     800     810
Cry1Ac RGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGKCGEPNRCAPHLEWNPDL
      800     810     820     830     840     850

      820     830     840     850     860     870
Cry1Ac DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGVVWVFKIKTQEGHARLGNLEFLEEKPL
      860     870     880     890     900     910

      880     890     900     910     920     930
Cry1Ac VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 LGEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHA
      920     930     940     950     960     970

      940     950     960     970     980     990
Cry1Ac ADKRVHSIREAYLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVVKNGDFNGLSCWN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 ADKLVHRIREAYLSELVPIPGVNAEIFEELGHIITAIISLYDARNVVKNGDFNGLTCWN
      980     990     1000    1010    1020    1030

      1000    1010    1020    1030    1040    1050
Cry1Ac VKGHVDVEEQNNQSRVSLVPEWEAEVSVQEVVCPGRGYLLRVYAYKEGYEGECVTIHEIE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|139 VKGHVDVQ-QSHHRSDLVIPWEAEVSVQAVRVCPCGCGYLLRVYAYKEGYEGECVTIHEIE
      1040    1050    1060    1070    1080    1090

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1060      1070      1080      1090      1100      1110
Cry1Ac  NNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVPA----D
gi|139  NNTDELKFKNREEEEVYPTDTGTTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
1100      1110      1120      1130      1140      1150

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1120      1130      1140      1150      1160      1170
Cry1Ac  YASVVEEKSYYTDGRRNCPENRNGYRDYTPLVGVYVTKLELYFPETDKVWIEIGETEGTF
gi|139  YKPTYEEETYYTDVRRDNHCEYDRGVVNYPPVPAGYVYVTKLELYFPETDVTWVIEIGETEGKF
1160      1170      1180      1190      1200      1210

```

```

1180
Cry1Ac  IVDSVELLLMEE
gi|139  IVDSVELLLMEE
1220

```

>>gi|4097878|gb|AAD10292.1| insecticidal crystal protein (1231 aa)  
 initn: 2934 initl: 1809 opt: 2652 Z-score: 3116.7 bits: 588.7 E(): 1.1e-164  
 Smith-Waterman score: 4672; 60.866% identity (79.248% similar) in 1224 aa overlap  
 (4-1182:30-1231)

```

10      20      30
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIE
gi|409  MTSNRKNEIINALSIPAVSNHSAQMDLSLDARIEDSLCIAEGNINPLV---SASTVQ
10      20      30      40      50

```

```

40      50      60      70      80      90
Cry1Ac  TGYPIDISLSLTQFLLESEFVPG-AGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIE
gi|409  TG---INIAGRILGLVGFVAGQLASFYSFLVGLWPS-GRDPWEIFLEHVQELIRQQVT
60      70      80      90      100     110

```

```

100      110      120      130      140      150
Cry1Ac  EFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFA
gi|409  ENTRNTAARLEGLGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFR
120      130      140      150      160      170

```

```

160      170      180      190      200      210
Cry1Ac  VQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVR
gi|409  IRNEEVPLLMVYAQAANLHLLLRDASLFGSEWGMASDVNYYQEQRIRYTEEYSNHCVQ
180      190      200      210      220      230

```

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220      230      240      250      260      270
Cry1Ac  WYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYT
gi|409  WYNTGLNNLRGTNAESWLRYNQFRDLTLGVLDLVALFPYDTRTYPIRTVSQLTREIYT
240      250      260      270      280      290

```

```

280      290      300      310
Cry1Ac  NPVLEN----FDGS--FRGSA---QGIEGSI-RSPHLMILNSITIIYTDHARGEY----
gi|409  DPIGRTNAPSGFASTNWFNNNAPSFAIEAAIFRPHLLDFPEQLTIYSASSRWSSTQHM
300      310      320      330      340      350

```

```

320      330      340      350      360      370
Cry1Ac  -YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLSST---LYRR
gi|409  NYWVGHRLNFRPIGGT---LNTSTQGLTNNNTSINPVTLQFTSRDVRTESNAGTNILFTT
360      370      380      390      400      410

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380      390      400      410      420      430
Cry1Ac  PFNIGINNQQLSVLDGTEFAYGTSNNLPSAVYRKSQT--VDSDLDEIPPNQNNVPRQGF
gi|409  PVN-GVPWARFNFINPQNI-YERGATTYSQPYQGVGIQLFDSETELPPETTERPNYESYS
420      430      440      450      460

```

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440      450      460      470      480      490
Cry1Ac  HRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSV
gi|409  HRLSHIGLI---IGNT---LRAPVYSWTHRSADRNTTIGPNRITQIPAVKGRFLFNGSV
470      480      490      500      510      520

```

```

500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWN
gi|409  ISGPGFTGGDVVRLNRNNGNIQNRGYIEVPIQFTSTSTRYRVRVRYASVTSIELNVNNGN
530      540      550      560      570      580

```

```

560      570      580      590      600      610
Cry1Ac  SSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGTAGVIIDRFEFIP
gi|409  SSIFTNTLPATAASLDNLQSGDFGYVEINNAFTSATGNIVGARNFNSANAEEVIIDRFEFIP
590      600      610      620      630      640

```

```

620      630      640      650      660      670
Cry1Ac  VTATLAEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRE
gi|409  VTATFEAEYDLERAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVAACLDEFCLDEKRE
650      660      670      680      690      700

```

```

680      690      700      710
Cry1Ac  LSEKVKHAKRLSDERNLLQD-----SNFKDINRQPERGWGGSTGITI
gi|409  LFEKVKYAKRLSDERNLLQDPNFTFISGQLSFASIDGQSNFTSINELSEHGWWGSENVTI
710      720      730      740      750      760

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720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|409  QEGNDVFKENYVTLPGTFNFCYPNLYQKIGESLKAAYTRYQLRGYIEDSQDLEIYLIRY
770      780      790      800      810      820

```

```

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHF
gi|409  NAKHETLDVPGTDSLWPLSVKSPIGRCGEPNRCAPHFEWNPDLDCSCRDEKCAHSHHF
830      840      850      860      870      880

```

```

840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|409  TLDIDVGCTDLHENLGVVWVFKIKTQEGYARLGNLEFIEEKPLIGALSVRKRAEKKWRD

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      890      900      910      920      930      940
Cry1Ac  900      910      920      930      940      950
KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELS
gi|409  KREKLEWETNIVYKEAKETVDALFVNSQYDQLQADTNIGMIHAADRLVHRIHEAYLPELP
      950      960      970      980      990      1000
Cry1Ac  960      970      980      990      1000      1010
VIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVDEEQQNRQSVL
gi|409  FIPGINAVIFEELENRISTAFSLYDARNVIKNGDFNNGLSWCWNVKGHVQVQ-QSHHRSDL
      1010      1020      1030      1040      1050      1060
Cry1Ac  1020      1030      1040      1050      1060      1070
VPEWEAEVSVQEVRRVCPGRGYILRVITAYKEGYGEGCVTIEHEIENNTDELKFSNCVEEVIY
gi|409  VPEWEAEVSVQAVRVCPCGRGYILRVITAYKEGYGEGCVTIEHEIENNTDELKFKNCEEEVY
      1070      1080      1090      1100      1110      1120
Cry1Ac  1080      1090      1100      1110      1120
PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVA---DYASVYEEKSYTDGRENPC
gi|409  PTDGTTCNDYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKPTYEEETVTDVRRDNHC
      1130      1140      1150      1160      1170
Cry1Ac  1130      1140      1150      1160      1170
EFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|409  EYDRGYVNYPPVAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVLELLMEE
      1180      1190      1200      1210      1220      1230
Cry1Ac  1180      1190      1200      1210      1220      1230
>>gi|22213635|gb|AAM93496.1| CryIBII [Bacillus thuringie (1231 aa)
  initn: 2934 initl: 1809 opt: 2652 Z-score: 3116.7 bits: 588.7 E(): 1.1e-164
Smith-Waterman score: 4670; 62.468% identity (80.766% similar) in 1175 aa overlap
(55-1182:72-1231)

      30      40      50      60      70      80
Cry1Ac  30      40      50      60      70      80
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPS---QWDAFL
gi|222  AEVNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFVLGELWPSGRDPWEIFL
      90      100      110      120      130      140
Cry1Ac  90      100      110      120      130      140
VQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|222  EHVEQLIRQVQVTEENTRNTAIARLEGLGRGYSYQQALETWLDNRNDARSRSIILERYVAL
      150      160      170      180      190      200
Cry1Ac  150      160      170      180      190      200
NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLT
gi|222  ELDIITTAIPLFRIRNEEVPPLMVYAQAANLHLLLRDASLFGSEWGMASSDVNQYQEQI
      210      220      230      240      250      260
Cry1Ac  210      220      230      240      250      260
RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDDIVSLFPNYSRTYPI
gi|222  RYTEEYSNHCVQWYNTGLNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPPSYDTRTYPI

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      230      240      250      260      270      280
Cry1Ac  270      280      290      300      310
RTVSQLTREIYTNPVLE-NFDGSGFRG-----SAQGIIEGSI-RSPHMLDILNSITIIY
gi|222  NTSAQLTREIYTDPIGRNTNAPSGFASTNWFNNNAPSFSFAIEAAIFRPPHLLDFPEQLTIY
      290      300      310      320      330      340
Cry1Ac  320      330      340      350      360
TDAHRGEY----YWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAQQRIVAQLGQGVYRT
gi|222  SASSRWSSTQHMMNYVWGHRLNFRPIGGT--LNTSTQGLTNNNTSINPVTLQFTSRDVYRT
      350      360      370      380      390
Cry1Ac  370      380      390      400      410
LSST---LYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQT--VDSLDEIIPP
gi|222  ESNAGTNILFTTPVN-GVPWDRFNFINPQNI-YERGATTYSQPYQGVGIQLFDSDELPP
      420      430      440      450      460      470
Cry1Ac  420      430      440      450      460      470
QNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIP
gi|222  ETTERPNYESYSHRSLSHIGLI---IGNT---LRAPVSWTHRSADRNTIGPNRITQIP
      480      490      500      510      520      530
Cry1Ac  480      490      500      510      520      530
AVKGNFLFNGSVISGPGFTGGDLVRLNNSGNNIQNRGYLEVPIHFPSTSTRYRVRVRYAS
gi|222  AVKGRFLFNGSVISGPGFTGGDVVLRNRRNGNIQNRGYLEVPIQFTSTRYRVRVRYAS
      540      550      560      570      580      590
Cry1Ac  540      550      560      570      580      590
VTFIHLNVNWNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVNRFSGT
gi|222  VTSIELNVNLGSSIFNTLPATAASLDNLQSGDFGYVEINNAFTSATNIVGARNFSAN
      600      610      620      630      640      650
Cry1Ac  600      610      620      630      640      650
AGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|222  AEVVIDRFEFIPVTATFEAEYDLERAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNMVC
      660      670      680      690      700
Cry1Ac  660      670      680      690      700
LSDEFCLDEKRELSEKVKHAKRLSDERNLLQD-----SNFKDINRQP
gi|222  LSDEFCLDEKRELSEKVKYAKRLSDERNLLQDPNFTFISGQLSFASIDGQSNFTSINELS
      710      720      730      740      750      760
Cry1Ac  710      720      730      740      750      760
ERGWGSGTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIE
gi|222  EHGWWGSENVTIQEGNDVFKENYVTLPGTFNFCYPNYLYQKIGESLQKAYTRYQLRGYIE
      770      780      790      800
Cry1Ac  770      780      790      800
DSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR

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gi|222 DSQDLEIYLIRYNAKHETLDVPGTDSLWPLSVKSPIGRCGEPNRCAPHFENWPDLDSCR
810      820      830      840      850      860

      830      840      850      860      870      880
Cry1Ac DGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEAL
.....
gi|222 DGERCAHSHHFTLDIDVGCTDLHENLGVVWVFKIKTQEGYARLGNLEFIEEKPLIGEAL
870      880      890      900      910      920

      890      900      910      920      930      940
Cry1Ac ARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRV
.....
gi|222 SRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRV
930      940      950      960      970      980

      950      960      970      980      990      1000
Cry1Ac HSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVH
.....
gi|222 HRIHEAYLPELFPFIPGINAVIFEELNRISTAFSLYDARNVIKNGDFNNGLSWVNVKGVH
990      1000      1010      1020      1030      1040

      1010      1020      1030      1040      1050      1060
Cry1Ac DVEEQNNQRSLVLPVEWAEVSVQEVVCPGRGYILRVTAAYKEGYEGCVTIHEIENNTDE
..
gi|222 DVQ-QSHRSDLVIPVEWAEVSVQEVVCPGRGYILRVTAAYKEGYEGCVTIHEIENNTDE
1050      1060      1070      1080      1090      1100

      1070      1080      1090      1100      1110
Cry1Ac LKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVA----DYASVYEE
.....
gi|222 LKFKNCEEEVPTDGTGTCNDYTAHQGT--AACNSRNAGYEDAYEVDTTASVNYKPTYEE
1110      1120      1130      1140      1150      1160

      1120      1130      1140      1150      1160      1170
Cry1Ac KSYTDGRENPECFNRYGRDYTPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVEL
.....
gi|222 ETYTDVRRDNHCEYDRGVVNYPPVPAGYVTKLEYFPETDVTWVIEIGETEGKFIIVDSVEL
1170      1180      1190      1200      1210      1220

1180
Cry1Ac LLMEE
::::
gi|222 LLMEE
1230

>>gi|146335684|gb|ABQ23438.1| Cry1B [Bacillus thuringien (1228 aa)
initn: 3593 initl: 1818 opt: 2642 Z-score: 3104.9 bits: 586.6 E(): 5e-164
Smith-Waterman score: 4138; 56.768% identity (77.327% similar) in 1182 aa overlap
(55-1182:67-1228)

      30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAG---FVLGLVDIIWGIFGSPQWDAF
:::
gi|146 AEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQLASFYSFLVGLWLP-RGRDQWEIF
40      50      60      70      80      90

      90      100      110      120      130      140
Cry1Ac LVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESPFEWADPTNPALREEMRIQFND
:

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gi|146 LEHVEQLINQITENARNTALARLQGLRHAFRAYQQSREDWLENRDDARTRRVLYTQYRA
100      110      120      130      140      150

      150      160      170      180      190      200
Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDL
..
gi|146 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLVLLRDASLFGSEFGLTSQEIQRYRYERQ
160      170      180      190      200      210

      210      220      230      240      250      260
Cry1Ac TRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYP
..
gi|146 VERTRDYSYCVWEYKTLGNSLRGTNAASWVRYNQFRDLTVGVLDLVALFSPYDTRTYP
220      230      240      250      260      270

      270      280      290      300      310
Cry1Ac IRTVSQLTREIYTNPVLE-----NFDGSFRGSAQGIEGS-IRSPHLMIDLNSITIYT
:
gi|146 INTSAQLTREVYTDIAGATGVNMARMNWNANNAPSFAIEAAAIRSPHLLDFLEQLTIFPS
280      290      300      310      320      330

      320      330      340      350      360
Cry1Ac DAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTL
:
gi|146 ASSRWSNTRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTIRFASRDVYRTE
340      350      360      370      380      390

      370      380      390      400      410
Cry1Ac SST-----LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV--DSLDEIP
:
gi|146 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQINISDRGTANY-SQPYESPLQLKDSSETELP
400      410      420      430      440

      420      430      440      450      460      470
Cry1Ac PQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
.....
gi|146 PETTERPNYESYSHRSLSHIGIILQ-----SRVNVVYVSWTHRSADRTNTIGPNRITQI
450      460      470      480      490      500

      480      490      500      510      520      530
Cry1Ac PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYR
:
gi|146 PMVKASELPQGTTVVRGPGFTGGDILLRRTNTGG---FGPIRVTVNGPLTQ-RYRIGFRY
510      520      530      540      550

      540      550      560      570      580      590
Cry1Ac ASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
.....
gi|146 ASTVDFDFVSRGGTIVNNFRFLRTMNSGDELKYGNFVRRAPFTTPTFTQIQDIRTSIQ
560      570      580      590      600      610

      600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVLDYHIDQVS
.....
gi|146 GLSGNGEVYIDKLEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
620      630      640      650      660      670

      660      670      680      690      700
Cry1Ac NLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP-----

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      ....
gi|146 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180
Cry1Ac -----ERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTLYLQKIDESKLFKAFTRYQL
gi|146 IHEQSEHGWGGSENITIQEGNDVFKENYVTLPGTFNECYPTLYLQKIGESLQKAYTRYQL
Cry1Ac RGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|146 RGYIEDSQDLEIYLIRYNAKHETLDVPGTESLWPLSVESPIGRGGEPNRCAPHLEWNPDL
Cry1Ac DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPL
gi|146 DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGVVWVFKIKTQEGHARLGNLEFLEEKPL
Cry1Ac VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHA
gi|146 LGEALSRGKRAKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIGMIHA
Cry1Ac ADKRVSIREAYLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWCWN
gi|146 ADKLVHRIREAYLSELPIPGVNAEIFEELGHIITAIISLYDARNVVKNGDFNNGLTWCWN
Cry1Ac VKGHVDVEEQNNQRSVLLVPEWAEVSVQEVVRCVPGRYILRVTAAYKEGYGEGCVTIHEIE
gi|146 VKGHVDVQ-QSHHRSDLVPEWAEVSVQAVRVCPGCGYILRVTAAYKEGYGEGCVTIHEIE
Cry1Ac NNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRGYNEAPSVA----D
gi|146 NNTDELKFKNREEEVEVPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
Cry1Ac YASVYEEKSYTDGRENPCFNRGYRDYTPLPVGYVTKLEYFPETDKVWVIEIGETEGTF
gi|146 YKPTYEBEYTDVRRDNHCEYDRGYVNYPPVAGYVTKLEYFPETDKVWVIEIGETEGTF
Cry1Ac IVDSVELLLMEE
gi|146 IVDSVELLLMEE
      1220
>>gi|119087867|gb|ABL60921.1| Cry1B [Bacillus thuringien (1228 aa)

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initn: 3581 init1: 1819 opt: 2632 Z-score: 3093.1 bits: 584.4 E(): 2.3e-163
Smith-Waterman score: 4126; 56.684% identity (77.157% similar) in 1182 aa overlap
(55-1182:67-1228)
      30 40 50 60 70 80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWIGIFGPSQWDAF
gi|119 AEGNNIDPFVFASTVQTGINIAGRILGLVGVPPFAGQLASFYSFLVGLWP-RGRDQWEIF
      40 50 60 70 80 90
Cry1Ac LVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
gi|119 LEHVEQLINQITENARNALARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLYTQYIA
      100 110 120 130 140 150
Cry1Ac MNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDL
gi|119 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQ
      160 170 180 190 200 210
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYP
gi|119 VERTRDYSYCVIEWYNTGLNSLRGTNAASWVRYNQFRRLTLGLVGLVALFSPSYDTRTYP
      220 230 240 250 260 270
Cry1Ac IRTVSQLTREIYTNPVLE-----NFDGSFRGSAQGIEGS-IRSPHMLDILNSITIYT
gi|119 INTSAQLTREVYTDIGATGVNMAASMNWYNNNAPSFAIEAAAIRSPHLLDFLEQLTIFPS
      280 290 300 310 320 330
Cry1Ac DAHRGEY-----YWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTL
gi|119 ASSRWSNTRHMTYWRGHTIQSRPIG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
      340 350 360 370 380 390
Cry1Ac SST-----LYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIP
gi|119 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPGLQKDSSETELP
      400 410 420 430 440
Cry1Ac PQNNVPPRQGFVSHRSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQI
gi|119 PETTERPNYESYSHRSLHIGIILQ-----SRVNVVYVSWTHRSADRINTIGPNRITQI
      450 460 470 480 490 500
Cry1Ac PAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRY
gi|119 PMVKASELPQGTTVVRGPGFTGGDILRRNTTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      510 520 530 540 550
      540 550 560 570 580 590

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Cry1Ac ASVTP IHLNVN WGNSSIFSNTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
gi|119 ASTVDFDF FASRGGTTVNNFRFLRMTMNSGDELKYGNFVRAFTTPTFTQIQNIIRTSIQ
560 570 580 590 600 610

600 610 620 630 640 650
Cry1Ac NFSGTAGVIIDRFEPVATATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|119 GLSGNGEVYIDKIEIIPVTATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVS
620 630 640 650 660 670

660 670 680 690 700
Cry1Ac NLVTVLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQP-----
gi|119 NLVACLSDDEFCLDEKRELESEKVKYAKRLSDERNLLQDPNFTSINKQPDFISTNEQSNFTS
680 690 700 710 720 730

710 720 730 740 750
Cry1Ac -----ERGWGGSTGITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQL
gi|119 IHEQSEHGWWGSENITIQEGNDVSKENYVTLPGTFNECYPTYLYQKIGESELKAYTRYQL
740 750 760 770 780 790

760 770 780 790 800 810
Cry1Ac RGYIEDSQDLEIYSIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDL
gi|119 EGYIEDSQDLEIYLIRYNKAKHETLDVPGTESLWPLSVESPIGRCGEPNRCAPHFEWNPDL
800 810 820 830 840 850

820 830 840 850 860 870
Cry1Ac DCSCRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLEEKPL
gi|119 DCSCRDGEKCAHSHHFLSLDIDVGCTDLHENLGWVVIKIKTQEGHARLGNLEFIEEKPL
860 870 880 890 900 910

880 890 900 910 920 930
Cry1Ac VGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHA
gi|119 LGEALSRVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIGMIHA
920 930 940 950 960 970

940 950 960 970 980 990
Cry1Ac ADKRVHSIREAYLPELSVIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWN
gi|119 ADKLVHRIREAYLSELPVIGVNAALFEELEGGHIIITAFSLYDARNVVKNGDFNNGLTWCWN
980 990 1000 1010 1020 1030

1000 1010 1020 1030 1040 1050
Cry1Ac VKGHVDVEEQNNQRSVLVPEWEAEVSVQEVRCVPGRYILRVTAAYKEGYGEGCVTIHEIE
gi|119 VKGHVDVQ-QSHHRSVLVPEWEAEVSVQAVRVCPCGYILSVTAAYKEGYGEGCVTIHEIE
1040 1050 1060 1070 1080 1090

1060 1070 1080 1090 1100 1110
Cry1Ac NNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYG--GAYTSRNRNGYNEAPSVA----D
gi|119 NNTDELKFKNREEEIVPTDTGTCNDYTAHQGTAGCADACNSRNAGYEDAYEVDTTASVN
1100 1110 1120 1130 1140 1150

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1120 1130 1140 1150 1160 1170
Cry1Ac YASVYEEKSYTDGRRENPCFENRGRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTF
gi|119 YKPTVEEETDVRDRNHCEYDRGVVNYPPVPAGYVTKLEYFPETDVTWVIEIGETEGKF
1160 1170 1180 1190 1200 1210

1180
Cry1Ac IVDSVELLLMEE
gi|119 MVDSVELLLMEE
1220

>>gi|436841|gb|AAA21121.1| CryIII delta-endotoxin (1138 aa)
initn: 1863 init1: 995 opt: 2606 Z-score: 3063.0 bits: 578.7 E(): 1.1e-161
Smith-Waterman score: 2689; 41.542% identity (67.081% similar) in 1206 aa overlap
(8-1182:29-1136)

10 20 30
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTP
gi|436 MNLNLLGGYEDSNRNLNNSLYPTQKALSPSLKNMNYQDFLSITERE--QPEALASGNTA
10 20 30 40 50

40 50 60 70 80 90
Cry1Ac IDISLSLTQFLSEF-VPGAGFVLGLVDI IWGIFGPSQ--WD AFLVQIEQLINQRIEEF
gi|436 INTVVSVTGATLSALGVPGASFITNFYFKITGLLWPHDKNIWDEFMTEVETLLEQKIEQY
60 70 80 90 100 110

100 110 120 130 140 150
Cry1Ac ARNQAISRLGLESLNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|436 ARNKALAELEGLGNLTIYQQALEDWLNPPDDPATITRVIDRFRILDALFESYMPFSRVA
120 130 140 150 160 170

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|436 GYEIPLLVYVQAANLHLLALLRDSTLYGDKWEFTQNNIEENYRQKKHISEYSNHCVKQY
180 190 200 210 220 230

220 230 240 250 260 270
Cry1Ac NTGLERVWGPDSRDWIRYNQFRRELTLTVDLIVSLFPNYSRTYPIRTVSQTLREIYTNP
gi|436 NSGLSRLNGSTYEQWINYRFRREMILMVLVDIAAVFPIYDPRMYSMETSTQTLTREVYTD
240 250 260 270 280 290

280 290 300 310 320
Cry1Ac VLENFDGSRFG-SAQGIEGS-IRSPHMDILNSITITYTDAHRGE-----YYWSGHQI
gi|436 ISLSISNPGIGSPFSQMENTAIRTPLHVDYLDDELVIYTSKYKAFSHEIQPDLFYWSAHKV
300 310 320 330 340 350

330 340 350 360 370 380
Cry1Ac MASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRPFNIGINNQQ
gi|436 SFKQSEQSN-LYTTGIYGKTSYIISGAYSFR-GNDIYRTLAAAPSVVVYPTQNYGVEQV
360 370 380 390 400 410

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390      400      410      420      430      440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSG---TVDSLDEIIPPQNNVPPROGFSHRLSHVSMF
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 -----EF-YGVKGVH---YRGDNKYDLTYDSIDQLPPDGE--PIHEKYTHRLCHATAI
      420      430      440      450      460

      450      460      470      480      490
Cry1Ac RSGFNSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTG
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 SKSTPDYDNATI--PIFSWTHRSAEYYNRIYPNKITKIPAVKMYKLGDTSTVVKGPGFTG
      470      480      490      500      510      520

      500      510      520      530      540      550
Cry1Ac GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRYASVTPIHNLVNWGNSSI-----
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 GDLVLRKGSNGYI---GDIKATVNSP-LSQNYRVRVRYATNVSGQFNV-YINDKITLQRK
      530      540      550      560      570

      560      570      580      590      600      610
Cry1Ac FSNTVPATATSLDNLQSSDFGYFESANA--FTSSLGNI-VGVRNFSGTAGVIIDRFEFIP
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 FQNTVETIGEGKD-LTYGSFGYIEYSTTIQFPDKHPKITLHLSDLNNSFFYVDSIEFIP
      580      590      600      610      620      630

      620      630      640      650      660      670
Cry1Ac VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 VDVNVDEKEKLEKAQKAVNTLTFTE-GRNALQKDVTDYKVDQVSIIVDCISGDLYPNEKRE
      640      650      660      670      680      690

      680      690      700      710      720      730
Cry1Ac LSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTF
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 LQNLVKYAKRLSYSRNLLEDPTFDSINSSEENGWYSGNGIVIGNGDFVFKGNYLIFSGTN
      700      710      720      730      740      750

      740      750      760      770      780      790
Cry1Ac DECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSSLWPL
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 DTQYPTYLYQKIDESKLFKEYTRYKLGFISSQDLEAVYIRYDAKHRTLVDV--SDNLLP-
      760      770      780      790      800      810

      800      810      820      830      840
Cry1Ac SAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSHHFFSLDIDVCGCTDLNEDL
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 -DILPENTCGEPNRCQAQYLDENPSSCQDQD--ILSDSHSFLNIDIGSINHNNEL
      820      830      840      850      860

      850      860      870      880      890      900
Cry1Ac GVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKE
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 GIWVLFKISTLEGYAKFGNLEVIDGPGVIGEALARVKRQETKWRNKLAQLTTETQAIYTR
      870      880      890      900      910      920

      910      920      930      940      950      960
Cry1Ac AKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPESLVPVGNAAIFEELEG
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 AKQALDNLFAQAQDSHLKIDVTFAEIAAARKIVQSIREAYMSWLVVPGVNHPIFTELSE
      930      940      950      960      970      980

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970      980      990      1000      1010      1020
Cry1Ac RIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLVVPEWEAEVSVQEVRV
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 RVQRAFQLYDVRNVVNRGRFLNGLSDWIVTSDVKVQEENGN-NVLVLNNWDAQVLQNVKL
      990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080
Cry1Ac CPGRGYILRVYTAYKEGYGECVTHIEIENNTDELKFSNCVVEEIIYPNNITVTCNDYTVNQE
      :::::::::::  ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 YQDRGYILRVTARKIGIGEGYITITDEEGHTVQLRFAC--EVIDASN-----
      1050      1060      1070      1080      1090

      1090      1100      1110      1120      1130      1140
Cry1Ac EYGGAYTSRRNGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYDTPLPVGYVTK
      ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|436 ----AFIS-----
      1100

      1150      1160      1170      1180
Cry1Ac ELEYPFETDKVWIEIGETEGTFIVDSVELLLMEE
      :::::::::::  :::::::::::  :::::::::::  ::
gi|436 ELEFPDTEKVVHIEIGETEGIFLVESIELFLMEELC
      1110      1120      1130

>>gi|490178|emb|CAA00646.1| toxin [Bacillus thuringiensis (1138 aa)
      initn: 1844 init1: 970 opt: 2601 Z-score: 3057.1 bits: 577.6 E(): 2.3e-161
      Smith-Waterman score: 2689; 41.591% identity (67.191% similar) in 1207 aa overlap
      (8-1182:29-1136)

      10      20      30
Cry1Ac          CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTP
      :::::::::::  :::::::::::  :::::::::::  ::
gi|490 MNLNLDGYEDSNRTLNNSLNYPTQKALSPSLKMMNYQDFLSITERE--QPEALASGNTA
      10      20      30      40      50

      40      50      60      70      80      90
Cry1Ac IDISLSLTQFLLSEF-VPGAGFVGLVLDI IWGIFGPSQ--WDAFLVQIEQLINQRIEEF
      ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|490 INTVSVTGATLSALGVPGASFITNFYLK IAGLLWPENGIWDEFMTEVEALIDQKIEEY
      60      70      80      90      100      110

      100      110      120      130      140      150
Cry1Ac ARNQAISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT'TAIPLFAVQ
      :::::::::::  :::::::::::  :::::::::::  :::::::::::  :::::::::::  ::
gi|490 VRNKAI AELDGLGSALDKYQKALADWLKQDDPEAILSVATEFRI IDSLFEPFSMP SFKVT
      120      130      140      150      160      170

      160      170      180      190      200      210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :::::::::::  :::::::::::  :::::::::::  :::::::::::  :::::::::::  ::
gi|490 GYEIPLLTYYAQAANLHLLALDRDSTLYGDKWGFTQNNIEENYRQKRISEYSDHCTKWY
      180      190      200      210      220      230

      220      230      240      250      260      270
Cry1Ac NTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQTLREIYTNP
      ::  ::  :::::::::::  :::::::::::  :::::::::::  ::
gi|490 NSGLSRLNGSTYEQWINYRFRREMILMALDLVAVFPFHDPRRYSMETSTQTLREYVYTD
      240      250      260      270      280      290

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      280      290      300      310      320
Cry1Ac VLENFDGSRG-SAQGI EGS-IRSPHLM DILNSIT IYD DAHRGE-----YYWSGHQI
: . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 VSLSISNPDIGPSFSQMENTAIRTPHLVDYLD ELYIYTSKYKAFSHEIQPDLFYWSAHKV
300      310      320      330      340      350

      330      340      350      360      370      380
Cry1Ac MASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGGQGVYRTLSS-TLYRRPFNIGINNOQL
: . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 SFKKSEQSN-LYTTGIYKGTSGYISSGAYS FPH-GNDIYRTL AAPS VVVVYPTQNYGVEQV
360      370      380      390      400      410

      390      400      410      420      430
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSG---TV DSLDEI PPQNNVPPRQGFSHRLSHVS-M
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 -----EF-YGVKGHVH---YRGDNKYD LTYDSIDQLPPDGE--PIHEKYTHRLCHATAI
420      430      440      450      460

      440      450      460      470      480      490
Cry1Ac FRSGFSNSSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPAVKGNFLFN GS-VISGPGFT
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 FKSTPDYDNATI---PIFSWTHRS AEY YNRIYPNK ITKIPAVKMYKLD DPSTVVKGPGFT
470      480      490      500      510      520

      500      510      520      530      540      550
Cry1Ac GGDVLRNLSSGNNIQNRGYIEVPIHFPST STRYRVRVRYASVTP IHLNVNWNSSNI----
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 GGDLVKRGSTGYI---GDIKATVNSP-LSQ KYRVRVRYAT NVSQGFNV-YINDKITLQT
530      540      550      560      570

      560      570      580      590      600      610
Cry1Ac -FSNTVPATATSLDNLQSSDFGYFESANA-- FTSSLGNI-VGVRNFSGTAGVIIDRFEFI
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 KFQNTVETIGEGKD-LTYGSFGYIEYSTT I QFPDEHPK I TLHLSDLSSNSSFYVDSIEFI
580      590      600      610      620      630

      620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLG LKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 PVDVNYAEKEKLEKAQKAVNTLFTE-GRN ALQKDVTDYKVDQV SILVDCISGDLYPNEKR
640      650      660      670      680      690

      680      690      700      710      720      730
Cry1Ac ELSEKVKHAKRLSDERNLLQDSNFKDINRQ PERGWGGSTGITIQGGDDVFKENYVTLSGT
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 ELQNLVKYAKRLSYSRNLLLDPTFDSINS SEENGWYGSNGVIGNGDFVFKGNYLIFS GT
700      710      720      730      740      750

      740      750      760      770      780      790
Cry1Ac FDECYPTYLYQKIDESKLFKAFTRYQLRGY IEDSQDLEIYSIRYNKAKHETVNVPGTGS LWP
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 NDTQYPTYLYQKIDESKLFKEYTRYKLGFI ESSQDLEAYVIRYDAKHRTL DV--SDNLLP
760      770      780      790      800      810

      800      810      820      830      840
Cry1Ac LSAQSPIGKCGEPNRCAP--HLEWNPDLDC SC-RDGEKCAHSHHFSLDIDVGC TDLNED
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 --DILPENTCGEPNRCAAQYLDENPSPEC SSMQDG--ILSDSHSFS LNI DTGS INHNEN

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      820      830      840      850      860
Cry1Ac LGVWVIFKIKTQDGHARLGNLEFLEEKPLVGE ALARVKRAEKKWRDKREKLEWETNIVYK
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 LGIWLWFKISTLEGYAKFGNLEVI EDGPVIG EALARVKRQETKWRNKL AQLTTETQAIYT
870      880      890      900      910      920

      910      920      930      940      950      960
Cry1Ac EAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPELSVIPGVNA AIFEELE
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 RAKQALDNLFANAQDSHLKR DVTFAEIAAARKIVQSIREAYMSWLSVVPVGNHPIFTELS
930      940      950      960      970      980

      970      980      990      1000      1010      1020
Cry1Ac GRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVL VVPEWEEVSQEV R
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 GRVQRAFQLYDVRNVVRNGRFLNGLSDW I VTS DVKVQEENGN-NVLVLNWD AQVLQNVK
990      1000      1010      1020      1030      1040

      1030      1040      1050      1060      1070      1080
Cry1Ac VCPGRGYILRV TAYKEGYEGECV T IHEIENNTDELKFSNCV EEEIYPNNVT CNDYTVNQ
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 LYQDRGYILHVTARKIGIGEGYITITDEB GHTDQLRFTAC--EEIDASN-----
1050      1060      1070      1080      1090

      1090      1100      1110      1120      1130      1140
Cry1Ac EEYGGAYTSRNRGYN EAPSPADYASVY EEKSYTDGRRENPC EFNRYR DYTPLPVGYVT
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 ----AFIS-----
1100

      1150      1160      1170      1180
Cry1Ac KELEYFPETDKVWIEIGETEGTFIVDSV ELLMEE
: : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|490 KELEFFPDTEKVHIEIGETEGIFLVESIE LFLMEELC
1110      1120      1130

>>gi|142761|gb|AAA22351.1| crystal protein (1138 aa)
initn: 1844 init1: 970 opt: 2601 Z-score: 3057.1 bits: 577.6 E(): 2.3e-161
Smith-Waterman score: 2689; 41.591% identity (67.191% similar) in 1207 aa overlap
(8-1182:29-1136)

      10      20      30
Cry1Ac CMQAMDNNPNINECIPYCNLSNPEVEVLG GERIETGYTP
: : . . . . . : : . . . . . : : . . . . .
gi|142 MNLNLDGYESNRTLNNLSNYPTQKALS PSLKNNMNYQDFLSITERE--QPEALASGNTA
10      20      30      40      50

      40      50      60      70      80      90
Cry1Ac IDISLSLTQFLLSEF-VPGAGFVLGLVDI IWGIFGPSQ---WDAFLVQIEQLINQRI EEF
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142 INTVVSVTGATLSALGVPASFITNFY LK IAGLLWPENGIWDEFMTEVEALIDQKIEEY
60      70      80      90      100      110

      100      110      120      130      140      150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREW EADPTNPALREEMRIQFNDMNSALT TAIPLFAVQ
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|142 VRNKAI AELDGLGSALDKYQKALADW LKGQDDPEAILS VATEFRIIDSLFEFSMP SFKV T

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120      130      140      150      160      170
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|142  GYEIPLLTVYAQAANLHLLALRDSTLYGDKWGFQNNIIBENYRQKKRRISEYSDHCTKWY
180      190      200      210      220      230
Cry1Ac  NTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNP
gi|142  NSGLSRLNGSTYEQWYINYNRFRREMILMALDLVAVFPFHDPRRYSMETSTQLTREVIYTD
240      250      260      270      280      290
Cry1Ac  VLENFDGSRFG-SAQGIEGS-IRSPHLMIDLNSITITYTDAHRGE-----YYWSGHQI
gi|142  VLSLSINPDIGPSFSQMENTAIRTPLHVDYLDDELYIYTSKYKAFSHEIQPDLFYWSAHKV
300      310      320      330      340      350
Cry1Ac  MASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRFPNIGINNOQL
gi|142  SFKKSEQSN-LYTTGIYKTSYISSGAYSFH-GNDIYRTLAAQSVVYVPTQNYGVEQV
360      370      380      390      400      410
Cry1Ac  SVLDGTEFAYGTSSNLPSAVYRKS-----TVDSLDEIPPQNNVPPRQGFSHRLSHVS-M
gi|142  -----EF-YGVKGVH-----YRGDNKYDLTYDSIDQLPPDGE--PIHEKYTHRLCHATAI
420      430      440      450      460
Cry1Ac  FRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNFS-VISGPGFT
gi|142  FKSTPDYDNATI---PIFSWTHRSAEYRNRIYPNKITKIPAVKMYKLDPPSTVVKPGGFT
470      480      490      500      510      520
Cry1Ac  GGDVLRNLSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSI----
gi|142  GGDLVKRGSTGYI---GDIKATVNSP-LSQKYRVRVRYATNVSGQFNV-YINDKITLQT
530      540      550      560      570
Cry1Ac  -FSNTVPATATSLDNLQSSDFGYFESANA--FTSSLGNI-VGVRNFSGTAGVIDRFEFI
gi|142  KFQNTVETIGEGKD-LTYGSFGYIEYSTTIQFPDEHPKILHLSDLSNNSFFYVDSIEFI
580      590      600      610      620      630
Cry1Ac  PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKR
gi|142  PVDVNYAEKEKLEKAQKAVNTLTFTE-GRNALQKDVTDYKVDQVSLVDCISGDLYPNEKR
640      650      660      670      680      690
Cry1Ac  ELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGT

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gi|142  ELQNLVKYAKRLSYSRNLLDPTFDSINSSEENGWYGSNGIVIGNGDFVFKGNLYLIFSQT
700      710      720      730      740      750
Cry1Ac  FDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWP
gi|142  NDTQYPTLYQKIDESKLFKEYTRYKLGFISSQDLEAYVIRYDAKHRTLDV--SDNLLP
760      770      780      790      800      810
Cry1Ac  LSAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSHHFSLDIDVGCTDLNED
gi|142  --DILPENTCGEPNRCQAQQYLDENPSPECSSMQDG--ILSDSHSFLNIDTGSINHNEN
820      830      840      850      860
Cry1Ac  LGVWVIFIKIKTQDGHARLGNLEFLEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYK
gi|142  LGIWVLFKISTLEGYAKFGNLEVIEDGPVIGEALARVKRQETKWRNKLAQLTETQAIYT
870      880      890      900      910      920
Cry1Ac  EAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYPELSVIPGVNAAIFEELE
gi|142  RAKQALDNLFAQAQDLSHLKRDVTFABEIAARKIVQSIREAYMSWLVVPGVNHPIFTELS
930      940      950      960      970      980
Cry1Ac  GRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVPEWAEVSEQEVR
gi|142  GRVQRAFQLYDVRNVVRNRFNGLSDWIVTSDVKVQEEENG-NVLVLNWDAAQVLQNVK
990      1000     1010     1020     1030     1040
Cry1Ac  VCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQ
gi|142  LYQDRGYILHVTARKIGIGEGYITITDEEGHTDQLRFTAC--EEIDASN-----
1050     1060     1070     1080     1090
Cry1Ac  EEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRDYTPLPVGYVT
gi|142  -----AFIS-----GYIT
1100
Cry1Ac  KELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|142  KELEFPDPTEKVHIEIGETEGIFLVEISIELFLMEELC
1110     1120     1130
>>gi|436839|gb|AAA21120.1| CryIII delta-endotoxin (1138 aa)
initn: 1877 initl: 1006 opt: 2588 Z-score: 3041.7 bits: 574.8 E(): 1.7e-160
Smith-Waterman score: 2676; 41.045% identity (66.998% similar) in 1206 aa overlap
(8-1182:29-1136)
Cry1Ac  CMQAMDNNPNINECIPYCNLSNPEVEVLGGERIETGYTP

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gi|436 MNLNLLGGYEDSNRTLNNLSNYPTQKALSPSLKMNMYQDFLSITERE--QPEALASGNTA
      10      20      30      40      50
Cry1Ac 40      50      60      70      80      90
IDISLSLTQFLLSEF-VPGAGFVLGLVDIIWGFIFGPSQ---WDAFLVQIEQLINQRIEEF
gi|436 INTVVSVTGATLSALGVPGASFITNFYLKITGLLWPHNKNIWDEFMTEVETLIEQKIEQY
      60      70      80      90      100     110
Cry1Ac 100     110     120     130     140     150
ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|436 ARNKALAELEGLGNNLTIIYQQALEDWLNPPDDPATITRVIDRFRILDALFESYMPSPFRVA
      120     130     140     150     160     170
Cry1Ac 160     170     180     190     200     210
NYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|436 GYEIPLLTVYAQAANLHLALLRDRSTLYGDKWGFTQNNIEENYRQKHHISEYSNHCVKWY
      180     190     200     210     220     230
Cry1Ac 220     230     240     250     260     270
NTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNP
gi|436 NSGLSRLNGSTYEQWINYNRFRREMILMVLDAIAVFPYIDPRMYSMETSTQLTREVYTD
      240     250     260     270     280     290
Cry1Ac 280     290     300     310     320
VLENFDGSRFG-SAQQIEGS-IRSPHLMIDILNSITITYDAHRGE-----YYWSGHQI
gi|436 ISLSISNPDIGSFSQMENTAFRTPHLVDYLDDELYIYTSKYKAFSHEIQPDLFYWCVKV
      300     310     320     330     340     350
Cry1Ac 330     340     350     360     370     380
MASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRPFNIGINNQQ
gi|436 SFKKSEQSN-LYTTGIYKTSGYISSGAYSFR-GNDIYRTLAAPSVVVYPYQNYGVEQV
      360     370     380     390     400     410
Cry1Ac 390     400     410     420     430     440
SVLDGTEFAYGTSSNLPSAVYRKSG---TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF
gi|436 -----EF-YGVKGHVH---YRGDNKYDLTYSDIDQLPPDGE--PIHEKYTHRLCHATAI
      420     430     440     450     460
Cry1Ac 450     460     470     480     490
RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFN-GSVISGPGFTG
gi|436 SKSTPDYDNATI--PIFSWTHRSAEYNNRIYPNKIKKIPAVKMYKLDLSTVVGKPGFTG
      470     480     490     500     510     520
Cry1Ac 500     510     520     530     540     550
GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWGNSSI----
gi|436 GDLVKRGSNGYI---GDIKATVNSP-LSQKYRVRVRYATSVSGLFNV-FINDEIALQKN
      530     540     550     560     570
Cry1Ac 560     570     580     590     600     610
FSNTVPATATSLDNLQSSDFGYFESANA--FTSSLGNI-VGVRNFSGTAGVIIDRFEPFIP

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gi|436 FQSTVETIGEGKD-LTYGSFGYIEYSTTIQFPNEHPKITLHLNHLNNSNPFVDSIEFIP
      580     590     600     610     620     630
Cry1Ac 620     630     640     650     660     670
VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
gi|436 VDVNVDKEKLEKAQKAVNTLFT-GRNALQKYVTDYKVDQVSIWDCISGDLYPNEKRE
      640     650     660     670     680     690
Cry1Ac 680     690     700     710     720     730
LSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTF
gi|436 LQNLVKYAKRLSYSRNLLEDPTFDSINSSEENGWYGSNGIVIGNGDFVFKGNYLIFSGTN
      700     710     720     730     740     750
Cry1Ac 740     750     760     770     780     790
DECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPL
gi|436 DTQYPTYLYQKIDESKLFKEYSRYKLGFISSQDLEAYVIRYDAKHRTLDV--SDNLLF-
      760     770     780     790     800     810
Cry1Ac 800     810     820     830     840
SAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSHHFFSLDIDVGCTDLNEDL
gi|436 -DILPENTCGEPNRCAAQQYLDENPSSECSMDDG--ILSDSHSFLNIDTGSINHNNEL
      820     830     840     850     860
Cry1Ac 850     860     870     880     890     900
GVWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKE
gi|436 GIWVLFKISTLEGYAKFNGLEVIEDGPVIGEALARVKRQETKWRNKLAQMTTETQAIYTR
      870     880     890     900     910     920
Cry1Ac 910     920     930     940     950     960
AKESVDALFVNSQYDQLQADTNLAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEG
gi|436 AKQALDNLFANAQDLSHLKIDVTFAEIAAARKIVQSIREVYMSWLSVVPVGNHPIFTELSG
      930     940     950     960     970     980
Cry1Ac 970     980     990     1000    1010    1020
RIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVPEWEAEVSVQEVRV
gi|436 RVQRAFQLYDVRNVVRNRFNLGLSDWIIVTSDVNVQEEENG-NVLVLNNWDAQVLRNVKL
      990     1000    1010    1020    1030    1040
Cry1Ac 1030    1040    1050    1060    1070    1080
CPGRGYILRVTAAYKEGYEGECVTIHEIENNTDELKFSNCVEEIEYPPNNTVTCNDYTVNQE
gi|436 YQDRGYVLRVTARKIGIGEGYITITDEEGHTDQLRFTAC--EIDASN-----
      1050    1060    1070    1080    1090
Cry1Ac 1090    1100    1110    1120    1130    1140
EYGGAYTSRNRGNYEAPSVPADYASVYEEKSYTDGRRENPCFENRNGYRDYTPPLVGVYTK
gi|436 ----AFIS-----GYITK
      1150    1160    1170    1180

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Regulatory Product Characterization Team

Cry1Ac 90 100 110 120 130 140  
INQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN PALREEMRIQFNDMNSALTT  
gi|118 INQKIEQQVVIIDAETALESVKLVNDVLYLNAFEWEKRPNTNEYSTELVYKRFDAYNYART  
80 90 100 110 120 130

Cry1Ac 150 160 170 180 190 200  
AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDA---ATINSRYNDLTRLI  
gi|118 SIPFFRVKTYEVSLLSVYAQAANISLLSRDAQIYGDWLGDFEHDKATFDSEK-LFR--  
140 150 160 170 180 190

Cry1Ac 210 220 230 240 250 260  
GNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTV  
gi|118 AEYIDHCTKYYKVGLDRKLGSSYGSVWVNYRNRREMTLMILDITIAAFPPYDIEEYPIEVS  
200 210 220 230 240 250

Cry1Ac 270 280 290 300 310  
SQLTREIYTNVPLENFDGSRFG-SAQGIEGS-IRSPHMLDILNSITITYDAHR---GEY-  
gi|118 TQLAREVYTDPIITSFVSDHGSPSFMESNAIRKPHLVLDLYIYTSRFRTPSNEFQ  
260 270 280 290 300 310

Cry1Ac 320 330 340 350 360 370  
----YWSGHQIMASVPGFSG-PEF-TFPLYGTMGNAAPQQRIVAQLGGVYRTLSSTLYR  
gi|118 PDLNVAHAKV---KYKYSQDPTLHETPIYGNASNYESTGNYSFR-GNSIYQTLA----  
320 330 340 350 360

Cry1Ac 380 390 400 410 420  
RPFNIGINQQLSVLDGTEFAYGTSSNLPSAVYRKS-----TVDSLDEIPPQNNVPPR  
gi|118 -PSAILTPNYIYIGIEQVEF-YGNKGN---VYRGGNKYPLSVDSANQLPDPVE--PIT  
370 380 390 400 410

Cry1Ac 430 440 450 460 470 480  
QGFSHRLSHVSMF--RSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG--  
gi|118 ENYNHVLCHATAVPVKDGGT-----VPIFSWTHRSADYNTIYDPKITQLPAVKSTP  
420 430 440 450 460

Cry1Ac 490 500 510 520 530 540  
NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTRYRVRVRYASVTP  
gi|118 SPEVEGLKVQEGPGFTGGDLVWAKSSNQTIIVR---LKVTVDSPGTQ-KYRIRLKYAATS  
470 480 490 500 510 520

Cry1Ac 550 560 570 580 590  
IHLNV---NWGNSSIFSNTVPATATSLDNLQSSDFGYFESANFTSSLGNIVGVR---N  
gi|118 FYLGAYAGSNGGNGIPGISTVPKTMNIEDPLSYTSFAYIDLPSYTFQKDEV-IRFTIN  
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650  
FSGTAGVII-DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS  
gi|118 IYESGGAVYADKVEFIPVDADYDEGVQLEKAQKAVNALFTA-GRNALQTDVTDYKVDQVS  
590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710  
NLVVTYLSDEFCLDEKREKLESEKVKHAKRRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ  
gi|118 ILVDCVSGELYPNEKRELQNLKYAKRRLSYSRNLLEDPTFDSINSNDENGWYGSNGIATIG  
650 660 670 680 690 700

Cry1Ac 720 730 740 750 760 770  
GGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN  
gi|118 SGNIVFKGNYLIFSGTNDQYPTYLYQKIDESKLFKEYTRYKLRGPIESSQDLEAVVIRVD  
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830  
AKHETVNVPGTGLWPLSAQSPIGKCGEPNRC--PHLEWNPDLDCSC-RDGEKCAHSH  
gi|118 AKHQITMDV--SNNL--FSDITPVNACGEPNRCALPYLDENPRLECSSIQDG--ILSDSH  
770 780 790 800 810

Cry1Ac 840 850 860 870 880 890  
HFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKW  
gi|118 SFSLHIDTGSIDFNENVGIWVLFKISTLEGYAKFGNLEVIDGPVIGEALARVKRQETKW  
820 830 840 850 860 870

Cry1Ac 900 910 920 930 940 950  
RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPE  
gi|118 RNKLTQLRTETQAIYTRAKQAIDNLFNEQDShLKI GTTFALIVAARKIVQSIREAYMSW  
880 890 900 910 920 930

Cry1Ac 960 970 980 990 1000 1010  
LSVIPGVNAAI FEELRIFTAFSLYDARNVIKNGDFNGLSCVNWVKGHV DVEEQNNQRS  
gi|118 LSVIPGVNYPITELNERVQAFQLYDVRNVVRNGRFQSGTSDWIVTSDVKVQEEENG-N  
940 950 960 970 980 990

Cry1Ac 1020 1030 1040 1050 1060 1070  
VLVVPWEAEVSGEVRVCPGRGYILRVTA YKEGYGEGCVTIHEIENNTDELKFSNCVEEE  
gi|118 VLVLSNWDAQVLCMTLYQDRGYILRV TARKEGLGEGYVITDEEGNTDQLRFGGC--EE  
1000 1010 1020 1030 1040 1050

Cry1Ac 1080 1090 1100 1110 1120 1130  
IYPNNTVTCDNYTVNQEYGGAYTSRNRGYNEAPSPADYASVYEKSYTDGRRNPCEP  
gi|118 IDASNS-----FVST-----  
1060

Cry1Ac 1140 1150 1160 1170 1180  
NRGYRDYTPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|118 -----GYVTKELEFFPDTEKVR IEIGETEGIFQVGSVELFLMEDLC  
1070 1080 1090 1100

>>gi|10053904|gb|AAE30811.1| Sequence 1 from patent US 5 (718 aa)  
initn: 2242 initl: 1024 opt: 2321 Z-score: 2729.8 bits: 516.4 E(): 4e-143  
Smith-Waterman score: 2395; 54.025% identity (76.262% similar) in 733 aa overlap  
(5-730:1-718)

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          10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . . . . .
gi|100  MENNIQ-NQCVPNCLNNEPEVEILNEER-STGRPLDLSLSLFRLLSEFVPGVGV
          10      20      30      40      50

          70      80      90     100     110     120
Cry1Ac VLGLVDIWIWGFPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
      . . . . .
gi|100  AFGLFDLWGFITPSDWSLFLQIEQLIEQRLETLELRNRAITTLRGLADSYEIIYIEALRE
          60      70      80      90     100     110

          130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi|100  WEANPNNAQLREDVRIRFANTDDALITAINNFLLTSFEIPLLSVYVQAANLHLSLLRDAV
          120     130     140     150     160     170

          190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      . . . . .
gi|100  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDLYNQLENLRGTNRQWARFNQFRRLD
          180     190     200     210     220     230

          250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQIEGSIKIRSP
      . . . . .
gi|100  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRPP
          240     250     260     270     280     290

          300     310     320     330     340     350
Cry1Ac HLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      . . . . .
gi|100  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSPYGVF-NPGGAIWAIED
          300     310     320     330     340     350

          360     370     380     390     400     410
Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSGTVDSLDEI
      . . . . .
gi|100  PRPFYRTLSDPVFVRG--GFGNPHYVLGLRGVAFQG-TGTN-HTRTFRNSGTIDSLDEI
          360     370     380     390     400

          420     430     440     450     460     470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
      . . . . .
gi|100  PPQDNSGAPWINDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
          410     420     430     440     450     460

          480     490     500     510     520     530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      . . . . .
gi|100  IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
          470     480     490     500     510     520

          540     550     560     570     580     590
Cry1Ac YASVTPIHNLNVNWNSSIFSNTVDPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      . . . . .
gi|100  YASTNLRIRYVTVAGERIFAGQFNKTMDTGDPLTFQSFYATINTAFTFPMQSSFTVGA

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          530     540     550     560     570     580
Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      . . . . .
gi|100  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTVDYHIDQV
          590     600     610     620     630     640

          660     670     680     690     700     710
Cry1Ac SNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      . . . . .
gi|100  SNLVDCLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFKGINRQLDRGWRGSDITIT
          650     660     670     680     690     700

          720     730     740     750     760     770
Cry1Ac QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
      . . . . .
gi|100  QRGDDVFKENYVTLPGT
          710

>>gi|594012|gb|AAA55619.1| Sequence 3 from Patent EP 034 (869 aa)
      initn: 2322 init1: 2322 opt: 2322 Z-score: 2729.7 bits: 516.6 E(): 4e-143
      Smith-Waterman score: 2322; 99.438% identity (99.438% similar) in 356 aa overlap
      (262-617:514-869)

          240     250     260     270     280     290
Cry1Ac RYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGI
      . . . . .
gi|594  MRCRAIDGVTFCRPKSPVYVNGVHANLFRTVSQLTREIYTNPVLENFDGSRGSAQGI
          490     500     510     520     530     540

          300     310     320     330     340     350
Cry1Ac EGSIRSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ
      . . . . .
gi|594  ERSIRSPHLMIDLNSITIIYTDHRGYYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ
          550     560     570     580     590     600

          360     370     380     390     400     410
Cry1Ac QRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV
      . . . . .
gi|594  QRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV
          610     620     630     640     650     660

          420     430     440     450     460     470
Cry1Ac DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIA
      . . . . .
gi|594  DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIA
          670     680     690     700     710     720

          480     490     500     510     520     530
Cry1Ac SDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRY
      . . . . .
gi|594  SDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRY
          730     740     750     760     770     780

          540     550     560     570     580     590
Cry1Ac RVRVRYASVTPIHNLNVNWNSSIFSNTVDPATATSLDNLQSSDFGYFESANAFTSSLGNIV
      . . . . .
gi|594  RVRVRYASVTPIHNLNVNWNSSIFSNTVDPATATSLDNLQSSDFGYFESANAFTSSLGNIV

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      790      800      810      820      830      840
Cry1Ac 600 610 620 630 640 650
GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
gi|594 GVRNFSGTAGVIIDRFEFIPVTATLE
      850      860
>>gi|15110439|gb|AAE68103.1| Sequence 11 from patent US (547 aa)
  initn: 2950 initl: 1829 opt: 2289 Z-score: 2693.8 bits: 509.3 E(): 4e-141
Smith-Waterman score: 3304; 88.482% identity (91.972% similar) in 573 aa overlap
(614-1182:1-547)

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      590      600      610      620      630      640
Cry1Ac TSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
gi|151 ATLEAESDLERAQKAVNALFTSSNQIGLKT
      10      20      30

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      650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER
gi|151 DVTDYHIDRVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDR
      40      50      60      70      80      90

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      710      720      730      740      750      760
Cry1Ac GWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDS
gi|151 GWRGSTDITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDS
      100      110      120      130      140      150

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      770      780      790      800      810      820
Cry1Ac QDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDG
gi|151 QDLEIYLIRYNAKHETVNVPGTGLWPLSAQSPIGK-----
      160      170      180

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      830      840      850      860      870      880
Cry1Ac EKCAHSHHFLSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
gi|151 ---AHHSHHFLSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
      190      200      210      220      230      240

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      890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
gi|151 VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHS
      250      260      270      280      290      300

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      950      960      970      980      990      1000
Cry1Ac IREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDV
gi|151 IREAYLPELSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDV
      310      320      330      340      350      360

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      1010      1020      1030      1040      1050      1060
Cry1Ac EEQNNQSVLVVPEWEAEVSVQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELK
gi|151 EEQNNHRSVLVPEWEAEVSVQEVVRCVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELK

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      370      380      390      400      410      420
Cry1Ac 1070 1080 1090 1100 1110
FNSCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKS
gi|151 FNSCVVEEIVPNNVTVCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKA
      430      440      450      460      470      480
      1120      1130      1140      1150      1160      1170
Cry1Ac YTDGRRENPCFNRYRDTPLPVGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLL
gi|151 YTDGRRDNPESNRGYDYPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLL
      490      500      510      520      530      540
      1180
Cry1Ac MEE
      1180
gi|151 MEE

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>>gi|42682717|gb|AAS28780.1| Sequence 11 from patent US (547 aa)
  initn: 2950 initl: 1829 opt: 2289 Z-score: 2693.8 bits: 509.3 E(): 4e-141
Smith-Waterman score: 3304; 88.482% identity (91.972% similar) in 573 aa overlap
(614-1182:1-547)

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      590      600      610      620      630      640
Cry1Ac TSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
gi|426 ATLEAESDLERAQKAVNALFTSSNQIGLKT
      10      20      30

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      650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER
gi|426 DVTDYHIDRVSNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDR
      40      50      60      70      80      90

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      710      720      730      740      750      760
Cry1Ac GWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDS
gi|426 GWRGSTDITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDS
      100      110      120      130      140      150

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      770      780      790      800      810      820
Cry1Ac QDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDG
gi|426 QDLEIYLIRYNAKHETVNVPGTGLWPLSAQSPIGK-----
      160      170      180

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      830      840      850      860      870      880
Cry1Ac EKCAHSHHFLSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
gi|426 ---AHHSHHFLSLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
      190      200      210      220      230      240

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      890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
gi|426 VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIIHAADKRVHS

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250      260      270      280      290      300
Cry1Ac  950      960      970      980      990      1000
IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDV
gi|426  IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDV
310      320      330      340      350      360

1010     1020     1030     1040     1050     1060
Cry1Ac  EEQNNQRSVLVVPEWEAEVSVQEVRRVCPGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELK
gi|426  EEQNNHRSVLVPEWEAEVSVQEVRRVCPGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELK
370      380      390      400      410      420

1070     1080     1090     1100     1110
Cry1Ac  FSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKS
gi|426  FSNCVVEEIVPNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEKA
430      440      450      460      470      480

1120     1130     1140     1150     1160     1170
Cry1Ac  YTDGRRENPCFNRGRYDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLL
gi|426  YTDGRDNPCEsnrgygdYTPPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLL
490      500      510      520      530      540

1180
Cry1Ac  MEE
gi|426  MEE

>>gi|1610952|gb|AAB13931.1| Sequence 27 from patent US 5 (1148 aa)
initn: 4513 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
(5-1182:1-1148)

10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGF
gi|161  MENNIQ-NQCVPNCLNNEVEILNEER-STGRPLDISLSLRFLLSEFVPGVGV
10      20      30      40      50

70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEIEFARNQAI SRLEGLSNLYQIYAESFRE
gi|161  AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
60      70      80      90      100     110

130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|161  WEANPNNAQLREDRVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
120     130     140     150     160     170

190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|161  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNTRQWARFNQFRRLD

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180      190      200      210      220      230
Cry1Ac  250      260      270      280      290
TLTVLDIVLSLFPNYDSRSTYPIRTVSQLTREIYTNVLEN--FDGFSFRGSAQGIEGSIRSP
gi|161  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSSVIEDSPVSANIPNGFNRAEFGVRRPP
240     250     260     270     280     290

300      310      320      330      340      350
Cry1Ac  HLMDDILNSITTYTDAHRGEYIYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|161  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPYSGVF--NPGGAIWADED
300     310     320     330     340     350

360      370      380      390      400      410
Cry1Ac  GQGVYRTLSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEI
gi|161  PRPFYRTLSDPVFVRG--GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360     370     380     390     400

420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|161  PPQDNSGAPWNDYSHVLNHVTFVVRWPEIISGSDSWRAPMFSWTHRSATPTNTIDERITQ
410     420     430     440     450     460

480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
gi|161  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
470     480     490     500     510     520

540      550      560      570      580      590
Cry1Ac  YASVTPIHNLNVNWNSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|161  YASTTNLRIVYTVAGERIFAGQFNKTMDTGDPPLTFQSFSYATINTAFTFPMSQSSFTVGA
530     540     550     560     570     580

600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQV
gi|161  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590     600     610     620     630     640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
gi|161  SNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSDTITI
650     660     670     680     690     700

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|161  QGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
710     720     730     740     750     760

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHSHF

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gi|161 NAKHETVNVPGTGLWPLSAPSPIGKC-----AHHSHHF
      770      780      790

      840      850      860      870      880      890
Cry1Ac SLDIDVGCIDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      .....
gi|161 SLDIDVGCIDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELS
      .....
gi|161 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHADKRVHSIREAYLPELS
      860      870      880      890      900      910

      960      970      980      990      1000      1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQRSVL
      .....
gi|161 VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDEEQNNHRSVL
      920      930      940      950      960      970

      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEY
      .....
gi|161 VVPEWAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEY
      980      990      1000      1010      1020      1030

      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEYEGGAYTSRNRGYNEA---PSPVADYASVYEEKSYTDGRRNCP
      .....
gi|161 PNNTVTCNDYTVNQEYEGGAYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNC
      1040      1050      1060      1070      1080      1090

      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDYTPPLVGVYTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      .....
gi|161 ESNRGYGDYTPPLVGVYTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100      1110      1120      1130      1140

>>gi|15110436|gb|AAE68100.1| Sequence 2 from patent US 6 (1148 aa)
  initn: 4513 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
Smith-Waterman score: 5059; 67.452% identity (82.338% similar) in 1189 aa overlap
(5-1182:1-1148)

      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|151 MENNIQ-NQCVPNCLNNEPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGV
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNLYQIYAESFRE
      .....
gi|151 AFGLFDLIWGFITPSDWLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIALRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....

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gi|151 WEANPNNAQLREDRVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDVA
      120      130      140      150      160      170

      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
      .....
gi|151 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDVTYNQGLENLRTNTRQWARFNQFRDL
      180      190      200      210      220      230

      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQGIIEGSIKSP
      .....
gi|151 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFGVRPP
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac HLMDDILNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      .....
gi|151 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF--NPGGAIWADED
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac GQGVRVRLSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI
      .....
gi|151 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQ
      .....
gi|151 PPQDMSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      .....
gi|151 IPLVKAHTLQSGTTVRGPFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520

      540      550      560      570      580      590
Cry1Ac YASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      .....
gi|151 YASTTNLRIYVTVAGERIFAGQFNKTMDDPLTFQSFYSATINTAFTFPMSQSSFTVGA
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      .....
gi|151 DTFSSGNEYVIDRFELIPVTATLEAESDLERAQKAVNALFTSSNQIGLKTVDYHIDRV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      .....
gi|151 SNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGRWGSTDITI
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY

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gi|151 QGGDDVFKENYVTLTLLGTFDECYPTLYLQKIDESKLAQTRYQLRGYIEDSQDLEIYLIRY
      710      720      730      740      750      760
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
      780      790      800      810      820      830
gi|151 NAKHETVNVPGTGSWPLSAPSPIGK-----AHSHHF
      770      780      790
Cry1Ac SLDIDVGCIDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      840      850      860      870      880      890
gi|151 SLDIDVGCIDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELS
      900      910      920      930      940      950
gi|151 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMHAADKRVHSIREAYLPELS
      860      870      880      890      900      910
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVEEQNNQRSVL
      960      970      980      990      1000     1010
gi|151 VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHDVEEQNNHRSVL
      920      930      940      950      960      970
Cry1Ac VVPEWAEVSEQVRRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCVEEEIY
      1020     1030     1040     1050     1060     1070
gi|151 VVPEWAEVSEQVRRVCPGRGYILRVYAYKEGYGEGCVTIEIENNTDELKFSNCVEEEVY
      980      990      1000     1010     1020     1030
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
      1080     1090     1100     1110     1120
gi|151 PNNTVTCNDYTATQEEYEGYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPC
      1040     1050     1060     1070     1080     1090
Cry1Ac EFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1130     1140     1150     1160     1170     1180
gi|151 ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100     1110     1120     1130     1140
>>gi|5973539|gb|AAE12819.1| Sequence 23 from patent US 5 (1148 aa)
  initn: 4513 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
(5-1182:1-1148)
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50      60
gi|597 MENNIQ-NQCVPINCLNPEVEILNEER-STGRLPLDISLSLFRLLSEFVPGVGV
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLBGLSNLYQIYAESFRE
      70      80      90      100     110     120

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gi|597 AFGLFDLIWGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALRE
      60      70      80      90      100     110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      130      140      150      160      170      180
gi|597 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
      120      130      140      150      160      170
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYQFRREL
      190      200      210      220      230      240
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRTNTRQWARFNFQFRDL
      180      190      200      210      220      230
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQGLEGSIRSP
      250      260      270      280      290
gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFVRRP
      240      250      260      270      280      290
Cry1Ac HLMDDILNSITITDAHRGEYYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQL
      300      310      320      330      340      350
gi|597 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWADED
      300      310      320      330      340      350
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSNNLPSAVYKSGTVDLDEI
      360      370      380      390      400      410
gi|597 PRPFYRTLSDDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
      360      370      380      390      400
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
      420      430      440      450      460      470
gi|597 PPQDNGAPWNDYSHVLNHVTVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460
Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRV
      480      490      500      510      520      530
gi|597 IPLVKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520
Cry1Ac YASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      540      550      560      570      580      590
gi|597 YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPLTFQSFYSATINTAFTFPMSSQSSFTVGA
      530      540      550      560      570      580
Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      600      610      620      630      640      650
gi|597 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
      590      600      610      620      630      640
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLBGLSNLYQIYAESFRE
      660      670      680      690      700      710

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Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI  
 gi|597 SNLVECLSDSEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI  
 650 660 670 680 690 700

Cry1Ac QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY  
 gi|597 QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLIYR  
 710 720 730 740 750 760

Cry1Ac NAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSHF  
 gi|597 NAKHETVNVPGTGSLSWPLSAPSPIGK-----AHHSHHF  
 770 780 790

Cry1Ac SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
 gi|597 SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
 800 810 820 830 840 850

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHAADKRVHSIREAYLPELS  
 gi|597 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIAHAADKRVHSIREAYLPELS  
 860 870 880 890 900 910

Cry1Ac VIPGVNAALFELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVL  
 gi|597 VIPGVNAALFELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNHRSVL  
 920 930 940 950 960 970

Cry1Ac VVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYI  
 gi|597 VVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYV  
 980 990 1000 1010 1020 1030

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC  
 gi|597 PNNTVTCNDYTVNQEEYEGTYTSRNRGYDGYENSSVPADYASVYEEKAYTDGRRDNPC  
 1040 1050 1060 1070 1080 1090

Cry1Ac EFNRYGRDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 gi|597 ESNRYGDDYTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
 1100 1110 1120 1130 1140

>>gi|5987871|gb|AAE17036.1| Sequence 35 from patent US 5 (1148 aa)  
 in1n: 4513 in1l: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141  
 Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap  
 (5-1182:1-1148)

10 20 30 40 50 60

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF  
 gi|598 MENNIQ-NQCVPYNCNLPNPEVEILNEER-STGRPLDIDISLSLTRFLLSEFVPGVGV  
 10 20 30 40 50

Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE  
 gi|598 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIYIALRE  
 60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|598 WEANPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV  
 120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL  
 gi|598 SPGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNRQWARFNQFRRLD  
 180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLEN--FDGSFRGSAQGIIEGSIKSP  
 gi|598 TLTVLDIVSLFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSNIPNGFNRAEFGRVPP  
 240 250 260 270 280 290

Cry1Ac HLMDFMNSLFTVTAETVRSQTVVGGH--LVSSRNTAGNRINFPVSYGVF-NPQGAIWADEI  
 gi|598 HLMDFMNSLFTVTAETVRSQTVVGGH--LVSSRNTAGNRINFPVSYGVF-NPQGAIWADEI  
 300 310 320 330 340 350

Cry1Ac GQGVYRTLSTLYRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI  
 gi|598 PRPFYRTLSDPVPVVRG--GFGNPHYVLGLRGVAFQO-TGTN-HTRTFRNSGTIDSLDEI  
 360 370 380 390 400

Cry1Ac PPQNNVPPRQGFSHRSLHVSFMFRSGFNSSSVSIIRAPMFSWIHRSAEFNIIASDSITQ  
 gi|598 PPQDNGAPWNDYSHVLNHVTFVWRPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ  
 410 420 430 440 450 460

Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRV  
 gi|598 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARR  
 470 480 490 500 510 520

Cry1Ac YASVTPIHNLNVNWNSSIFSNTPATATSLDNLQSSDFGFESANAFNTSSLGN---IVGV  
 gi|598 YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPDLPQSFYSATINTAFTFPMSSQSSFTVGA  
 530 540 550 560 570 580

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600      610      620      630      640      650
Cry1Ac  RNFSTAGVVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQV
      . . . . .
gi | 598  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAKAVNELFTSSNIGLKTVDVTDYHIDRV
      590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      . . . . .
gi | 598  SNLVECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
      650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKILKAFTRYQLRGIYIEDSQDLEIYSIRY
      . . . . .
gi | 598  QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKILKAYTRYQLRGIYIEDSQDLEIYLIRY
      710      720      730      740      750      760

780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHF
      . . . . .
gi | 598  NAKHETVNVPGTGSWPLSAPSPIGK-----AHHSHHF
      770      780      790

840      850      860      870      880      890
Cry1Ac  SLDIDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      . . . . .
gi | 598  SLDIDVGCIDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850

900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS
      . . . . .
gi | 598  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVHSIREAYLPELS
      860      870      880      890      900      910

960      970      980      990      1000     1010
Cry1Ac  VIPGVNAAIFEELEGRIFTAFLSYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVL
      . . . . .
gi | 598  VIPGVNAAIFEELEGRIFTAFLSYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNHRSVL
      920      930      940      950      960      970

1020     1030     1040     1050     1060     1070
Cry1Ac  VVPEWAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVIY
      . . . . .
gi | 598  VVPEWAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVIY
      980      990      1000     1010     1020     1030

1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEYEGGAYTSRNRGYNEA----PSPADYASVYEEKSYTDGRENPC
      . . . . .
gi | 598  PNNTVTCNDYTATQEEYEGTYTSRNRGYDGAYESNSVPADYASVYEEKAYTDGRRDNPC
      1040     1050     1060     1070     1080     1090

1130     1140     1150     1160     1170     1180
Cry1Ac  EFNRGYRDYTPLVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi | 598  ESNRGYGDYTPLVAGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100     1110     1120     1130     1140

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>>gi|42682714|gb|AAS28777.1| Sequence 2 from patent US 6 (1148 aa)
  initn: 4513  initl: 1829  opt: 2289  Z-score: 2689.0  bits: 509.5  E(): 7.4e-141
  Smith-Waterman score: 5059;  67.452% identity (82.338% similar) in 1189 aa overlap
  (5-1182:1-1148)

      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      . . . . .
gi | 426  MENNIQ-NQCVPNCLNNPEVEILNEER-STGRLLPLDISLSLTRFLLEFVPGVGV
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEFPARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi | 426  AFGLFDLWGFITPDSWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi | 426  WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRLDAV
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFREL
      . . . . .
gi | 426  SPGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRTNTRQWARFNQFRDL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSRFGSAQGIIEGSIKSP
      . . . . .
gi | 426  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFVGRPP
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac  HLMDDILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      . . . . .
gi | 426  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWIADED
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac  GQGVYRTLSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPASAVYRKSQGTVDLSLDEI
      . . . . .
gi | 426  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRFRNSGTIDSLDEI
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAPFNIIASDSITQ
      . . . . .
gi | 426  PPQDNGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHR.SATPTNTIDPERITQ
      410     420     430     440     450     460

      480     490     500     510     520     530
Cry1Ac  IPAVKGNFLFNGS-VISPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      . . . . .
gi | 426  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470     480     490     500     510     520

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410      420      430      440      450      460
Cry1Ac  IPAVKGNFLFNNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
gi|160  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470      480      490      500      510      520
Cry1Ac  YASVTPIHLNVNWNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|160  YASTNLRILYVTVAGERIFAGQFNKIMDTGDPDPLTFQSFYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580
Cry1Ac  RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|160  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590      600      610      620      630      640
Cry1Ac  SNLVTYLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
gi|160  SNLVCLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
650      660      670      680      690      700
Cry1Ac  QGGDDVFKENYVTLGTFDECYPTLYQKIDESKLIKAPTRYQLRGIYEDSQDLEIYSIRY
gi|160  QGGDDVFKENYVTLGTFDECYPTLYQKIDESKLIKAYTRYQLRGIYEDSQDLEIYLYIRY
710      720      730      740      750      760
Cry1Ac  NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
gi|160  NAKHETVNVPGTGSWPLSAPSPIGK-----AHSHHF
770      780      790      800      810      820
Cry1Ac  SLDIDVGCTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|160  SLDIDVGCTDLNEDLGVVWIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
830      840      850      860      870      880
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS
gi|160  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAAADKRVHSIREAYLPELS
890      900      910      920      930      940
Cry1Ac  VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVL
gi|160  VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNHRSVL
950      960      970      980      990      1000
Cry1Ac  VVPEWEAEVSVQEVVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVY
gi|160  VVPEWEAEVSVQEVVRCVPCGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVY
1010     1020     1030     1040     1050     1060

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980      990      1000     1010     1020     1030
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|160  PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPC
1040     1050     1060     1070     1080     1090
Cry1Ac  EFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|160  ESNRGYGDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1100     1110     1120     1130     1140
>>gi|5973541|gb|AAE12821.1| Sequence 27 from patent US 5 (1148 aa)
initn: 4513 init1: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
(5-1182:1-1148)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNFEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|597  MENNIQ-NQCVPYNCNNEVEVEILNEER-STGRLPLDISLSLTRLFLSEFVPGVGV
10      20      30      40      50
Cry1Ac  VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFRE
gi|597  AFGLFDLIWGITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIEALRE
60      70      80      90      100     110
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|597  WEANPNNAQLREDVIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
120     130     140     150     160     170
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|597  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLNLRGTNTRQWARFNQFRDL
180     190     200     210     220     230
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGLEGSIRSP
gi|597  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSNPNPNGFNRAEFGVRPP
240     250     260     270     280     290
Cry1Ac  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSYGVF-NPGGAIWIADSD
gi|597  HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPVSYGVF-NPGGAIWIADSD
300     310     320     330     340     350
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPASVYRKSQTVVSLDEI
gi|597  GQGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPASVYRKSQTVVSLDEI

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gi|598 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPYSYGVF--NPGGAIWAIEDI
      300      310      320      330      340      350
Cry1Ac QQGVYRTLSSSTLYRRFPFNIGINNQQLSV-LDGTEFAYGTSSNLPSSAVYRKSQTVDSLDEI
gi|598 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
      360      370      380      390      400
Cry1Ac PPQNNVPPRQGFSHRLSHVMSFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|598 PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNNSGNNIQNRGYLEVPIHFPSTSTRYVRVR
gi|598 IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520
Cry1Ac YASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|598 YASTTNLRYYVTVAGERIFAGQFNKTMDDTGDPLTFQSPSYATINTAFTFPMSQSSFTVGA
      530      540      550      560      570      580
Cry1Ac RNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|598 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
      590      600      610      620      630      640
Cry1Ac SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|598 SNLVECLSDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
      650      660      670      680      690      700
Cry1Ac QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYSIRY
gi|598 QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYIEDSQDLEIYLIRY
      710      720      730      740      750      760
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
gi|598 NAKHETVNVPGTGSWPLSAPSPIGK-----AHSHHF
      770      780      790
Cry1Ac SLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|598 SLDIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850
Cry1Ac VFGQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|160 SFGQWGLDIATVNNHYNRLINLIHRYTKHCLDVTYNQGLENLRTGTRQWARFNRDRL
      180      190      200      210      220      230
Cry1Ac VPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIIY
gi|598 VPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIVY
      980      990      1000      1010      1020      1030
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|598 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVADYASAYEEKAYTDGRRDNPC
      1040      1050      1060      1070      1080      1090
Cry1Ac EFNRRGYRDTPLPVGYVTKLELYFPETDKVWVIEIGETEGTFIVDSVELLMEE
gi|598 ESNRGGYDYPPLPAGYVTKLELYFPETDKVWVIEIGETEGTFIVDSVELLMEE
      1100      1110      1120      1130      1140

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Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|598 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELS
      860      870      880      890      900      910
Cry1Ac VIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVVEEQNNQRSVL
gi|598 VIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVVEEQNNHRSVL
      920      930      940      950      960      970
Cry1Ac VVPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIIY
gi|598 VVPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIVY
      980      990      1000      1010      1020      1030
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|598 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVADYASAYEEKAYTDGRRDNPC
      1040      1050      1060      1070      1080      1090
Cry1Ac EFNRRGYRDTPLPVGYVTKLELYFPETDKVWVIEIGETEGTFIVDSVELLMEE
gi|598 ESNRGGYDYPPLPAGYVTKLELYFPETDKVWVIEIGETEGTFIVDSVELLMEE
      1100      1110      1120      1130      1140
>>gi|1608058|gb|AAB11013.1| Sequence 27 from patent US 5 (1148 aa)
      initn: 4513 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
      Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
      (5-1182:1-1148)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|160 MENNIQ-NQCVPNCLNPEVEILNEER-STGRPLDISLSLTRLFLSEFVPGVGV
      10      20      30      40      50
Cry1Ac VLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIEIEFARNQAIISRLGLSNLYQIYAESFRE
gi|160 AFGLFDLIWGFITPDSWLSFLQIEQLIEQRIETLERNRAITLRLGLADSYEIIYIEALRE
      60      70      80      90      100      110
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSLVRDVS
gi|160 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYQAAANLHLSLRLDAV
      120      130      140      150      160      170
Cry1Ac VFGQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFREL
gi|160 SFGQWGLDIATVNNHYNRLINLIHRYTKHCLDVTYNQGLENLRTGTRQWARFNRDRL
      180      190      200      210      220      230
Cry1Ac VPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIIY
gi|598 VPEWEAEVQEVVRCVPCGRGYILRVTAAYKEGYEGECVTTIHEIENNTDELKFSNCVEEIVY
      250      260      270      280      290

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Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQGIIEGSIRSP
gi|160 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPP
      240      250      260      270      280      290

      300      310      320      330      340      350
Cry1Ac HLMIDLNSITIIYDHAHRGEYYWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQL
gi|160 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFP SYGVF--NPGGAIWIADDEI
      300      310      320      330      340      350

      360      370      380      390      400      410
Cry1Ac GQGVYRTLSSTLYRRFPNIGINNQQLSV-LDGTEFAYGTSSNLPSAVYKSGTVDLSLDEI
gi|160 PRPFYRTLSLSDPVFVRG--GFGNPHYVLGLRGVAFQQ--TGTN-HTRTFRNSGTIDSLDEI
      360      370      380      390      400

      420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|160 PPQDNSGAPWNDYSHVLNHTVFRVWPGEISGSDSWRAPMFSWTHRSATPINTIDPERITQ
      410      420      430      440      450      460

      480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVR
gi|160 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
      470      480      490      500      510      520

      540      550      560      570      580      590
Cry1Ac YASVTPIHNLNWNNGSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|160 YASTNLRIYVTVAGERIFAGQFNKTMDTGDDPLTFQSFYATINTAFTFPMSQSSFTVGA
      530      540      550      560      570      580

      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|160 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGKTDVTDYHIDRV
      590      600      610      620      630      640

      660      670      680      690      700      710
Cry1Ac SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|160 SNLVECLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
      650      660      670      680      690      700

      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIEDSDLEIYSIRY
gi|160 QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIEDSDLEIYLIRY
      710      720      730      740      750      760

      780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSRRDGEKCAHSHHF
gi|160 NAKHETVNVPGTGSWPLSAPSIGK-----AHHSHHF
      770      780      790

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      840      850      860      870      880      890
Cry1Ac SLDIDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|160 SLDIDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|160 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELS
      860      870      880      890      900      910

      960      970      980      990      1000      1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNQRSVL
gi|160 VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDVEEQNNHRSVL
      920      930      940      950      960      970

      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWEAEVSQEVVRCVPGRYILRVTAAYKEGYEGCVTIHEIENNTDELKFSNCEVEEIIY
gi|160 VVPEWEAEVSQEVVRCVPGRYILRVTAAYKEGYEGCVTIHEIENNTDELKFSNCEVEEIVY
      980      990      1000      1010      1020      1030

      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|160 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPC
      1040      1050      1060      1070      1080      1090

      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|160 ESNRGYDGYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100      1110      1120      1130      1140

>>gi|5973548|gb|AAE12828.1| Sequence 35 from patent US 5 (1148 aa)
      initn: 4513 init1: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
      Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
      (5-1182:1-1148)

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|597 MENNIQ-NQCVPYNCLNPEVEILNEER-STGRPLPLDISLSLTLRFLLEFVPGVGV
      10      20      30      40      50

      70      80      90      100      110      120
Cry1Ac VLGLVDIINGIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFRE
gi|597 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRLETLEARNRAITTLRGLADSYEITYEALRE
      60      70      80      90      100      110

      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSLVRDVS
gi|597 WEANPNNAQLREDVIRFANTDDALITAINNFTLSFEIPLLSVYVQAANLHLSLRLDAV
      120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac VFGQRWGPDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
gi|597 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRRLD
180      190      200      210      220      230

250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPLEN--FDGSRFSAQIEGSIKIRSP
gi|597 TLTVLDIVALFPNVDVRYPIQTSSQLTREIYTSVIEDSPVANIPNGFNRAEFGVRRPP
240      250      260      270      280      290

300      310      320      330      340      350
Cry1Ac HLMIDILNSITIIYTDHARGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|597 HLMDFMNSLFVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWADED
300      310      320      330      340      350

360      370      380      390      400      410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQLSV-LDGTFAFYGTSSNLPASAVYKSGTVDLDEI
gi|597 PRPFYRTLSDPVVFVRG--GFGNPHYVLGLRGVAFQQ-TGNT-HTRTFRNSGTIDSLDEI
360      370      380      390      400

420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|597 PPQDNSGAPWNDYSHVLNHVTFVRWVPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410      420      430      440      450      460

480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRVVRV
gi|597 IPLVKAHTLQSGTTVVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
470      480      490      500      510      520

540      550      560      570      580      590
Cry1Ac YASVTPIHNLNVWGNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|597 YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPDPLTFQSPSYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580

600      610      620      630      640      650
Cry1Ac RNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|597 DTFSSGNVEVYIDRFELIPVTATFEAEYDLERAQKAVNELFTSSNIQGLKTDVTDYHIDRV
590      600      610      620      630      640

660      670      680      690      700      710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITI
gi|597 SNLVECLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
650      660      670      680      690      700

720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAFTRYQLRGIEDSQDLEIYSIRY
gi|597 QGGDDVFKENYVTLTSGTFDECYPTLYQKIDESKLFKAFTRYQLRGIEDSQDLEIYLRIR
710      720      730      740      750      760

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780      790      800      810      820      830
Cry1Ac NAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGKCAHSHSHF
gi|597 NAKHETVNVPGTGSLSWPLSAPSPIGKC-----AHSHSHF
770      780      790

840      850      860      870      880      890
Cry1Ac SLDIDVGCITDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|597 SLDIDVGCITDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
800      810      820      830      840      850

900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|597 KREKLEWETNIVYKEAKESVDALFVNSQYDRQLQADTNIAMIHAADKRVHSIREAYLPELS
860      870      880      890      900      910

960      970      980      990      1000      1010
Cry1Ac VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
gi|597 VIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
920      930      940      950      960      970

1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEYI
gi|597 VVPEWEAEVSEQEVRVCPGRGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEVY
980      990      1000      1010      1020      1030

1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEYEGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|597 PNNTVTCNDYATQEEYEGYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPC
1040      1050      1060      1070      1080      1090

1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|597 ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1100      1110      1120      1130      1140

>>gi|5987864|gb|AAE17029.1| Sequence 27 from patent US 5 (1148 aa)
initn: 4513 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141
Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap
(5-1182:1-1148)

10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNFEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
gi|598 MENNIQ-NQCVPYCNLNNPEVEILNEER-STGRPLDLSLSLTRFLLEFVPGVGV
10      20      30      40      50

70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFRE
gi|598 AFGLFDLIWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEYIEALRE
60      70      80      90      100      110

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Regulatory Product Characterization Team

Cry1Ac 130 140 150 160 170 180  
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
gi|598 WEANPNNAQLREDVRIQFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV  
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240  
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL  
gi|598 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGNTNRQWARFNQFRDL  
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290  
TLTVLDIVLSLFPNYSRTPYPIRTVSQLTREIYTNPLEN--FDGSRGSAQIEGSIKRS  
gi|598 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFVGRPP  
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350  
HLMIDLNSITITYTDAHRGEYVWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQL  
gi|598 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSPYGVF--NPGGAIWAIED  
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400 410  
GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPASAVYKSGTVDLSDEI  
gi|598 PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQG--TGTN-HTRTFRNSGTIDLSDEI  
360 370 380 390 400

Cry1Ac 420 430 440 450 460 470  
PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ  
gi|598 PPQDNGSAPWNDYSHVLNHVTFVVRWPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ  
410 420 430 440 450 460

Cry1Ac 480 490 500 510 520 530  
IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR  
gi|598 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR  
470 480 490 500 510 520

Cry1Ac 540 550 560 570 580 590  
YASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGFESANAFTSSLGN---IVGV  
gi|598 YASTINLRIYVTVAGERIFAGQFNKMTDGTGDLTPQSFYSYATINTAFTFPMSQSSFTVGA  
530 540 550 560 570 580

Cry1Ac 600 610 620 630 640 650  
RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV  
gi|598 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV  
590 600 610 620 630 640

Cry1Ac 660 670 680 690 700 710  
SNLVTYLSDFECLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI  
gi|598 SNLVECLSDFECLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI

650 660 670 680 690 700  
Cry1Ac 720 730 740 750 760 770  
QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY  
gi|598 QGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYLIRY  
710 720 730 740 750 760

Cry1Ac 780 790 800 810 820 830  
NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSHF  
gi|598 NAKHETVNVPGTGLWPLSAPSPIGKC-----AHSHSHF  
770 780 790

Cry1Ac 840 850 860 870 880 890  
SLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
gi|598 SLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
800 810 820 830 840 850

Cry1Ac 900 910 920 930 940 950  
KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS  
gi|598 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAAMIHAADKRVHSIREAYLPELS  
860 870 880 890 900 910

Cry1Ac 960 970 980 990 1000 1010  
VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQRSVL  
gi|598 VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNHRSVL  
920 930 940 950 960 970

Cry1Ac 1020 1030 1040 1050 1060 1070  
VVPWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYI  
gi|598 VVPWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYI  
980 990 1000 1010 1020 1030

Cry1Ac 1080 1090 1100 1110 1120  
PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC  
gi|598 PNNTVTCNDYTVNQEEYEGTYTSRNRGYDGAYESNSVSPADYASVYEEKAYTDGRRDNPC  
1040 1050 1060 1070 1080 1090

Cry1Ac 1130 1140 1150 1160 1170 1180  
EFNRGRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
gi|598 ESNRGYDYPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE  
1100 1110 1120 1130 1140

>>gi|1610950|gb|AAB13929.1| Sequence 23 from patent US 5 (1148 aa)  
initn: 4513 init1: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141  
Smith-Waterman score: 5059; 67.368% identity (82.338% similar) in 1189 aa overlap  
(5-1182:1-1148)

Cry1Ac 10 20 30 40 50 60  
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF  
gi|161 MENNIQ-NQCVYPNCLNPEVEILNEER-STGRLEPLDISLSLTRLLESEFVPGVGV

Regulatory Product Characterization Team

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10      20      30      40      50
70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
gi|161 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSVEIYIEALRE
60      70      80      90      100     110
130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|161 WEANPNNAQLREDVRIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRLDAV
120     130     140     150     160     170
190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
gi|161 SFGQWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLENLRGTRTRQWARFNQFRRLD
180     190     200     210     220     230
250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLEN--FDGSRGSAQGIIEGSIKSP
gi|161 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPSANIPNGFNRAEFGVRRPP
240     250     260     270     280     290
300     310     320     330     340     350
Cry1Ac HLMIDIINSITIIYTDHARGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|161 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRLNFPVSYGVF--NPGGAIWIADED
300     310     320     330     340     350
360     370     380     390     400     410
Cry1Ac GQGVYRTLSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPASAVYRKSQVDSLDEI
gi|161 PRPFYRTLSDPVVFVRG--GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360     370     380     390     400
420     430     440     450     460     470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|161 PPQDNSGAPWNDYSHVLNHTVFRVWPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
410     420     430     440     450     460
480     490     500     510     520     530
Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNLSGNNIQNRGYLEVPIHFPSTSTRYRVRVR
gi|161 IPLVKAHTLQSGTIVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
470     480     490     500     510     520
540     550     560     570     580     590
Cry1Ac YASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGV
gi|161 YASTTNLRIYVTVAGERIFAGQFNKMTDGTGDLPTQSPSYATINTAFTFPMQSSFTVGA
530     540     550     560     570     580
600     610     620     630     640     650
Cry1Ac RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV

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gi|161 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590     600     610     620     630     640
660     670     680     690     700     710
Cry1Ac SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGSTGITI
gi|161 SNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
650     660     670     680     690     700
720     730     740     750     760     770
Cry1Ac QGGDDVFKENYVTLSTGTFDECYPTLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|161 QGGDDVFKENYVTLSTGTFDECYPTLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
710     720     730     740     750     760
780     790     800     810     820     830
Cry1Ac NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDEKCAHSHHF
gi|161 NAKHETVNVPGTGLWPLSAPSPIGK-----AHSHSHF
770     780     790
840     850     860     870     880     890
Cry1Ac SLDIDVGCITDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|161 SLDIDVGCITDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
800     810     820     830     840     850
900     910     920     930     940     950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
gi|161 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELS
860     870     880     890     900     910
960     970     980     990     1000    1010
Cry1Ac VIPGVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVL
gi|161 VIPGVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNHRSVL
920     930     940     950     960     970
1020    1030    1040    1050    1060    1070
Cry1Ac VVPEWEAEVSQEVRCVPCGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCV EEEIY
gi|161 VVPEWEAEVSQEVRCVPCGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCV EEEVY
980     990     1000    1010    1020    1030
1080    1090    1100    1110    1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|161 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSVSPADYASAYEEKAYTDGRRDNPC
1040    1050    1060    1070    1080    1090
1130    1140    1150    1160    1170    1180
Cry1Ac EFNRGYRDYTPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|161 ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1100    1110    1120    1130    1140

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>>gi|5987861|gb|AAE17026.1| Sequence 21 from patent US 5 (1150 aa)
initn: 4951 init1: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141

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Regulatory Product Characterization Team

Smith-Waterman score: 5341; 71.068% identity (83.600% similar) in 1189 aa overlap (5-1182:1-1150)

Sequence alignment for Cry1Ac and gi|598. Includes positions 10-60, 70-120, 130-180, 190-240, 250-290, 300-350, 360-410, 420-470, 480-530, 540-590.

Sequence alignment for Cry1Ac and gi|598. Includes positions 530-580, 600-650, 660-710, 720-770, 780-830, 840-890, 900-950, 960-1010, 1020-1070, 1080-1120, 1130-1180.





Regulatory Product Characterization Team

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1020      1030      1040      1050      1060      1070
Cry1Ac  VVPEWEAEVSEQVRRVCPGRGYLLRVYAYKEGYGEGCVTIHEIENNTDELKFNCSVVEEELY
gi|160  VVPEWEAEVSEQVRRVCPGRGYLLRVYAYKEGYGEGCVTIHEIENNTDELKFNCSVVEEELY
980      990      1000      1010      1020      1030

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1080      1090      1100      1110      1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRENPC
gi|160  PNNTVTCNDYTVNQEEYGGAYTSRNRGYDYGAYESSNSVPADYASVYEEKAYTDGRRDNPC
1040      1050      1060      1070      1080      1090

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1130      1140      1150      1160      1170      1180
Cry1Ac  EFNRYGRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|160  ESNRYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
1100      1110      1120      1130      1140      1150

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>>gi|1610949|gb|AAB13928.1| Sequence 21 from patent US 5 (1150 aa)  
 initn: 4951 initl: 1829 opt: 2289 Z-score: 2689.0 bits: 509.5 E(): 7.4e-141  
 Smith-Waterman score: 5341; 71.068% identity (83.600% similar) in 1189 aa overlap  
 (5-1182:1-1150)

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10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|161  MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

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70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFRE
gi|161  VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFRE
60      70      80      90      100      110

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130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNMDMSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|161  WEADLNNAQLREDVRIQFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLRDAV
120      130      140      150      160      170

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190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRREL
gi|161  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDLYNQLENLRGNTNRQWARFNQFRRLD
180      190      200      210      220      230

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250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN--FDGSFRGSAQIEGSIRSP
gi|161  TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRP
240      250      260      270      280      290

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300      310      320      330      340      350
Cry1Ac  HLMIDIILNSITIIYTDHARGBYWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQL
gi|161  HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINPFSYGVF--NPGGAIWAIED
300      310      320      330      340      350

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360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKSQTVDSLDEI
gi|161  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQO-TGTN-HTRTFRNSGTIDSLDEI
360      370      380      390      400

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420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|161  PPQDNSGAPWNDYSHVLNHVTFVRWPGEISGSDSWRAPMFSWTHR SATPTNTIDPERITQ
410      420      430      440      450      460

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480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVR
gi|161  IPLVKAHTLQSGTTVVRGPGFTGGDILRRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
470      480      490      500      510      520

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540      550      560      570      580      590
Cry1Ac  YASVTPHILNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|161  YASTTNLRIYVTVAGERIFAGQFNKTMDTGDPDLPQSFYSYATINTAFTFPMSQSSFTVGA
530      540      550      560      570      580

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600      610      620      630      640      650
Cry1Ac  RNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|161  DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNALFTSINQIGIKTDVTDYHIDRV
590      600      610      620      630      640

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660      670      680      690      700      710
Cry1Ac  SNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGGTGITI
gi|161  SNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGRWGSTDITI
650      660      670      680      690      700

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720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|161  QGGDDVFKENYVTLSTGFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
710      720      730      740      750      760

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780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHSHF
gi|161  NAKHETVNVPGTGLSWPLSAPSPIGKC-----AHSHSHF
770      780      790

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840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|161  SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
800      810      820      830      840      850

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900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELS
gi|161  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADNTIAMIHAADKRVHSIREAYLPELS

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      860      870      880      890      900      910
Cry1Ac  960      970      980      990      1000     1010
VIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVL
gi|161  VIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNHRSVL
920      930      940      950      960      970

      1020     1030     1040     1050     1060     1070
Cry1Ac  VVPEWAEVSVQEVRRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVIY
gi|161  VVPEWAEVSVQEVRRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEVIY
980      990      1000     1010     1020     1030

      1080     1090     1100     1110     1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPC
gi|161  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEEKSYTDGRRENPC
1040     1050     1060     1070     1080     1090

      1130     1140     1150     1160     1170     1180
Cry1Ac  EFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|161  EFNRGYRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1100     1110     1120     1130     1140     1150

>>gi|42682719|gb|AAS28782.1| Sequence 21 from patent US (1163 aa)
initn: 4388 initl: 1829 opt: 2289 Z-score: 2688.9 bits: 509.5 E(): 7.5e-141
Smith-Waterman score: 5020; 66.612% identity (81.074% similar) in 1210 aa overlap
(5-1182:1-1163)

      10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGF
gi|426  MEEN-NQNQCIPYNCLSNPEEVLLDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac  VLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESPFE
gi|426  LVGLIDFVWGVGSPQWDAFLVQIEQLINERIAEFARNAIANLEGLGNNFNIIYVEAFKE
60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|426  WEEDPNPATRTRVIDRFRILDGLLERDIPSRISGFEVPLLSVYAQAANLHLAILRDSV
120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDRDWRIRYNQFRREL
gi|426  IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRNLNLPKSTYQDWITYNLRRDL
180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac  TLTVLVDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRFRGSAQG-----IEGS-
gi|426  TLTVLVDIAAFFPNYDNRYPYIQQVQGLTREVYTDPLI-NFNPQLQSVQALPTFNVMESSA

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      240      250      260      270      280      290
Cry1Ac  300      310      320      330      340      350
IRSPHLMIDLNSITIYTDADR-GE-YYWSGHQIMASPVVFGSGPEFTFPLYGTMGNAAPQQ
gi|426  IRNPHLFDILNLTIFTDWFSVGRNFYWGHRVVISLIG--GGNITSPIYGREANQEPFR
300      310      320      330      340      350

      360      370      380      390      400
Cry1Ac  RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPASVAVYKSG
gi|426  SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360      370      380      390      400

      410      420      430      440      450      460
Cry1Ac  TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
gi|426  QVDSLTELPPEDNSVPPREGYSHRLCHATFVQSRGTPFLTTGVV---FSWTHRSATLTN
410      420      430      440      450      460

      470      480      490      500      510      520
Cry1Ac  IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
gi|426  TIDPERINQIPLVKGRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPT
470      480      490      500      510

      530      540      550      560      570      580
Cry1Ac  STRYRVRVRYASVTPHILNVNWNSSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
gi|426  Q-RYRLRFRYASSRDARVILVTGAASTGVGGQVSVNMPLQKMEIGENLTSRTFRYTDPS
520      530      540      550      560      570

      590      600      610      620      630
Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTTALEAEYNLERAQKAVNAL
gi|426  NPF'SFRANPDIIGISEQPLFGAGSISSGELYIDKIEIILADATLEAESDLERAQKAVNAL
580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
gi|426  FTSSNQIGLKTVDYHIDRVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
gi|426  NFRGINRQLDRGWRGSDITIQGGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLAFT
700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac  RYQLRGIYIEDSDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEW
gi|426  RYQLRGIYIEDSDLEIYLIRYNAKHETVNVPGTGLWPLSAPSPIGK-----
760      770      780      790      800

      820      830      840      850      860      870
Cry1Ac  NPDLDSCSRDGEKCAHSHHFSLDIDVGCITDLNEDLGWVWIFKIKTQDGHARLGNLEFLE

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gi|426 -----AHSHHFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLE
810 820 830 840

Cry1Ac 880 890 900 910 920 930
EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA

gi|426 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIA
850 860 870 880 890 900

Cry1Ac 940 950 960 970 980 990
MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL

gi|426 MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
910 920 930 940 950 960

Cry1Ac 1000 1010 1020 1030 1040 1050
SCWNVKGVHVDVEEQNNQSVLVPVEWAEVSVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTI

gi|426 SCWNVKGVHVDVEEQNNHRSVLPVEWAEVSVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTI
970 980 990 1000 1010 1020

Cry1Ac 1060 1070 1080 1090 1100
HEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSPV

gi|426 HEIENNTDELKFSNCVVEEIVYPNNTVTCNDYATQEEYEGYTSRNRGYDYGAYESNSSVP
1030 1040 1050 1060 1070 1080

Cry1Ac 1110 1120 1130 1140 1150 1160
ADYASVYEEKSYTDGRENPCFNRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEG

gi|426 ADYASAYEEKAYTDGRRDNPCESNRGYDYPPLPAGYVTKLEYFPETDKVWIEIGETEG
1090 1100 1110 1120 1130 1140

Cry1Ac 1170 1180
TFIVDSVELLLMEE

gi|426 TFIVDSVELLLMEE
1150 1160

>>gi|15110441|gb|AAE68105.1| Sequence 21 from patent US (1163 aa)
initn: 4388 initl: 1829 opt: 2289 Z-score: 2688.9 bits: 509.5 E(): 7.5e-141
Smith-Waterman score: 5020; 66.612% identity (81.074% similar) in 1210 aa overlap
(5-1182:1-1163)

Cry1Ac 10 20 30 40 50 60
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF

gi|151 MEEN-NQNCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac 70 80 90 100 110 120
VLGLVDIIWGIWGFQSDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFRE

gi|151 LVGLIDFVWGIWGFQSDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac 130 140 150 160 170 180
WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS

gi|151 WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
::: . . . . .

gi|151 WEEDPNPATRTRVIDRFRILDGLLERDIPFRISGFVPLLVSVAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac 190 200 210 220 230 240
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL

gi|151 IFGERWGLTTINVNENYRNLIRHIDEYADHCANTYRGLNPLKSTYQDWITYNRLRDL
180 190 200 210 220 230

Cry1Ac 250 260 270 280 290
TLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRFSAQG-----IEGS-

gi|151 TLTVLDIAAFFPNYDNRRIPIQPVGQLTREVYTDPLI-NFNPQLQSVLQPTFNVMESSA
240 250 260 270 280 290

Cry1Ac 300 310 320 330 340 350
IRSPHLMIDLNSITYTDAHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQ

gi|151 IRNPHLFDILNLTIFTDWFVSVGRNFYWGHRVSSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac 360 370 380 390 400
RIVAQLQGQVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSG

gi|151 SFT--FNGPVFRTLSNPTLRLQPPWAPPFN--LRGVEGVFES--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac 410 420 430 440 450 460
TVDSLDEIPPQNNVPPRQGFSHRSLHVSMSF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN

gi|151 QVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac 470 480 490 500 510 520
IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSST

gi|151 TIDPERINQIPLVKGFVRVWGGTSVITGPGFTGGDILRRNTFGDFVS---LQVNIINSPIT
470 480 490 500 510

Cry1Ac 530 540 550 560 570 580
STRYRVRYASVTPPIHLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA

gi|151 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMEIGENLTSRTFRYTDFS
520 530 540 550 560 570

Cry1Ac 590 600 610 620 630
NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL

gi|151 NPFSSFRANPDIIGISEQPLFAGSISGELYIDKIEIILADATLEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac 640 650 660 670 680 690
FTSTNQLGKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS

gi|151 FTSSNQIGLKTVDVTDYHIDRVSNLVECLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDP
640 650 660 670 680 690

Cry1Ac 700 710 720 730 740 750
NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKFT

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gi|151 NFRGNNRQLDRGWRGSDTITIQGGDDVFKENYVTLGLTFDECYPTYLQKIDESLKKAYT
700 710 720 730 740 750

Cry1Ac RYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGSWPLSAQSPIGKCEPNRCAPHLEW
760 770 780 790 800 810

gi|151 RYQLRGYIEDSDLEIYLIRYNAKHETVNVPGTGSWPLSAPSPIGKC-----
760 770 780 790 800

Cry1Ac NPDLDCSCRDGEKCAHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
820 830 840 850 860 870

gi|151 -----AHSHHFLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLE
810 820 830 840

Cry1Ac EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
880 890 900 910 920 930

gi|151 EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIA
850 860 870 880 890 900

Cry1Ac MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
940 950 960 970 980 990

gi|151 MIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGL
910 920 930 940 950 960

Cry1Ac SCWNVKGHV DVEEQNNQRSVLVVPEWEAEVVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
1000 1010 1020 1030 1040 1050

gi|151 SCWNVKGHV DVEEQNNHRSVLVPEWEAEVVSQEVRCVCPGRGYILRV TAYKEGYGEGCVTI
970 980 990 1000 1010 1020

Cry1Ac HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
1060 1070 1080 1090 1100

gi|151 HEIENNTDELKFSNCVEEIVPNNTVTCNDYTATQEEYEGYTSRNRGYD GAYESNSSVP
1030 1040 1050 1060 1070 1080

Cry1Ac ADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEG
1110 1120 1130 1140 1150 1160

gi|151 ADYASAYEEKAYTDGRDNPCESNRGYD YTPLPAGYVTKELEYFPETDKVWIEIGETEG
1090 1100 1110 1120 1130 1140

Cry1Ac TFIVDSVLELLMEE
1170 1180

gi|151 TFIVDSVLELLMEE
1150 1160

>>gi|1831475|gb|AAB45929.1| Sequence 11 from patent US 5 (1163 aa)
initn: 4384 initl: 1829 opt: 2289 Z-score: 2688.9 bits: 509.5 E(): 7.5e-141
Smith-Waterman score: 5022; 66.612% identity (81.157% similar) in 1210 aa overlap
(5-1182:1-1163)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10 20 30 40 50 60

gi|183 MEEN-NQNQCIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQFLVSNFVPGGGF
10 20 30 40 50

Cry1Ac VLGLVDIIWGI FGPSSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
70 80 90 100 110 120

gi|183 LVGLIDFVWGI FGPSSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60 70 80 90 100 110

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
130 140 150 160 170 180

gi|183 WEEDPNPATRTRVIDRFRILDGLLERDIPSPRISGFVEPPLLSVYAQAANLHLAILRDSV
120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
190 200 210 220 230 240

gi|183 IFGERWGLTTINVNENYNRLIRIHIDEYADHCANTYNRGLNNLPKSTYQDWITYNRLRRDL
180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQG-----IEGS-
250 260 270 280 290

gi|183 TLTVLDIAAFFPNYDNRRYPIQPVGQLTREVYTDPLI-NFNPLQLSVAQLPTFNVMESSA
240 250 260 270 280 290

Cry1Ac IRSPHLMIDILNSITIIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLLYGTMGNAAPQQ
300 310 320 330 340 350

gi|183 IRNPHLFDILNLTIFTDFWFSVGRNFYWGGRVVISSLIG--GGNITSPIYGREANQEPFR
300 310 320 330 340 350

Cry1Ac RIVAQLGQGVYRTLSSTLYR---RPFNIGINNQLSVLDGTEFAYGTSNLP SAVA YRKSG
360 370 380 390 400

gi|183 SFT--FNGPVFRTLSNPTLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRG
360 370 380 390 400

Cry1Ac TVDSLDEIPPQNNVPPRQGFSHRLSHVSMF-RSGFSSNSVSIIRAPMFSWIHRSAEFNN
410 420 430 440 450 460

gi|183 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHPFST
470 480 490 500 510 520

gi|183 TIDPERINQIPLVKGFVWGGT SVITGPGFTGGDILRRNTFGDFVS---LQVNINSPIT
470 480 490 500 510

Cry1Ac STRYRVRVRYASVTPIHLLNVNWNSSI-----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|183 Q-RYRLRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDS
520 530 540 550 560 570

590 600 610 620 630

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Cry1Ac  NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
gi|183  NPFSSFRANPDIIGISEQPLFGAGSISGELYIDKIEIILADATFAESDLERAQKAVNAL
      580      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDS
gi|183  FTSSNQIGLKTVDYHIDRVSNLVECLSEDFCLDEKRELSKVKHAKRLSDERNLLQDP
      640      650      660      670      680      690

      700      710      720      730      740      750
Cry1Ac  NFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKPKAFT
gi|183  NFRGINRQLDRGWRGSTDITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKPKAYT
      700      710      720      730      740      750

      760      770      780      790      800      810
Cry1Ac  RYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW
gi|183  RYQLRGYIEDSQDLEIYLIRYNAKHETVNVPGTGSWLPLSAPSPIGKC-----
      760      770      780      790      800

      820      830      840      850      860      870
Cry1Ac  NPDLDSCSRDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
gi|183  -----AHSHHFLSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNLEFLE
      810      820      830      840

      880      890      900      910      920      930
Cry1Ac  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIA
gi|183  EKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIA
      850      860      870      880      890      900

      940      950      960      970      980      990
Cry1Ac  MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
gi|183  MIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGL
      910      920      930      940      950      960

      1000     1010     1020     1030     1040     1050
Cry1Ac  SCWNVKGHVDVEEQNNQRSVSVLVPWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
gi|183  SCWNVKGHVDVEEQNNHRSVSVLVPWEAEVSVQEVVCPGRGYILRVYAYKEGYGEGCVTI
      970      980      990      1000     1010     1020

      1060     1070     1080     1090     1100
Cry1Ac  HEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVP
gi|183  HEIENNTDELKFSNCVEEIVPNNTVTCNDYATQEEYEGYTSRNRGYDYGAYESNSSVP
      1030     1040     1050     1060     1070     1080

      1110     1120     1130     1140     1150     1160
Cry1Ac  ADYASVYEEKSYTDGRRENPCFENRGYRDYTPPLVGYVTKLEYFPETDKVWIEIGETEG
gi|183  ADYASAYEEKAYTDGRDNPCESNRGYGDYTPPLPAGYVTKLEYFPETDKVWIEIGETEG
      1090     1100     1110     1120     1130     1140

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      1170     1180
Cry1Ac  TFIVDSVELLLMEE
gi|183  TFIVDSVELLLMEE
      1150     1160

>>gi|15110442|gb|AAE68106.1| Sequence 23 from patent US (1186 aa)
      initn: 3876 init1: 1829 opt: 2289 Z-score: 2688.8 bits: 509.5 E(): 7.6e-141
Smith-Waterman score: 4455; 62.532% identity (78.725% similar) in 1161 aa overlap
(55-1182:72-1186)

      30      40      50      60      70      80
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDI IWGIFGP---SQWDAFL
gi|151  AEGNNIDPFVSASTVQTGINIAGRILGVLGVFPAGQIASFYSLVGLWPRGRDPWEIFL
      50      60      70      80      90      100

      90      100     110     120     130     140
Cry1Ac  VQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN PALREEMRIQFNDM
gi|151  EHVQLIRQQVTENTRDTALARLQGLGNSFRAYQSSLEDWLENRDDARTSRVLYTQYIAL
      110     120     130     140     150     160

      150     160     170     180     190     200
Cry1Ac  NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLT
gi|151  ELDFLNAMPLFAIRNQEVP LLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYRQV
      170     180     190     200     210     220

      210     220     230     240     250     260
Cry1Ac  RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|151  EKTREYSDYCARWYNTGLNLRGTNAESWLRYNQFRRLTLGLVLDLVALFPYSYDTRVYPM
      230     240     250     260     270     280

      270     280     290     300     310
Cry1Ac  RTVSQTLTREIYTNPVLE-NFDGSGFRG-----SAQGI EGS-IRSPHMDILNSITIIY
gi|151  NTSAQLTREIYTDPIGRTNAPSGFASTNWFNANNAPSFSAIEAAVIRPPHLLDFPEQLTIF
      290     300     310     320     330     340

      320     330     340     350     360
Cry1Ac  TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQORIVAQLGQGVYRT
gi|151  SVLSRWSNTQYMMYVWGHRLSRTIRGS---LSTSTHGNT-NTSINPVTLQFTSRDVIYRT
      350     360     370     380     390

      370     380     390     400     410
Cry1Ac  LS---STLYRRPFNIGINNQLSVLDGTFEYAGTSSNLP SAVA YRKS GT--VDSLDEIIPP
gi|151  ESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTI GYTGVTGQLFDS ETELPP
      400     410     420     430     440     450

      420     430     440     450     460     470
Cry1Ac  QNNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIP
gi|151  ETTERPNYESYSHRLSNIRLI-SG-----NTLRAPVYSWTHRSADRTINTISSDSITQIP
      460     470     480     490     500

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480      490      500      510      520      530
Cry1Ac AVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTST-RYRVRVRY
      . . . . .
gi |151 LVKSFNLNSGTSVVSVPSTMSANESLTSQSFRFAEFPVVGISASGSQTAGISISN
510      520      530      540      550      560

      540      550      560      570      580      590
Cry1Ac ASVTPIHNLNVNMGNSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--N
      . . . . .
gi |151 AASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAEFPVVGISASGSQTAGISISN
      570      580      590      600      610      620

      600      610      620      630      640      650
Cry1Ac FSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
      . . . . .
gi |151 NAGRQTFHFDKIEFIPITATLEAESDLERAQKAVNALFTSSNQIGLKTVDVTDYHIDRVSN
      630      640      650      660      670      680

      660      670      680      690      700      710
Cry1Ac LVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQG
      . . . . .
gi |151 LVECLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITIQG
      690      700      710      720      730      740

      720      730      740      750      760      770
Cry1Ac GDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNA
      . . . . .
gi |151 GDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLRIRYNA
      750      760      770      780      790      800

      780      790      800      810      820      830
Cry1Ac KHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSL
      . . . . .
gi |151 KHETVNVPGTGLWPLSAQSPIGK-----AHHSHHFFSL
      810      820      830

      840      850      860      870      880      890
Cry1Ac DIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKR
      . . . . .
gi |151 DIDVGCTDLNEDLGWVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKR
      840      850      860      870      880      890

      900      910      920      930      940      950
Cry1Ac EKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPPELSVI
      . . . . .
gi |151 EKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMHAADKRVHSIREAYLPPELSVI
      900      910      920      930      940      950

      960      970      980      990      1000      1010
Cry1Ac PGVNAAIPEELEBGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLWV
      . . . . .
gi |151 PGVNAAIPEELEBGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNHRSVLWV
      960      970      980      990      1000      1010

      1020      1030      1040      1050      1060      1070
Cry1Ac PEWEAEVVSQEVVRCPRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVIYPN
      . . . . .
gi |151 PEWEAEVVSQEVVRCPRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEVEYPN
      1020      1030      1040      1050      1060      1070

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1080      1090      1100      1110      1120      1130
Cry1Ac NTVTCNDYTVNQEEYGGAYTSRNRGYNEA----PSVPADYASVYEKSYTDGRRENPCF
      . . . . .
gi |151 NTVTCNDYTATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEKAATDGRRRNPCE
      1080      1090      1100      1110      1120      1130

      1140      1150      1160      1170      1180
Cry1Ac NRGYRDYTPPLVGVYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi |151 NRGYGDYTPPLPAGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170      1180

>>gi|42682720|gb|AAS28783.1| Sequence 23 from patent US (1186 aa)
      initn: 3876 init1: 1829 opt: 2289 Z-score: 2688.8 bits: 509.5 E(): 7.6e-141
      Smith-Waterman score: 4455; 62.532% identity (78.725% similar) in 1161 aa overlap
      (55-1182:72-1186)

      30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGFVLGLVDIIWGFIP---SQWDAFL
      . . . . .
gi |426 AEGNNDPFFVSASTVQTGINIAGRILGVLPVFPAGQIASFYSFLVGLWPRGRDPWEIFL
      50      60      70      80      90      100

      90      100      110      120      130      140
Cry1Ac VQIEQLINRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
      . . . . .
gi |426 EHVQLIRQVQVNTENTRDTALARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIAL
      110      120      130      140      150      160

      150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLT
      . . . . .
gi |426 ELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTQEIQRYYERQV
      170      180      190      200      210      220

      210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPI
      . . . . .
gi |426 EKTREYSYCARWYNTGLNLRGTNAESWLRYNQFRRLTLGLVLDLVALFPYSYDTRVYPM
      230      240      250      260      270      280

      270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPVLE-NFDGSRG-----SAQGIEGS-IRSPHLMIDLNSITIIY
      . . . . .
gi |426 NTSAQLTREIYTDPIGRNTAPSGFASTNWFNNAPSFSIAEAAVIRPPHLLDFPEQLTIF
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
      . . . . .
gi |426 SVLSRWSNTQYMNWVWGHRLSRTIRGS--LSTSTHGNT-NTSINPVTLQFTSRDQVYRT
      350      360      370      380      390

      370      380      390      400      410
Cry1Ac LS----STLYRRPFNIGINNQLSVLDGTFEYAGTSSNLPASAVYRKSQT--VDSLDEIPP
      . . . . .
gi |426 ESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTIYGTGVGQLFDSSETLPP
      400      410      420      430      440      450

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300      310      320      330      340      350
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEI
gi|598  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
360      370      380      390      400      410
Cry1Ac  GQGVYRTLSSSTLYRRPFNIGINNQQLSV-LDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEI
gi|598  PRPFYRTLSDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI
420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
gi|598  PPQDMSGAPWNDYSHVLNHFVFRWVPEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
480      490      500      510      520      530
Cry1Ac  IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR
gi|598  IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
540      550      560      570      580      590
Cry1Ac  YASVTPIHNLVNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
gi|598  YASTNLRITYVTAGERIFAGQFNKTMDTGDLTFQSFYATINTAFTFPMSSQSSFTVGA
600      610      620      630      640      650
Cry1Ac  RNFSGTAGVIIDRFFPIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|598  DTFSSGNEVYIDRFLIPVTATFEAEYDLERAQKAVNELFTSTNQLGLKTDVTDYHIDRV
660      670      680      690      700      710
Cry1Ac  SNLVITYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
gi|598  SNLVECLSDDEFCLDEKEELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
720      730      740      750      760      770
Cry1Ac  QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY
gi|598  QGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY
780      790      800      810      820      830
Cry1Ac  NAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHF
gi|598  NAKHETVNVPGTGSWPLSVQSPIGK-----AHHSHHF
840      850      860      870      880      890
Cry1Ac  SLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
gi|598  SLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRD
900      910      920      930      940      950
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS

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gi|598  KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELS
860      870      880      890      900      910
960      970      980      990      1000      1010
Cry1Ac  VIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQORSVL
gi|598  VIPGVNADIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNHRSVL
920      930      940      950      960      970
1020      1030      1040      1050      1060      1070
Cry1Ac  VVPEWAEVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEIY
gi|598  VVPEWAEVSQEVVRCVPCGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEEVY
980      990      1000      1010      1020      1030
1080      1090      1100      1110      1120
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
gi|598  PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSVSPADYASAYEEKAYTDGRRDNPC
1040      1050      1060      1070      1080      1090
1130      1140      1150      1160      1170      1180
Cry1Ac  EFNRGYRDYTPLVGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|598  ESNRGYGDYTPLVAGYVTKELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1100      1110      1120      1130      1140
>>gi|5973551|gb|AAE12831.1| Sequence 38 from patent US 5 (1148 aa)
initn: 4517 initl: 1822 opt: 2282 Z-score: 2680.7 bits: 508.0 E(): 2.1e-140
Smith-Waterman score: 5063; 67.452% identity (82.422% similar) in 1189 aa overlap
(5-1182:1-1148)
10      20      30      40      50      60
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|597  MENNIQ-NQCVYINCLNNEVEILNEER-STGRPLPLDISLSLTFLLSEFVPGVGV
10      20      30      40      50
70      80      90      100      110      120
Cry1Ac  VLGLVDIIWGFPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFRE
gi|597  AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSEYIYIEALRE
60      70      80      90      100      110
130      140      150      160      170      180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|597  WEANPNNAQLREDVRIRFANTDDALITAINNF'TLTSFEIPLLSVYVQAANLHLSLRDAV
120      130      140      150      160      170
190      200      210      220      230      240
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDRWIRYNQFRREL
gi|597  SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDTYNQGLLENLRTNTRQWARFNQFRDRL
180      190      200      210      220      230
250      260      270      280      290
Cry1Ac  TLTVLVDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLEN--PDGSRFGSAQGLEGSIRSP

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gi|597 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRPP
      240      250      260      270      280      290
      300      310      320      330      340      350
Cry1Ac HLM DILNSIT IYTD AHRGEY YW SGHQIMAS PVFGSGPEFT FPLYGTMGNAAPQQRIVAQL
      .....
gi|597 HLMDFMNSL FVTAET VRSQTVWGGH--LVSSRNTAGNR INFPSYGVF-NPGGAIWIADED
      300      310      320      330      340      350
      360      370      380      390      400      410
Cry1Ac GQGVYRTL SSTLYRRPFNIGINNQLSV-LDGTEFAYGTSSNLPSAVYRKS GTVDSLDEI
      .....
gi|597 PRPFYRTL SDPVFVRG---GFGNPHYVLGLRGVAFQQ-TGNT-HTRTFRNSGTIDSLDEI
      360      370      380      390      400
      420      430      440      450      460      470
Cry1Ac PPQNNVPP RQGF SHRLSHVSMFRSGFSNS SVSII RAPMFSWIHRSAEFNNIIASDSITQ
      .....
gi|597 PPQDNSGAP WNDYSHV LNHVTFVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      410      420      430      440      450      460
      480      490      500      510      520      530
Cry1Ac IPAVKGNFL FNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVR
      .....
gi|597 IPLVKAHTL QS GTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ---RYRARIR
      470      480      490      500      510      520
      540      550      560      570      580      590
Cry1Ac YASVTP IHLNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      .....
gi|597 YASTNLR IYVTVAGERIFAGQFNK TMDTGDPLTFQSPSYATINTAFTFPMSQSFTVGA
      530      540      550      560      570      580
      600      610      620      630      640      650
Cry1Ac RNFSGTAG V IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
      .....
gi|597 DTFSSGNE VYIDRFELIPVTATFEAEYDLERAQKAVNELFTSTNQIGLKTVDVTDYHIDRV
      590      600      610      620      630      640
      660      670      680      690      700      710
Cry1Ac SNLVTYLS DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      .....
gi|597 SNLVECLS DEFCLDEKEELS KVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITI
      650      660      670      680      690      700
      720      730      740      750      760      770
Cry1Ac QGGDDVFKEN YVTL SGT FDECYPTYLYQKIDESK LKAFTRYQLRGI EDSQDLEIYSIRY
      .....
gi|597 QGGDDVFKEN YVTL SGT FDECYPTYLYQKIDESK LKAYTRYQLRGI EDSQDLEIYLIRY
      710      720      730      740      750      760
      780      790      800      810      820      830
Cry1Ac NAKHETVNV PGTGSLWPLSAQSP I GKGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHSHF
      .....
gi|597 NAKHETVNV PGTGSLWPLSVQSP I GKC-----A HSHSHF
      770      780      790
      840      850      860      870      880      890
Cry1Ac SLDIDVGC TDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD

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      .....
gi|597 SLDIDVGC TDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850
      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAM IHAADKRVHSIREAYLPELS
      .....
gi|597 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAM IHAADKRVHSIREAYLPELS
      860      870      880      890      900      910
      960      970      980      990      1000      1010
Cry1Ac VIPGVNAAL FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
      .....
gi|597 VIPGVNADIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
      920      930      940      950      960      970
      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCVEE EYI
      .....
gi|597 VVPEWEAEVSQEVVRVCPGRGYILRV TAYKEGYGEGCVT IHEIENNTDELKFSNCVEE EVY
      980      990      1000      1010      1020      1030
      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNPC
      .....
gi|597 PNNTVTCNDYATQEEYEGYTYSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNPC
      1040      1050      1060      1070      1080      1090
      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRGYRDY TPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      .....
gi|597 ESNRGYGDY TPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1100      1110      1120      1130      1140
>>gi|5973550|gb|AAE12830.1| Sequence 37 from patent US 5 (1148 aa)
      initn: 4511 initl: 1822 opt: 2282 Z-score: 2680.7 bits: 508.0 E(): 2.1e-140
      Smith-Waterman score: 5057; 67.368% identity (82.338% similar) in 1189 aa overlap
      (5-1182:1-1148)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNIN ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      .....
gi|597 MENNIQ-NQCVPYNCLNNEVEILNEER-STGR LPLDISLSLTRFLLEFVPGVGV
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIE EFARNQAI SREGLSNLYQIYAESFR E
      .....
gi|597 AFGLFDLIWGFITPSDWSLFLQIEQLIEQRIETLERNRAITTLRGLADSYE IYIEALRE
      60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTN PALREEMRIQFNDMNSALTTA IPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      .....
gi|597 WEANPNNAQLRE D V RIRFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV
      120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDH A VRWYNTGLERWVGPDSRDWIRYNQFRREL

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      180      190      200      210      220      230
gi|597 SFGQGWGLDIATVNNHNYRNLINLIHRYTKHCLDLYNQLENLRGNTNRQWARFNGFRDRD
      250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLEN--FDGSRFRGSAQIEGSIKSP
      240      250      260      270      280      290
gi|597 TLTVLDIVALFPNVDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPNGFNRAEFGVRRP
      300      310      320      330      340      350
Cry1Ac HLMIDLNSITIIYTDARHGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
      300      310      320      330      340      350
gi|597 HLMDFMNSLFTVTAETVRSQTVWGGH--LVSSRNTAGNRINFPSYGVF-NPGGAIWADED
      360      370      380      390      400      410
Cry1Ac GQGVYRTLSSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPASVYRKSQTVDSLDEI
      360      370      380      390      400
gi|597 PRPFYRTLSDPVVFVRG---GFGNPHYVLGLRGVAFQQ-TGTTN-HTRTFRNSGTIDSLDEI
      420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQ
      410      420      430      440      450      460
gi|597 PPQDMSGAPWNDYSHVLNHVTFVVRWPGEISGSDSWRAPMFSWTHRSATPTNTIDPERITQ
      480      490      500      510      520      530
Cry1Ac IPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYLEVPIHPSTSTRYRVRVR
      470      480      490      500      510      520
gi|597 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR
      540      550      560      570      580      590
Cry1Ac YASVTPIHNLNVNWNSSIFSNTVVPATATSLDNLQSSDFGYFESANAFTSSLGN---IVGV
      530      540      550      560      570      580
gi|597 YASTINLRIYVTVAGERIFAGQFNKMTMDTGDELTFQSFYATINTAFTFPMSQSSFTVGA
      600      610      620      630      640      650
Cry1Ac RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDVYHIDQV
      590      600      610      620      630      640
gi|597 DTFSSGNEVYIDRFELIPVTATFEAEYDLERAQKAVNELFTSINQIGLKTVDVTDVYHIDRV
      660      670      680      690      700      710
Cry1Ac SNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI
      650      660      670      680      690      700
gi|597 SNLVECLSDDEFCLDEKEELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWRGSTDITII
      720      730      740      750      760      770
Cry1Ac QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY
      710      720      730      740      750      760
gi|597 QGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAYTRYQLRGIYEDSQDLEIYLRIR
      780      790      800      810      820      830

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Cry1Ac NAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHSHF
      770      780      790
gi|597 NAKHETVNVPGTGLWPLSVQSPIGKC-----AHSHSHF
      840      850      860      870      880      890
Cry1Ac SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      800      810      820      830      840      850
gi|597 SLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNMIAMIHAADKRVHSIREAYLPELS
      860      870      880      890      900      910
gi|597 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNMIAMIHAADKRVHSIREAYLPELS
      960      970      980      990      1000      1010
Cry1Ac VIPGVNAEIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
      920      930      940      950      960      970
gi|597 VIPGVNADIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNHRSVL
      1020      1030      1040      1050      1060      1070
Cry1Ac VVPEWEAEVSQEVRRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYI
      980      990      1000      1010      1020      1030
gi|597 VVPEWEAEVSQEVRRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCEVEEYI
      1080      1090      1100      1110      1120
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRENPC
      1040      1050      1060      1070      1080      1090
gi|597 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNSSVPADYASAYEEKAYTDGRRDNC
      1130      1140      1150      1160      1170      1180
Cry1Ac EFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1100      1110      1120      1130      1140
gi|597 ESNRNGYDTPPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
>>gi|5987873|gb|AAE17038.1| Sequence 37 from patent US 5 (1148 aa)
  initn: 4511 init1: 1822 opt: 2282 Z-score: 2680.7 bits: 508.0 E(): 2.1e-140
  Smith-Waterman score: 5057; 67.368% identity (82.338% similar) in 1189 aa overlap
  (5-1182:1-1148)
      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEPIYCNLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50
gi|598 MENNIQ-NQCVPNCLNPEVEILNEER-STGRPLDISLSLTRFLLSEFVPGVGV
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFPSQWDAFLVQIEQLINQRIEIEFARNQAIISREGLSNLYQIYAESFRE
      60      70      80      90      100      110
gi|598 AFGLFDLIWGFITPDSWLSFLQIEQLIEQRIETLERNRAITTLRGLADSYEIIYIALRE
      130      140      150      160      170      180

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Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS  
 gi|598 WEANPNNAQLREDVRIREFANTDDALITAINNFTLTSFEIPLLSVYVQAANLHLSLLRDAV  
 120 130 140 150 160 170

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVGPDSRDWIRYNOFRREL  
 gi|598 SFGQGWGLDIATVNNHYNRLINLIHRYTKHCLDLYNQGLENLRGNTNRQWARFNQFRDDL  
 180 190 200 210 220 230

Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQTLREIYTNPLEN--FDGSRGSAQGIIEGSIRSP  
 gi|598 TLTVLDIVALFPNYDVRTYPIQTSSQLTREIYTSVIEDSPVSANIPGNFRAEFGVRPP  
 240 250 260 270 280 290

Cry1Ac HLMIDLNSITIIYDHAHRGEYVWVSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL  
 gi|598 HLMDFMNSLFTVAETVRSQTVWGGH--LVSSRNTAGNRINFPSPYGVF--NPGGAIWIADSD  
 300 310 320 330 340 350

Cry1Ac GQGVYRTLSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPASAVYRKSQTVDSLDEI  
 gi|598 PRPFYRTLSDPVVFVRG--GFGNPHYVLGLRGVAFQQ-TGTN-HTRTFRNSGTIDSLDEI  
 360 370 380 390 400 410

Cry1Ac PFQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQ  
 gi|598 PFQDNSGAPWVNDYSHVNLHVTFVVRWPEIGSSDSWRAPMFSWTHRSATPTNTIDPERITQ  
 420 430 440 450 460 470

Cry1Ac IPAVKGNFLNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVR  
 gi|598 IPLVKAHTLQSGTTVVRGPGFTGGDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIR  
 480 490 500 510 520 530

Cry1Ac YASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGN--IVGV  
 gi|598 YASTNLRIYVTVAGERIFAGQFNKTMDTGDLTFQSFYATINTAFTFPMQSSFTVGA  
 540 550 560 570 580 590

Cry1Ac RNFSGTAGVIDRFEFIPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV  
 gi|598 DTFSSGNEVYIDRFELIPVTTATFEAEYDLERAQKAVNELFTSINQIGLKTVDVTDYHIDRV  
 600 610 620 630 640 650

Cry1Ac SNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITI  
 gi|598 SNLVECLSDDEFCLDEKEELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWGSTDITI  
 660 670 680 690 700 710

Cry1Ac QGGDDVFKENYVTLSGTFDECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRY  
 gi|598 QGGDDVFKENYVTLSGTFDECYPTLYLQKIDESKLFKAYTRYQLRGYIEDSQDLEIYLIRY  
 720 730 740 750 760 770

Cry1Ac NAKHETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRGEKCAHSHHF  
 gi|598 NAKHETVNVPGTSLWPLSVQSPIGKC-----AHSHSHHF  
 780 790 800 810 820 830

Cry1Ac SLDIDVGCTDLNEDLGVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
 gi|598 SLDIDVGCTDLNEDLGVVWVIFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD  
 840 850 860 870 880 890

Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS  
 gi|598 KREKLEWETNIVYKEAKESVDALFVNSQYDRLQADTNIAMIHAADKRVHSIREAYLPELS  
 900 910 920 930 940 950

Cry1Ac VIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSVL  
 gi|598 VIPGVNADIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNHRSVL  
 960 970 980 990 1000 1010

Cry1Ac VVPEWAEVSVQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEII  
 gi|598 VVPEWAEVSVQEVVRCVPCGRGYILRVTAAYKEGYGEGCVTTHEIENNTDELKFSNCVVEEIV  
 1020 1030 1040 1050 1060 1070

Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNENP  
 gi|598 PNNTVTCNDYATQEEYEGTYTSRNRGYDGAYESNNSVPADYASAYEEKAYTDGRRDNPC  
 1080 1090 1100 1110 1120 1130

Cry1Ac EFNRGYRDYTPLPVGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 gi|598 ESNRGYGDYTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE  
 1140 1150 1160 1170 1180 1190

>>gi|81302556|gb|ABB70817.1| insecticidal crystal protei (1154 aa)  
 initn: 2296 init1: 640 opt: 2168 Z-score: 2546.2 bits: 483.1 E(): 6.6e-133  
 Smith-Waterman score: 2493; 40.482% identity (67.528% similar) in 1161 aa overlap  
 (64-1182:90-1152)

Cry1Ac ETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIGWIFGPSQ-WDAFLVQIEQLINQRI  
 gi|813 GTAVLATARKIGGKIVKAIGEQLSKILKEILDYLPWSSSSSNWEEEMKVEYVLDKKI  
 40 50 60 70 80 90

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100      110      120      130      140      150
Cry1Ac EEFARNQALISRLLEGLSNLYQIYAESFRWEADPTNPALREEM-RIQFNDMNSALTTAIPL
gi|813 EEYARNKALAVLEGIGNAVESYSALEAWELESSERSLELVLERYQFA-VQFA-RSSMPS
120      130      140      150      160      170

160      170      180      190      200      210
Cry1Ac FAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHA
gi|813 FAIINYEIPLLATYANAANVHLLMRDIQIYGDRWGISQNDMNLFLKEQEIYTSYSEHC
180      190      200      210      220      230

220      230      240      250      260
Cry1Ac VRWYNTGLERVW---GPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLT
gi|813 VKWYNEGLNQLKTKGASGLVWENYNSFRTEMTIMVLDLVAIFPAYNMSKYP IESTVELT
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac REIYTNPLENFDG-----SFRGSAQ---GIEG-SIRSPHMDILNSITIYTD--AHR
gi|813 RTIYTDPL--GYTGSNDHEPTYYSKAPFSSIESRAVLAPSLFKWITQLEVYTKKYSYS
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL-GQGVYRTLSTSLYR
gi|813 SQYTTLWTGLRVIAOPT---KDFTDTVYDYGSSSGSENKDVFDLYGNDVYDTSQVSSVY
360      370      380      390      400      410

380      390      400      410      420
Cry1Ac RPFNIG-INNQLSVL----DGT-EFAYGTSSNLPs-AVYRKSQGTVDLSLDEIPPQNNV
gi|813 KPTGGGHFVGPQFRLFWITKSNGLREQIFNYANNMGSYSAYRFSK----DELPIELLQ-
420      430      440      450      460

430      440      450      460      470      480
Cry1Ac PPRQG----FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|813 PPLFGDIEEYSHRLSHVSEVIKDYGEGII----PVLGWTHVSVTRDNR IYDPDKITQLPA
470      480      490      500      510      520

490      500      510      520      530
Cry1Ac VKGNFLFNGSVI-SGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTSTRYRVRYAS
gi|813 VKMYELLSSAVVVKGPGFTGGDLVKRTGNGGI----GHFNVSVESPGTQ-RYRLRIRYSS
530      540      550      560      570

540      550      560      570      580      590
Cry1Ac -VTPI-HLVNWNWGNSSIFSNTPATATSLDNLQSSDFGYFESANAFT---SSLGNV-VGVR
gi|813 EVSGVFHMQIN--DIETIQGEFSSSTADSTSTLSSEAFQLREYSTTFTFPPTNMTKIKVSLG
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEP I PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|813 AIEGAGGFYLDRIEFPVDENHDNRVTLEKAQKAVNALFTA-GRNALQTDVTDYKVDQVS
640      650      660      670      680      690

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660      670      680      690      700      710
Cry1Ac NLVVTYLSDEFCLDEKRELSEKVKHAKRRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
gi|813 ILVDCVSGELYPNEKRELLSLVKYAKRRLSYSRNLLDPTFDSINSSDENGWYSGNGIATG
700      710      720      730      740      750

720      730      740      750      760      770
Cry1Ac GGDDVFKENYVTLSGTFDECPYTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYN
gi|813 NGNFVFKGNLYLIFSGTNDTQYPTLYLYQKIDESKLFKEYTRYKLRGFIENSQDLEAVVIRVD
760      770      780      790      800      810

780      790      800      810      820      830
Cry1Ac AKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSH
gi|813 AKHETLDV--SNLLP--DISPVNACGEPNRCALQYLDENPRLECSSIQDG--ILSDSH
820      830      840      850      860

840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKW
gi|813 SFSLNIDTGSIDFNENVGIWVLFKISTPEGYAKFGNLEVIEDSPVIGEALARVKRQETKW
870      880      890      900      910      920

900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPE
gi|813 RNKLTQLRTETQAIYTRAKQAIQDNVFTNAQDQSHLKIQTFAAIVAAARKVQSIREAYMSW
930      940      950      960      970      980

960      970      980      990      1000      1010
Cry1Ac LSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRS
gi|813 LSVIPGVNYPITELNERVQRAFQLYDVRNVVRNGRFLNGVSDWIVTSDVKVQEEENG-N
990      1000      1010      1020      1030      1040

1020      1030      1040      1050      1060      1070
Cry1Ac VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCEVEE
gi|813 VLVLSNWDQVQLQCLKLYQDRGYILRVTAARKEGLGEGYITITDEEGHTDQLTFGTC--EE
1050      1060      1070      1080      1090      1100

1080      1090      1100      1110      1120      1130
Cry1Ac IYPNNTVTCDNYTVNQEYEGGAYTSRNRGYNEAPSPADYASVYEKSYTDGRRNPCEP
gi|813 IDASNTF-----
1110

1140      1150      1160      1170      1180
Cry1Ac NRGYRDYTPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|813 -----VTTGYITKELEFFPDTEKVRIEIGETEGTFQVESIELFLMEDLC
1120      1130      1140      1150

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>>gi|3993437|gb|AAC86865.1|AR006381 Sequence 2 from pate (1149 aa)
initn: 1550 initl: 503 opt: 2094 Z-score: 2459.0 bits: 466.9 E(): 4.8e-128
Smith-Waterman score: 2127; 36.372% identity (66.483% similar) in 1086 aa overlap
(22-1067:59-1109)

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Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL  
gi|399 LANDQTNTLQNMNYKDYLMKTESTNAELSRNPGTFISAQDAVGTG---IDIVSTIISGL-  
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVLGLVDIIWGFIFGPSQ---WDAFLVQIEQLINQRIEEFARNQAISRLEGL  
gi|399 --GIPVLGEVFSILGSLIGLLWPSNNENVWQIFMNRVEELIDQKILDSVRSRAIADLANS  
90 100 110 120 130 140

Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ  
gi|399 RIAVEYYQNALEDWRKNPHSTRSAALVKERFGNAEAILRTNMGFSQTNYEPTLLPTYAQ  
150 160 170 180 190 200

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSD  
gi|399 AASLHLLVMRDVQIYGKEWGYPQNDIDLIFYKEQVSYTARYSDHCVQWYNAGLNKLRGTGA  
210 220 230 240 250 260

Cry1Ac RDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRFG-  
gi|399 KQWVDYNRFRREMMVMVLDLVALFPNYDARIYPLETNAELTREIFTDVPVGSYVTTQSSSTL  
270 280 290 300 310 320

Cry1Ac -----SAQIEGSIKSPHMLDILNSITITYTDAHRG---EYY--WSGHQIMASP  
gi|399 ISWYDMIPAAALPSFSTLENLLRKPDPFTLLQEIRMYTSFRQNGTIEYYNYWGGQRLTLYS  
330 340 350 360 370 380

Cry1Ac VGFSGPEPTFFPLYGTMGNAAPQQRIVAQLGQG-VYRTLSSTLYRPFNI-GINNQLSVL  
gi|399 IYGS---SFKYIS--GVLAGAEDIIP-VGQNDIYRVVWYTYIGRYTNSLLGVNPTVTFYFS  
390 400 410 420 430 440

Cry1Ac DGTEFAYGTSNLPASAVYRKSQGTVDLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNS  
gi|399 NNTQKTYSKPKQFAGGI---KTIDSGEELTYEN-----YQSYSHRVSYITSFEIKSTGG  
440 450 460 470 480

Cry1Ac SVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRL  
gi|399 TVLGV-VPIFGWTHSSASRNNFIYATKISQIPINKASRTSGGAVWNFQEBLYNGGPFVMKL  
490 500 510 520 530 540

Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNWNWG---NSSIFSNTVPAT  
gi|399 SSGSQVIN---LRVATDAKGASQRYSRIRIRYASDRAGKFTISSRSPENPATYSASIAYT

Cry1Ac ATSLDN--LQSSDFGYFESANAFTSSLGNI---VGVRFNSGTAGVIIDRFEFIPVTATL  
gi|399 NTMSTNASLTYSTFAYAESGPINLGLSGSSRTFDISITKEAGAANLYIDRIEFIPVNTLTF  
610 620 630 640 650 660

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTVYLSDEFCLDEKRELSKV  
gi|399 EAEEDLDVAKKAVNGLFTNEKD-ALQTSVTDYQVQANLIECLSDLEYPNKRLMWDVA  
670 680 690 700 710 720

Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGTDFD---E  
gi|399 KEAKRLVQARNLLQDTGFNRIN--GENGWGTSTGIEVVEGDVLFKDRSLRLTSAREIDTE  
730 740 750 760 770

Cry1Ac CYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSA  
gi|399 TYPTYLYQQIDESLLKPYTRYKLGFIGSSQDLEIKLIRHRANQIVKNVPD--NLLP--D  
780 790 800 810 820 830

Cry1Ac QSPIGKCGEPNRCAP--HLEWNPDLDCSCRDEKCAHSHHFLSLDIDVGTDLNEDLGVW  
gi|399 VRFVNSCGVDRCSQYVDANLALENNGENGMSSD-SHAFSFHIDTGEIDLNENTGIW  
840 850 860 870 880 890

Cry1Ac VIFKIKTQDGHARLGNLFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKE  
gi|399 IVFKIPTTNGNATLGNLEFVEEGPLSGETLEWAQQQEQWQDKMARKRAASEKTYAAKQ  
900 910 920 930 940 950

Cry1Ac SVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIF  
gi|399 AIDRLFADYQDQKLNKSGVEMSDLLAAQNLVQSIPIVYNDALPEIPGMNYTSFTELNRLLQ  
960 970 980 990 1000 1010

Cry1Ac TAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVPEWEAEVVSQEVRCVCPG  
gi|399 QAWNLYDLQNAIPNGDFRNGLSNWNATSDVNVQ-QLSDTSLVIVPNWNSQVVSQFTVQPN  
1020 1030 1040 1050 1060 1070

Cry1Ac RGYILRVTAAYKEGYGECVTEIHEIENNTDELKFSNCVVEEIIYNNVTVCNDYTVNQEYEG  
gi|399 YRYVLRVTRARKEGVGDYVVIIRDGANQTEITLTFNICDDDTGVLSTDQTSYITKTVEFTPS  
1080 1090 1100 1110 1120 1130

Cry1Ac GAYTSRNRGYNEAPSPADYASVYEKSYTDGRRENPCFENRGRDYTPPLVGYVTKLE

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gi|399 TEQVWIDMSETEVYST
1140
>>gi|5972897|gb|AAE12788.1| Sequence 2 from patent US 58 (1149 aa)
initn: 1550 initl: 503 opt: 2094 Z-score: 2459.0 bits: 466.9 E(): 4.8e-128
Smith-Waterman score: 2127; 36.372% identity (66.483% similar) in 1086 aa overlap
(22-1067:59-1109)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLF
gi|597 LANDQTNTLQNMNYKDYLMKMTTESTNAELSRNPGTFISAQDAVGTG---IDIVSTIIISGL-
Cry1Ac SEFVPGAGFVLGLVDIIWGFGPSQ---WDAFLVQIEQLINQRIIEFARNQAI RLEGL
gi|597 --GIPVLGEVFSILGSLIGLLWPSNNENVWQIFMNRVEELIDQKILDSVRSRAIADLANS
Cry1Ac SNLQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|597 RIAVEYYQNALEDWRKNPHSTRSAALVKERFGNAEAILRTNMGFSQ'NYETPLLPYTAQ
Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDS
gi|597 AASLHLLVMRDVQIYGKEWGYPQNDIDLKYEQVSYTARYSDHCQVQWYNAGLNKLRGTGA
Cry1Ac RDWIRYNFRRELTLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSRFG-
gi|597 KQWVDYNRFRREMMVLDLVALFPNYDARIYPLETNAELTREIFDTPVGSYVTVQSSTL
Cry1Ac -----SAQGI EGSIRSPHLM DILNSITIYTD AHRG---EYY--WSGHQIMASP
gi|597 ISWYDMIPAALPSFSTLENLLRKPDPFTLLQEIRMYTSFRQNGTIEYYNYWGGQRLTLSY
Cry1Ac VGFSGPEPTFFPLYGTMGNAAPQQRIVAQLGQG-VYRTLSSTLYRRPFNI-GINNQQLSVL
gi|597 IYGS---SFKNYS--GVLAGAEDIIP-VGQNDIYRVVWYTYIGRYTNSLLGVNPNVTFYFS
Cry1Ac DGTEFAYGTSSNLP S AVYRKS GTVDSLDEIIPPQNNVPPRQGF SHRLSHVSMFRSGFSNS
gi|597 NNTQKTYSKPKQFAGGI----KTIDSGEELTYEN-----YQSYSHRVSYITSFEIKSTGG
Cry1Ac SVSII RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRL

gi|597 TVLGV-VPIFGWTHSSASRNNFIYATKISQIPINKASRTSGGAVWNFQEGLYNGGPVMKL
490 500 510 520 530 540
Cry1Ac NSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWG---NSSIFSNTVPAT
gi|597 SGSGSQVIN---LRVATDAKGASQRYRIRIRYASDRAGKFTISSRSPENPATYSASIAYT
Cry1Ac ATSLDN--LQSSDFGYFESANAFTSSLGNI---VGVRFNSGTAGVIIDRFEFIPVTATL
gi|597 NTMSTNASLTYSTFAYAESGPI NLGISGSSRTFDISITKEAGAANLYIDRIEFIPVNTLTF
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKV
gi|597 EAEEDLDVAKKAVNGLFTNEKD-ALQTSVTDYQVNAANLIECLSD ELYPNEKRLMWDVA
Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDVFKENYVTLSGTFD---E
gi|597 KEAKRLVQARNLLQDTGFNRIN--GENGWTGSTGIEVVEGDVLFKDRSLRLT SAREIDTE
Cry1Ac CYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSA
gi|597 TYPTYLYQQIDESLLKPYTRYKLGKFIGSSQDLEIKLIRHRANQIVKNVPD--NLLP--D
Cry1Ac QSPIGKCGEPNRCAP--HLEWNPDLDCSRDGEKCAHSHHFLSDIDV GCTDLNEDLGVW
gi|597 VRPVNSCGGVDRCS EQYVDANLAL ENNGENGMSSD-SHAF SFHIDTGEIDL NENTGIW
Cry1Ac VIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKE
gi|597 IVFKIPTTNGNATLGNLEFVEEGPLSGETLEWAQQEQQWQDKMARKRAASEKTYAARKQ
Cry1Ac SVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLP ELSVIPGVNAAIFEELEGRIF
gi|597 AIDRLFADYQDQKLNLSGVEMSDLLAQNLVQSIPIVYNDALPEIPGMNYSPTLNTNRLQ
Cry1Ac TAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVVP EWEAEVSVQEVRCPG
gi|597 QAWNLYDLQNAIPNGDFRNGLSNWNATSDVNVQ-QLSDTSVLV IPNWNSQVQQFTVQPN
Cry1Ac RGYILRVTA YKGEYGBGCVTIHEIENNTDELKFSNCV EEEIYPNNTVTCNDYTVNQEEYG

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gi|597 YRYVLRVLTARKEGVGDGYVIIRDGANQTFETLTFNICDDDTGVLSTDQTSYITKTVEFTPS
1080 1090 1100 1110 1120 1130

Cry1Ac GAYTSRNRGYNAPSVPADYASVYEEKSYTDGRRENPCFNRGRYRDYTPLVGVYVTKLE
1100 1110 1120 1130 1140 1150

gi|597 TEQVWIDMSETEVYST
1140

>>gi|41056817|gb|AAR98783.1| HBF-1 CryIII delta-endotoxi (1160 aa)
initn: 1458 initl: 503 opt: 2094 Z-score: 2458.9 bits: 466.9 E(): 4.8e-128
Smith-Waterman score: 2147; 35.054% identity (63.697% similar) in 1201 aa overlap
(22-1182:59-1160)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
10 20 30 40 50

gi|410 LANDQTNTLQNMNYKDYLKMTTESTNAELSRNPGTFISAQDAVGTG---IDIVSTIISGLG
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVLGLVDIIWIGIFGPSQ---WDAFLVQIEQLINQRIEAFARNQAIIRLEGL
60 70 80 90 100

gi|410 ---IPVLGEVFSILGSLIGLLWPSNNENVWQIFMNRVEELIDQKILDVSRRAIADLANS
90 100 110 120 130 140

Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQ
110 120 130 140 150 160

gi|410 RIAVEYYQNALEDWRKNPHSTRSAALVKERFGNAEAILRTNMGSFSQTYETPLPTAQAQ
150 160 170 180 190 200

Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS
170 180 190 200 210 220

gi|410 AASLHLLVMRDVQIYGKEWGYPQNDIDLPHYEQVSYTARYSDHCVQWYNAGLNKLRGTGA
210 220 230 240 250 260

Cry1Ac RDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRFG-
230 240 250 260 270 280

gi|410 KQWVDYNRFRREMNMVLDLVALFPNYDARIYPLETNAELTREIFTDPVGSVVTGQSSTL
270 280 290 300 310 320

Cry1Ac -----SAQIEGSIRSPHLMIDLNSITIYTDHRG---EYY--WSGHQIMASP
290 300 310 320

gi|410 ISWYDMIIPAALPSFSTLENLLRKPDPFTLLQEIRMYTSFRQNGTIEYNYWGGQRLTLSY
330 340 350 360 370 380

Cry1Ac VGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG-VYRTLSSTLYRRPFNI-GINNQQLSVL
330 340 350 360 370 380

gi|410 IYGS---SFKNYS--GVLAGAEDIIP-VGQNDIYRVVWTYIGRYTNSLLGVNVPVTFYFS
390 400 410 420 430

Cry1Ac DGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNS
390 400 410 420 430 440

gi|410 NNTQKTYSKPKQFAGGIK----TIDSGEELTYEN----YQYSHRVSYITSFEEKSTGG
440 450 460 470 480

Cry1Ac SVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNQSVIS-GPG-FTGGDLVRL
450 460 470 480 490 500

gi|410 TVLGV-VPIFGWTHSSASRNNFIYATKISQIPINKASRTSGGAVWNFQEGLYNGGVPVVKL
490 500 510 520 530 540

Cry1Ac NSSGNNIQNRGYIEVPIHFSTSTRYRVRYASVTPIHLNVNWG---NSSIFSNTVPAT
510 520 530 540 550 560

gi|410 SGSGSQVIN---LRVATDAKGASQRYRIRIRYASDRAGFTISSRSPENPATYSASIAYT
550 560 570 580 590 600

Cry1Ac ATSLDN--LQSSDFGYFESANAFSTSLGNI---VGVNRFSGTAGVIIDRFEFIPVTATL
570 580 590 600 610

gi|410 NTMSTNASLTYSTFYAYESGPINLIGSGSSRTFDISITKEAGANLYIDRIEFIPVNTLIF
610 620 630 640 650 660

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKV
620 630 640 650 660 670

gi|410 EAEEDLDVAKKAVNGFLTNEKD-ALQTSVTDYQVNQAANLIECLSEDELYPNEKRLMWDVA
670 680 690 700 710 720

Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---E
680 690 700 710 720 730

gi|410 KEAKRLVQARNLLQDTGFNRIN--GENGWGTSGTIEVVEGDVLFKDRSLRLTNAREIDTE
730 740 750 760 770

Cry1Ac CYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSA
740 750 760 770 780 790

gi|410 TYPTLYLQKIDESLLKPYTRYKLGKFIGSSQDLEIKLIRHRANQIVKNVPD--NLLP--D
780 790 800 810 820 830

Cry1Ac QSPIGKCGEPNRCAP--HLEWNPDLDCSCRDGKCAHSHHFLSLDIDVCTDLNEDLGVW
800 810 820 830 840 850

gi|410 VRPVNSCGGVDRCSQQYVDANLALENNNGENGMSSD-SHAFSFHIDTGEIDLNENTGIW
840 850 860 870 880 890

Cry1Ac VIFKIKTQDGHARLGNLFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKE
860 870 880 890 900 910

gi|410 IVFKIPTTNGNATLGNLFEVVEGPLSGETLEWAQQEQWQDKMARKRAASEKTYAAQAQ
900 910 920 930 940 950

Cry1Ac SVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSPVPGVNAAFEELEGRIF
920 930 940 950 960 970

gi|410 AIDRLFADYQDKLNSGVEMSDLLAAQNLVQSIPIVYVNDALPEIPGMNYSPTLNTLRLO
960 970 980 990 1000 1010

gi|410 980 990 1000 1010 1020 1030

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Cry1Ac TAFSLYDARNVIKNGDFNNGLSWCNVKGHVDVEEQNNQRSLVVPWEAEVSEQEVRVCPG  
gi|410 QAWNLYDLQNAIPNGDFRNLGSLSNWNATSDVNVQ-QLSDTSLVLPVFNWNSQVSOQFTVQFN  
1020 1030 1040 1050 1060 1070

Cry1Ac RGYILRVLTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYNNNTVTCNDYTVNQEYEG  
gi|410 YRYILRVLTARKEGVDGYVVIIRDGANQTETLTFN-----ICDDDT-----  
1080 1090 1100 1110

Cry1Ac GAYTSRNRGYNEAPVSPADYASVYEEKSYTDGRRENPCFNRGRYRDYTPPLVGVYVTKELE  
gi|410 GVLST-----DQTS-----YITKTVE  
1120

Cry1Ac YFPETDKVWIEIGETEGTFIVDSVELLLMEE  
gi|410 FTPSTEQVWIDMSETEGVFNIESVELVLEEE  
1130 1140 1150 1160

>>gi|532524|gb|AAA21119.1| CryIII delta-endotoxin (1160 aa)  
initn: 1460 initl: 503 opt: 2094 Z-score: 2458.9 bits: 466.9 E(): 4.8e-128  
Smith-Waterman score: 2147; 35.054% identity (63.697% similar) in 1201 aa overlap  
(22-1182:59-1160)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLL  
gi|532 LANDQTNTLQNMNYKDYLKMTESTNAELSRNPGTFISAQDAVGTG--IDIVSTIISGLG  
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVLGLVDIIWIGIFGPSQ---WDAFLVQIEQLINQRIEAFARNQAIISRLLEGL  
gi|532 ---IPVLGEVFSILGSLIGLLWPSNNENVWQIFMNRVEELIDQKILDSVRSRAIADLANS  
90 100 110 120 130 140

Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ  
gi|532 RIAVEYYQNALEDWRKNPHSTRSAALVKERFGNAEAILRTNMGSFSQTYETPLPITYAQ  
150 160 170 180 190 200

Cry1Ac AANLHLSVLRDVSFVQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS  
gi|532 AASLHLLVMRDVQIYGKEWGYPQNDIDLPHYKEQVSYTARYSDHCVCQWYNAGLNKLRGTGA  
210 220 230 240 250 260

Cry1Ac RDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRFG-  
gi|532 KQWVDYNRFRREMNVMVLDLVALFPNYDARIYPLETNAELTREIFTPDVGSVYVTSQSSLT  
270 280 290 300 310 320

290 300 310 320

Cry1Ac -----SAQGIIEGSIRSPHLMIDLNSITIYTDHARG---EYY--WSGHQIMASP  
gi|532 ISWYDMIPALPSPFTLENLLRKPDPFLLQEIIRMYTSFRQNGTIEYYNYWGGQRLLTSLY  
330 340 350 360 370 380

Cry1Ac VGFSGPEFTFPLGYTMGNAAPQQRIVAVLQGG-VYRSLSTLYRRFPNI-GINNQQLSVL  
gi|532 IYGS---SFKNYS--GVLGAEDIIP-VGQNDIYRVVWYIYGRYTNSSLGVPVTFYFYS  
390 400 410 420 430

Cry1Ac DGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLHVSFMRSGFSNS  
gi|532 NNTQKTYSKPKQFAGGIK---TIDSGEELTYEN----YQSYSHRVSYITSFEKSTGG  
440 450 460 470 480

Cry1Ac SVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRL  
gi|532 TVLGV-VPIFGWTHSSASRNNFIYATKISQIPINKASRTSGGAVWNFQEGLYNGGPEVMKL  
490 500 510 520 530 540

Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWG--NSSIFSNTVPAT  
gi|532 SGSGSQVIN---LRVATDAKGASQRYRIRIRYASDRAGKFTTSSRSPENPATYSASIAYT  
550 560 570 580 590 600

Cry1Ac ATSLDN--LQSSDFGYFESANAFTSSLGNI---VGVRNFGTAGVIIDRFEFIPVTATL  
gi|532 NTMSTNASLTYSTFAYAESGPIINLGISGSSRTFDISITKEAGAANLYIDRIEFIPVNTLFL  
610 620 630 640 650 660

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRESEKV  
gi|532 EAEEDLDVAKAVNGLFTNEKD-ALQTSVTDYQVQAANLIECLSDSELYPNEKRMMLWDAV  
670 680 690 700 710 720

Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD--E  
gi|532 KEAKRLVQARNLLQDGTGFNRIN--GENGWGTSTGIEVVEGDVLFKDRSRLRLTSAREIDTE  
730 740 750 760 770

Cry1Ac CYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSA  
gi|532 TYPTYLYQQIDESLLKPYTRYKLGKFGSSQDLEIKLIRHRANQIVKNVPD--NLLP--D  
780 790 800 810 820 830

Cry1Ac QSPIGKCGEPNRCAP--HLEWNPDLDCSRDGEKCAHSHHFSLDIDVGCTDLNEDLGVW  
gi|532 VRPVNSCGGVDRCSQYVDANLALENNGENGMSSD-SHAFSFHIDTGEIDLNENTGIW  
840 850 860 870 880 890

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      860      870      880      890      900      910
Cry1Ac VIFKIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKE
      . . . . .
gi|532 IVFKIPTTNGNATLGNLEFVEEGPLSGETLEWAQQEQQWQDKMARKRAASEKTYAAKQ
      900      910      920      930      940      950

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      920      930      940      950      960      970
Cry1Ac SVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIF
      . . . . .
gi|532 AIDRLFADYQDQKLNLSGVMSDLLAAQNLVQSIPIVYVNDALPEIPGMNYTSFTELTLNRLQ
      960      970      980      990      1000     1010

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      980      990      1000     1010     1020     1030
Cry1Ac TAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQSRVSVLVPWEAEVSVQEVVRCVCPG
      . . . . .
gi|532 QAWNLYDLQNAIPNGDFRNLGNLWVNSVQVQ-QLSDTSLVLPVWNSQVSVQVQVTPVQPN
      1020     1030     1040     1050     1060     1070

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      1040     1050     1060     1070     1080     1090
Cry1Ac RGYILRVYTAYKEGEGCVTIHEIENNTDELKFSNCVEEIIYPNNVTVCNDYTVNQEEYQ
      . . . . .
gi|532 YRYVLRVITARKEGVDGYVIIRDGANQTELTFTN-----ICDDDT-----
      1080     1090     1100                               1110

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      1100     1110     1120     1130     1140     1150
Cry1Ac GAYTSRNRGYNAPSVPADYASVYEEKSYTDGRRENPCFNRGRYDYTPPLVGVYVTKELE
      . . . . .
gi|532 GVLST-----DQTS-----YITKTVE
      1120

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```

      1160     1170     1180
Cry1Ac YFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi|532 FTPSTEQVWIDMSETEGVFNIESVELVLEEE
      1130     1140     1150     1160

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>>gi|118628703|emb|CAL85374.1| unnamed protein product [ (1131 aa)
  initn: 2439 init1: 624 opt: 2086 Z-score: 2449.6 bits: 465.2 E(): 1.6e-127
Smith-Waterman score: 2527; 41.341% identity (65.620% similar) in 1178 aa overlap
(40-1182:36-1129)

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      10      20      30      40      50      60
Cry1Ac NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVL---GL
      . . . . .
gi|118 YEIIGASTNGTIELPEDYNTIVSPYDAPASVTTTIEITGTLISDLGVPGASSVSLLNKL
      10      20      30      40      50      60

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      70      80      90      100     110     120
Cry1Ac VDIIWGFPGSQWDAFLVQIEQLINQRI--EAFARNQALSRLEGLSNLYQIYAESFREWE
      . . . . .
gi|118 INLLWPNDTNTVWGTFGKETADLLNEVLSPDDPVVKDANTILKGINSLNLYLNALEIWK
      70      80      90      100     110     120

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      130     140     150     160     170     180
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVF
      . . . . .
gi|118 KDPNNLTTIENVTDYFRSLNVVFTHDMPSFAVPGYETKLLTIYAQAANLHLLLRDASRF
      130     140     150     160     170     180

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      190      200      210      220      230      240
Cry1Ac GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELT
      . . . . .
gi|118 GEGWGLTQEIIINTNYNDQLRLTAEYTDHCVKWNAGLEKLGKGLTGENWYTYNRFREMT
      190      200      210      220      230      240

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      250      260      270      280      290
Cry1Ac LTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV-LENFDGSGFRGSA---QGIEGS-IR
      . . . . .
gi|118 LMLVDVVALFPNYDTRMYPIGTSSSELTRMIYTDPIAYTQSDPWYKITSLSFSNIENSAIP
      250      260      270      280      290      300

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      300      310      320      330      340      350
Cry1Ac SPHLMIDILNSITITYTD---AHRGEYVWSGHQIMASPVGFSGPEFTFPL-YGTMGNAAPQ
      . . . . .
gi|118 SPSFFRWLKSVSINSQWWSGSPSQTYVWVGHVLSN---SNSNQLVKVYGDPNFIEP
      310      320      330      340      350      360

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      360      370      380      390      400
Cry1Ac QRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSVLDGT---EFAYGTSSNLPSAVYRK
      . . . . .
gi|118 PDSFSPSSTDVYRTIS-VVRNSVSNYIVSEVRFNSISSTNQISEEIKHQSNWSRQETKD
      370      380      390      400      410      420

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      410      420      430      440      450      460
Cry1Ac SGTVDLSLDEIIPPQN-NNVPPRQGFSHRLSHVS-MFRSGFSNSSVSIIRAPMFSWIHRSAE
      . . . . .
gi|118 SITELSLAANPPTTFGNVAE---YSHRLAYISEAYQS--HNPSKYPTYIPVPGWHTTSVR
      430      440      450      460      470

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      470      480      490      500      510      520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGS---VISGPGFTGGDLVRLNSSGNINQNRGYIEVPI
      . . . . .
gi|118 YDNKIFPDKITQIPAVKSSSAQGGSWKNIVKGGFTGGD-VITAVSPATVTDIIKIQVTL
      480      490      500      510      520      530

```

```

      530      540      550      560      570
Cry1Ac HFPSTSTRYRVRYAS--VTPIHLMNVNNGNSSIFSNTPATA--TSLDNLQSSDF-GYF
      . . . . .
gi|118 DPNSLSQKYRARLRYASNAFVPATLYTNTSSNYNFELKKGTTTEQFTTYSYQYVDIPGSI
      540      550      560      570      580      590

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      580      590      600      610      620      630
Cry1Ac ESANAFTSSLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTN
      . . . . .
gi|118 QFNN--TSDTVSVYLHMDSTSNVNVHVDRIEFIPIDENYDERFQLEKAQKAVNALFTA-G
      600      610      620      630      640      650

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      640      650      660      670      680      690
Cry1Ac QLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDI
      . . . . .
gi|118 RNALQTDVTDYKVDQVSIILVDCVSGELYPNEKRELLSLVKYAKRLSYSRNLLDPTFDSI
      660      670      680      690      700      710

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```

      700      710      720      730      740      750
Cry1Ac NRQPERGWGSGTIGITIQGGDDVFKENYVTLSGTFDECPYTYQKIDESKLFKAFTRYQLR
      . . . . .
gi|118 NSPEENGWYGSNGIATGSGNIVFKGNYLIFSGTNDQYPTYLYQKIDETKLFKEYTRYKLR
      720      730      740      750      760      770

```

```

760      770      780      790      800      810
Cry1Ac GYIEDSQLLEIYSIRYNAKHETVNVPGTGSLSWPLSAQSPIGKCGEPNRCA--PHLEWNPD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 GFISSQDLEAYVIRYDAKHQTMVD--SNNL--FSDITPVNACGEPNRCAALPYLDENPR
      780      790      800      810      820

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820      830      840      850      860      870
Cry1Ac LDCSC- RDGEKCAHSHHFLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 LECSSIQDG--ILSDSHSFLHIDTGSIDFNENVGIWVLFKISTPEGYARFGNLEVIDEG
      830      840      850      860      870      880

```

```

880      890      900      910      920      930
Cry1Ac PLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAESVDALFVNSQYDQLQADTNIAAMI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 PVIGEALARVKRQETKWRNKLTQLRTETQAIYTRAKQAIIDNLFNTAQDShLKIGATFASI
      890      900      910      920      930      940

```

```

940      950      960      970      980      990
Cry1Ac HAADKRVHSIREAYLPELSVIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 VAARKIVQSIREAYMSWLSIVPGVNYPIVTELNERIQQAFQLYDVRNVRRNGRFQSGTSD
      950      960      970      980      990      1000

```

```

1000     1010     1020     1030     1040     1050
Cry1Ac WNVKGVHVDVEEQNNQSVLVVPEWEAEVSQEVVRCVGRGYLLRVYAYKEGYGEGCVTIHE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 WIVTSDVRVQENGNG--NVLVLSNWDQVLCQMTLYQDRGYILRVYARKEGLGEGYVTTID
      1010     1020     1030     1040     1050     1060

```

```

1060     1070     1080     1090     1100     1110
Cry1Ac IENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 EEGNTDQLRFGGC--EEIDASNS-----FVST
      1070     1080     1090

```

```

1120     1130     1140     1150     1160     1170
Cry1Ac YEEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 -----GYMKELEFFPDTEKVRIEIGETEGTFQVES
      1100     1110     1120

```

```

1180
Cry1Ac VELLMLME
: : : : :
gi|118 VELFLMEDLC
      1130

```

>>gi|125172656|gb|ABN37588.1| Sequence 6 from patent US (1152 aa)  
 initn: 1572 initl: 474 opt: 2038 Z-score: 2392.9 bits: 454.7 E(): 2.3e-124  
 Smith-Waterman score: 2157; 36.926% identity (61.988% similar) in 1197 aa overlap  
 (22-1182:59-1152)

```

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 LARDPNAVFQNMHYKDYLTQYDGDYTGSIINPNLSINPRDLVLTQ---INIVGRLLGLG
      30      40      50      60      70      80

```

```

60      70      80      90      100
Cry1Ac SEFVPGAG----FVLGLVDIIWIGIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 ---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELINQRISEAVVGTAAADHLTGL
      90      100      110      120      130      140

```

```

110     120     130     140     150     160
Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPLLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 HDNYELYVEALEEELERP--NAARTNLLFNRFTTLDLSLFTQFMPSFGTGPQSQNYAVPLLT
      150     160     170     180     190     200

```

```

170     180     190     200     210     220
Cry1Ac VYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 VYAQAANLHLLLLKDAEIIYGARWGLNQNQINSFHTROQERTQYYTNHCVTYNTGLDRLR
      210     220     230     240     250     260

```

```

230     240     250     260     270     280
Cry1Ac GPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNENF---
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 GTNTESWLNHYRFRREMTLMAMDVLALFPYYNVRQYPNGANPQLTREIYTDPIVYNPPAN
      270     280     290     300     310     320

```

```

290     300     310     320
Cry1Ac DGSFR-----GSAQGIIEGS--IRSPHMLDILNSITI---YDHAHRGEY--YWSGHQIM
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 QGICRRWGNPNYNTFSELENAFIRPHLFDRLNRLTISRNYTAPTNTSYLDYWSGHTLQ
      330     340     350     360     370     380

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330     340     350     360     370     380
Cry1Ac ASPVFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPF--NIGINNQQLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 SQ---YANNPTTYET--SYGQITSNTRLF--NTTNGANAIDSRA---RNFGNLYANLYGVS
      390     400     410     420     430     440

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390     400     410     420     430     440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 YLNI--FPTGVMSIETSAFNTCWQDLTTTEELPLVNNNF-----NLLSHVTFLRFNNT
      440     450     460     470     480

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450     460     470     480     490     500
Cry1Ac NSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SVISGPGFTGGDL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 QGGPLATVGFVPTYVWTRQDVFNNIITPNRITQIPVVKAYELSSGATVVKGPGFTGGDV
      490     500     510     520     530     540

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510     520     530     540     550     560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSII--FSNTVP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 IRRNTTGG---FGAIRVSVTGTLTQ--RYRIRFRYASTIDDFVFRGTTINNFRFTRT
      550     560     570     580     590

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570     580     590     600     610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRFNSGTAGVIIDRFEFIPVTATLEAE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|125 MNRQBSRYESYRTVEFTTFFNFQTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAE

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600      610      620      630      640      650
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  EDLEAAKKAVALFTRTRD-GLQVNVTDYQVDQAANLVSLCLSEQYAHDKKMLLEAVRAA
      660      670      680      690      700      710

680      690      700      710      720      730
Cry1Ac  KRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  KRLSRERNLLQDPDFNTINSTENGWKASNGVTISEGGPFYKGRALQLASA-RENYPTYI
      720      730      740      750      760      770

740      750      760      770      780      790
Cry1Ac  YQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLWPLSAQSPIGK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  YQKVDASELKPYPYTRYRLDGFVKSSQDLEIDLHSHKVLVKNV--LDNL--VSDTYPDDS
      780      790      800      810      820      830

800      810      820      830      840      850
Cry1Ac  CGEPNRCAPHLEWNPDLDCSCRDEKGC--AHSHHFSLDIDVGCTDLNE--DLGVWVIFK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  CSGINRCEEQQMVNAQLETEHHHPMDCCEAAQTHEFSSYIDTG--DLNSTVDQGIWVIFK
      840      850      860      870      880      890

860      870      880      890      900      910
Cry1Ac  IKTDQGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  VRTTDGYATLGNLELVEVGPLLGEPLEREQRENAKWAELGRKRAETDRVYQDAKQSIINH
      900      910      920      930      940      950

920      930      940      950      960      970
Cry1Ac  LFNVSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIPTAFS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  LFDVYDQDQLNPQIGMADIMDAQNLVASISDVYSDAVLQIPGINYEIYTELSNRLLQQASY
      960      970      980      990      1000      1010

980      990      1000      1010      1020      1030
Cry1Ac  LYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQRSVLVPEWEAEVSEQEVRVCPGRGYI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  LYTSRNAVQNGDFNNGLDWNAATAGASVQDGNTH-FLVLSHWDAQVSSQQFRVQPNCKYV
      1020      1030      1040      1050      1060

1040      1050      1060      1070      1080      1090
Cry1Ac  LRVTAKEGYEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCDNYTVNQEEYGGAYT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  LRVTAKEVGGDGYVTIRDGAHHTETLTFNAC-----DYDIN-----GTYV
      1070      1080      1090      1100      1110

1100      1110      1120      1130      1140      1150
Cry1Ac  SRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGRDYTPLPVGYVTKLEYFPE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|125  TDNT-----YTKEVIFYSH
      1120

1160      1170      1180
Cry1Ac  TDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : . . . . . :

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gi|125  TEHMWVEVNETEGAFHIDSIEFVETEK
      1130      1140      1150

>>gi|15143043|emb|CAC50780.1| unnamed protein product [B (1152 aa)
      initn: 1572 init1: 474 opt: 2038 Z-score: 2392.9 bits: 454.7 E(): 2.3e-124
Smith-Waterman score: 2157; 36.926% identity (61.988% similar) in 1197 aa overlap
(22-1182:59-1152)

10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  LARDPNAVFQNMHYKDYLTQYDGDYTGSGFINPNLSINPRDVLQGTG--INIVGRLLGFLG
      30      40      50      60      70      80

60      70      80      90      100
Cry1Ac  SEFVPGAG----FVLGLVDIIWGFIFGPSQWDAFLVQIEQLINRIEFAFNQAISRLEGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  ---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELINQRISEAVVGTAAADHLTGL
      90      100      110      120      130      140

110      120      130      140      150      160
Cry1Ac  SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIFLFAV---QNYQVPLLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  HDNYELYVEALEEWLERP-NAARTNLLFNRFITLDSLFTQFMPSFGTGPQSNYAVPLLT
      150      160      170      180      190      200

170      180      190      200      210      220
Cry1Ac  VVYQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  VYAQAANLHLLKDAEIIYGARWGLNQNSFHTRQERTQYTNHCVTTTYNTGLDRLR
      210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac  GPDSDWIRYNQFRRELTTLVLDIVSLFPNYSRTPYIRTVSQTREIYTNVLENF---
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  GTNTESWLNYHRFRREMTLMAMDVLFPPYVNRQYPNGANPQLTREIYTDPIVYVPPAN
      270      280      290      300      310      320

290      300      310      320
Cry1Ac  DGSFR-----GSAQGI EGS-IRSPHLM DILNSITI---YD AHRGEY--YWSGHQIM
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  QGICRRWGNPNYTFSELENAFIRPPHLPDRLNRLTISRNRYPAPTNSYLDYWSGHTLQ
      330      340      350      360      370      380

330      340      350      360      370      380
Cry1Ac  ASPVGSFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLTSSLYRRPF-NIGINQQLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  SQ---YANNPTTYET--SYGQITSNTRLF-NTTNGANAIDSRA---RNFGNLYANLYGVV
      390      400      410      420      430

390      400      410      420      430      440
Cry1Ac  VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

gi|151  YLNI--FPTGVMSEITSPANTCWQDLTTTEELPLVNNNF-----NLLSHVTFVLRFNNT
      440      450      460      470      480

450      460      470      480      490      500
Cry1Ac  NSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

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gi|151 QGGPLATVGFVPTYVWTRQDQVDFNNIITPNRITQIPVVKAYELSSGATVVKGPGFTGGDV
      490      500      510      520      530      540
      510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHLNWNWGNSSI--FSNTVP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 IRRNTTGG---FGAIRVSVTGPLTQ-RYRIRFRYASTIDDFVFRGGTTINNFRFTRT
      550      560      570      580      590
      570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 MNRGQESRYESYRTVEFTTFFNFQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAE
      600      610      620      630      640      650
      620      630      640      650      660      670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDSDFCLDEKRELSEKVKHA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 EDLEAAKAVASLFRTRD-GLQVNVTDYQVDQAAANLVSLCLSDQYAHDKMLLEAVRAA
      660      670      680      690      700      710
      680      690      700      710      720      730
Cry1Ac KRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 KRLSRERNLLQDPDFNTINSTEENGWKASNGVTISEGGFFYKGRALQLASA-RENYPTYI
      720      730      740      750      760      770
      740      750      760      770      780      790
Cry1Ac YQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLSLWPLSAQSPIGK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 YQKVDASELKPYTRRLDGFVKSSQDLEIDLHSHHKVHLVKNV--LDNL--VSDTYPDDS
      780      790      800      810      820      830
      800      810      820      830      840      850
Cry1Ac CGEPNRCAPHLEWNPDLDCSCRDEKGC--AHSHHFLSLDIDVGCDDLNE--DLGVVWVIFK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 CSGINRCEEQVMNAQLETEHHHPMDCCEAAQTHEFSSYIDTG--DLNSTVDQGIWVIFK
      840      850      860      870      880      890
      860      870      880      890      900      910
Cry1Ac IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 VRTTDGYATLGNLELVEVGPLLGEPLEREQRENAKWNAELGRKRAETDRVYQDAKQSIH
      900      910      920      930      940      950
      920      930      940      950      960      970
Cry1Ac LFNVSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LFDVYQDQQLNPQIGMADIMDAQNLVASISDVYSDAVLQIPGINVYIYTELNRQLQASYS
      960      970      980      990      1000      1010
      980      990      1000      1010      1020      1030
Cry1Ac LYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVPWEAEVSVQEVRCVCPGRGYI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LYTSRNVAQNGDFNGLSDSWNATAGASVQDGNTH-FLVLSHWDAQVQQFRVQPNCKYV
      1020      1030      1040      1050      1060
      1040      1050      1060      1070      1080      1090
Cry1Ac LRVTAYKEGYGBCVVTIHEIENNTDELKFSNCVEEIEYPNNVTVCNDYTVNQEYGGAYT

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      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 LRVTAEKVGGGQDGYVTIRDAHHTETLTFNAC-----DYDIN-----GTVY
      1070      1080      1090      1100      1110
      1100      1110      1120      1130      1140      1150
Cry1Ac SRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYTPLPVGYVTKLEYFPE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 TDNT-----YLTKEVIFYSH
      1120
      1160      1170      1180
Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151 TEHMMVEVNETEGAFHIDSIEFVETEK
      1130      1140      1150
>>gi|33731258|gb|AAQ37321.1| Sequence 72 from patent US (1156 aa)
      initn: 2028 init1: 719 opt: 2019 Z-score: 2370.4 bits: 450.6 E(): 4.1e-123
      Smith-Waterman score: 2263; 37.112% identity (63.812% similar) in 1191 aa overlap
      (22-1182:59-1156)
      10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 LASDPNAAALQNMNYKDYLMQMTDEDYTDYSINPSLSISGRDAVQ TALTVVGRILGALGVFP
      30      40      50      60      70      80
      60      70      80      90      100      110
Cry1Ac SEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI SRLGLS NLY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 SQQI--VSFYQLLNTLWPNVDTAIWEAFMRQVEELVQQITEFARNQALARLQGLGDSF
      90      100      110      120      130      140
      120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 NVYQRSLQNLADRNDTRNLSVVRAQFIALDLDFVNAIPLFAVNGQVPLLSVYAQAVNL
      150      160      170      180      190      200
      180      190      200      210      220      230
Cry1Ac HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 HLLLLKDALFEGEGWFTQGEISTYYDRQLELTAKYTNYCETWYNTGLDRLRGTNTESWL
      210      220      230      240      250      260
      240      250      260      270      280
Cry1Ac RYNQFRRELTTLVLDIVLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD---GSFR--G
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 RYHQFRREMTLVVLDVVALFPYDYVRLYPTGSPQLTREVVYTDPIVFNPPANVGLCRRWG
      270      280      290      300      310      320
      290      300      310      320      330      340
Cry1Ac SA----QIEGS-IRSPHMDILNSITTYTDAH--RGEY--YWSGHQIMASPVGFSGPE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 TNPYNTFSELENAFIRPPHFLDRLNLSLTISSNRFVSSNFMDYWSGHTLRRSYLNDASVQ
      330      340      350      360      370      380
      340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY

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Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD--GSFR--G  
gi|337 RYHQFRREMTLVVLDVVALFPYDVRVLYPTGSNPQLTREYVTDPIVFNPPANVGLCRRWG  
270 280 290 300 310 320

Cry1Ac SA----QGIEGS-IRSPHLMIDLNSITTYTDAH--RGEY--YWSGHQIMASPVGFSGPE  
gi|337 TNPYNTFSELENAFIRPPHLDRLNLSLTISSNRFVSSNFMDYWSGHTLRRSYLNDLSAVQ  
330 340 350 360 370 380

Cry1Ac FTFPLYGTMGNAAPQRIVAQLG-QGVYRTLSSTLYRRPFNIGINN-QQLSVLDGTEFAY  
gi|337 ED--SYGLITTT---RATINPGVDGTNRRIESTAVDFRSALIGIYGVNRAFVPGGLFN-  
390 400 410 420 430

Cry1Ac GTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLHVMFRSFGSFSNSSVSIIRA  
gi|337 GTTS--PANGGCRD-LYDNDLPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA  
440 450 460 470 480 490

Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNFS-VISGPGFTGGDLVRLNSSGN  
gi|337 GSVPTYVWTRRDVLDLNTITPNRITQLPLVKASAPVSGTTLVKGPGFTGGGILRRRTTNGT  
500 510 520 530 540 550

Cry1Ac NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWNSSI----FSNTVP-ATATS  
gi|337 ---FGTLRVTVNSPLTQ-RYRVRVRFASSGNFSTRILRGNTSIAYQRFSGTMMNRGQELT  
560 570 580 590 600

Cry1Ac LDNLQSSDFGYFES--ANAFTSSLGNI-VGVRNFGTAGVIIDRFEFIPVTATLEAEYNL  
gi|337 YESFVTSEFTTNQSDLPPTFTQAQENLTILAEVSTGSEYFIDRIEIIIPVNPAREAEEDL  
610 620 630 640 650 660

Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRL  
gi|337 EAAKAVANLFTTRRD-GLQVNVTDYQVDQAANLVSCLSDEQYGHDKMKMLLEAVRAAKRL  
670 680 690 700 710 720

Cry1Ac SDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQK  
gi|337 SRERNLLQDPPFNTINSTEENGWKAASNGVTISEGGPFKGRALQLASA-RENYPTYIYQK  
730 740 750 760 770 780

Cry1Ac IDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNKAKHETVNVPGTGLWPLSAQSPIGKCGE  
gi|337 VDASVLKPYTRYRLDGFVKSSQDLEIDLHHKHLVKNVDPNL---VSDTYSYDGS CSG  
790 800 810 820 830 840

Cry1Ac PNRCAHPLEWNPDLDCSCRDKGKC-AHSHHFLSLDIDVGCCTDLNEDLGWVVFVKIKTQDG  
gi|337 INRCDEQHQVDMQLDAEHPMDCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTDG  
850 860 870 880 890 900

Cry1Ac HARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQ  
gi|337 YATLGNLELVEVGPLSGESLEREQRDQNAKWAELGRKRAEIDRVYLAQKQAINHLFVDYQ  
910 920 930 940 950 960

Cry1Ac YDQLQADTNIAMIHADKRVHSIREAYLPELSVIPGVNAAIFEELRIFTAFSLYDARN  
gi|337 DQQLNPEIGLAEINEASNLVESISGVYSDTLQLIPGINVEIYTELSDRLQQASLYTSRN  
970 980 990 1000 1010 1020

Cry1Ac VIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVPEWEAEVSEVVRVCPGRGYILRVYAY  
gi|337 AVQNGDFNSGLDSWNTTMDASVQDGNMH-FLVLSHWDQVSVQQLRVNPNCKYVLRVTAR  
1030 1040 1050 1060 1070

Cry1Ac KEGYGEQCVTIEIENNTDELKFSNCEVEEIIYPNNVTVCNDYTVNQEYGGAYTSRNRGY  
gi|337 KVGGGDGYVTIRDGAHQETLTFNAC-----DYDVN-----GTVVDN---  
1080 1090 1100 1110

Cry1Ac NEAPSVPADYASVYEEKSYTDGRENPECFNRYRDRYDTPLPVGYVTKLEYPFETDKVWI  
gi|337 -----SYITEEVVFPETKHMV  
1120 1130

Cry1Ac EIGETEGTFIVDSVELLMEE  
gi|337 EVSESEGSFYIDSIEFIETQE  
1140 1150

>>gi|21504423|gb|AAM57117.1| Sequence 72 from patent US (1156 aa)  
initn: 2028 init1: 719 opt: 2019 Z-score: 2370.4 bits: 450.6 E(): 4.1e-123  
Smith-Waterman score: 2263; 37.112% identity (63.812% similar) in 1191 aa overlap  
(22-1182:59-1156)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL  
gi|215 LASDPNAAQLNMYKDYLMQTDDEYDTSYINPSLSISGRDAVQALTVVGRILGALGVFP  
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVGLVDIIWGI FGPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLY  
gi|215 SQGI--VSFYQFLNLTLPVNDTAIWEAFMRQVEELVNQOITEFARNQALARLQGLGDSF  
90 100 110 120 130 140

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120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|215 N VYQ RSLQNLADRNDTRNLSVVRAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNL
150      160      170      180      190      200

180      190      200      210      220      230
Cry1Ac HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
gi|215 H L L L L K D A S L F G E G W G F T Q G E I S T Y Y D R Q L E L T A K Y T N Y C E T W Y N T G L D R L R G T N T E S W L
210      220      230      240      250      260

240      250      260      270      280
Cry1Ac RYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD---GSFR--G
gi|215 R Y H Q F R E M T L V V L D V V A L F P Y Y D V R L Y P T G S N P Q L T R E V Y T D P I V F N P P A N V G L C R R W G
270      280      290      300      310      320

290      300      310      320      330
Cry1Ac SA----QGI EGS-IRSPHLM DILNSITTYTDAH--RGEY--YWSGHQIMASPVGFSGPE
gi|215 T N P Y N T F S E L E N A F I R P P H L F D R L N S L T I S S N R F P V S S N F M D Y W S G H T L R R S Y L N D S A V Q
330      340      350      360      370      380

340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSSTLYRRPFNIGINN-QQLSVLDGTEFAY
gi|215 E D -- S Y G L I T T T --- R A T I N P G V D G T N R I E S T A V D F R S A L I G I Y G V N R A S F V P G G L F N -
390      400      410      420      430

400      410      420      430      440      450
Cry1Ac GTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
gi|215 G T T S -- P A N G G C R D - L Y D T N D E L P P D E S T --- G S T H R L S H V T F F - S F Q T N Q A G S I A N A
440      450      460      470      480      490

460      470      480      490      500      510
Cry1Ac ---PMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN
gi|215 G S V P T Y V W T R R D V L N N T I T P N R I T Q L P L V K A S A P V S G T T V L K G P G F T G G G I L R R T T N G T
500      510      520      530      540      550

520      530      540      550      560
Cry1Ac NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSSI----FSNTVP-ATATS
gi|215 ---F G L T R V T V N S P L T Q - R Y R V R V R F A S S G N F S I R I L R G N T S I A Y Q R F G S T M N R G Q E L T
560      570      580      590      600

570      580      590      600      610      620
Cry1Ac LDNLQSSDFGYFES--ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLAEAYNL
gi|215 Y E S F T S E F T T N Q S D L P F T F T Q A Q E N L T I L A E G V S T G S E Y F I D R I E I I P V N P A R E A E E D L
610      620      630      640      650      660

630      640      650      660      670      680
Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL
gi|215 E A A K A V A N L F T R T R D - G L Q V N V T D Y Q V D Q A A N L V S C L S D E Q Y G H D K M L L E A V R A A K R L
670      680      690      700      710      720

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690      700      710      720      730      740
Cry1Ac SDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTLYLQK
gi|215 S R E R N L L Q D P D F N T I N S T E E N G W K A S N G V T I S E G G F F F K G R A L Q L A S A - R E N Y P T Y I Y Q K
730      740      750      760      770      780

750      760      770      780      790      800
Cry1Ac IDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLWPLSAQSPIGKCGE
gi|215 V D A S V L K P Y T R Y R L D G F V K S S Q D L E I D L I H H K V H L V K N V P D N L --- V S D T Y S D G S C S G
790      800      810      820      830      840

810      820      830      840      850      860
Cry1Ac PNRCAPHLEWNPDLDCSCRDGEKC-AHSHHFSLDIDVGCTDLNEDLGVWVIFKIKTQDG
gi|215 I N R C D E Q H Q V D M Q L D A E H H P M D C C E A A Q T H E F S S Y I N T G D L N A S V D Q G I W V V L K V R T T D G
850      860      870      880      890      900

870      880      890      900      910      920
Cry1Ac HARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQ
gi|215 Y A T L G N L E L V E V G P L S G E S L E R E Q R D N A K W N A E L G R K R A E I D R V Y L A A K Q A I N H L F V D Y Q
910      920      930      940      950      960

930      940      950      960      970      980
Cry1Ac YDQLQADTNIAMHAADKRVSIREAYLPELSVIPGVNAAI FEEL EGRIFTAFSLYDARN
gi|215 D Q L N P E I G L A E I N E A S N L V E S I S G V Y S D T L L Q I P G I N Y E I Y T E L S D R L Q Q A S Y L Y T S R N
970      980      990      1000      1010      1020

990      1000      1010      1020      1030      1040
Cry1Ac VIKNGDFNGLSCWNVKGHV DVEEQNQRSVLVVP EWEAEVSEQVRCVGRGYILRVTA Y
gi|215 A V Q N G D F N S G L D S W N T T M D A S V Q D G N M H - F L V L S H W D A Q V S Q Q L R V N P N C K Y V L R V T A R
1030      1040      1050      1060      1070

1050      1060      1070      1080      1090      1100
Cry1Ac KEGYGEQCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGY
gi|215 K V G G D G Y V T I R D G A H H Q E T L T F N A C --- D Y D V N --- G T Y V N D N ---
1080      1090      1100      1110

1110      1120      1130      1140      1150      1160
Cry1Ac NEAPSPADYASVYEKSYTDGRRENPCFNRGYRDYTPLPVGYVTKELEYFPETDKVNI
gi|215 -----SYITEVVVFYPETKHMVW
1120      1130

1170      1180
Cry1Ac EIGETEGTFIVDSVELLLMEE
gi|215 E V S E S E G S F Y I D S I E F I E T Q E
1140      1150

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>>gi|53970041|gb|AAV19134.1| Sequence 72 from patent US (1156 aa)  
 initn: 2028 initl: 719 opt: 2019 Z-score: 2370.4 bits: 450.6 E(): 4.1e-123  
 Smith-Waterman score: 2263; 37.112% identity (63.812% similar) in 1191 aa overlap  
 (22-1182:59-1156)

Regulatory Product Characterization Team

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLF  
gi|539 LASDPNAAALQNMNYKDYLMQMTDEDYTDYSINPFLSISGRDAVQATALTAVVGRILGALGVFP  
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVLGLVDIIWGIIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLY  
gi|539 SGQI--VSFYQFLNLTLPVNDTAIWEAFMRQVEELVQITTEFARNQALARLQGLGDSF  
90 100 110 120 130 140

Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLVSYYQAANL  
gi|539 NVYQRSLOQNLADRNDTRNLSVVRQAQFIALDLDFVNAIPLFAVNGQQVPLLVSYYQAANL  
150 160 170 180 190 200

Cry1Ac HLSVLRDVSVFQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI  
gi|539 HLLLLKDAASLFGEGWGFTQGEISTYYDRQLELTAKYNTNYCETWYNTGLDRLRGTNTESWL  
210 220 230 240 250 260

Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD---GSFR--G  
gi|539 RYHQFRREMTLVVLDVVALFPYDVRLYPTGSGNPQLTREYVTDPIVFNPPANVGLCRRWG  
270 280 290 300 310 320

Cry1Ac SA----QGIIEGS-IRSPHLMIDLNSITTYTDAH--RGEY--YWSGHQIMASPVFGSFGPE  
gi|539 TNPYNTFSELENAFIRPPHFDRLNSLTISSNRFVSSNFMFYWSGHTLRRSYLNDASVQ  
330 340 350 360 370 380

Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY  
gi|539 ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRASFVPGGLFN-  
390 400 410 420 430

Cry1Ac GTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA  
gi|539 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTFP-SFQTNQAGSIANA  
440 450 460 470 480 490

Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN  
gi|539 GSVPTYVWTRRDVLDLNNITPNRITQLPLVKASAPVSGTTVLKGPFGFTGGGILRRRTNGT  
500 510 520 530 540 550

Cry1Ac NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNNGNSSI----FSNTVP-ATATS  
gi|539 ---FGTLRVTVNSPLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFGSTMNRGQELT

Cry1Ac LDNLQSSDFGYFES--ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNL  
gi|539 YESFVTSEFTTNQSDLPFTFTAQENLTLAEGVSTGSEYFIDRIEIIIPVNPAREAEEDL  
610 620 630 640 650 660

Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRL  
gi|539 EAAKAVANLFTTRTRD-GLQVNVTDYQVDQANLVSCLSDEQYGHDKMLLEAVRAAKRL  
670 680 690 700 710 720

Cry1Ac SDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQK  
gi|539 SRERNLLQDPDFNTINSTEENGWKAASNGVTISEGGPFFKGRALQLASA-RENYPTYIYQK  
730 740 750 760 770 780

Cry1Ac IDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWLPLSAQSPIGKCGE  
gi|539 VDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVVHLVKNVDPNL---VSDTYSDBGSCSG  
790 800 810 820 830 840

Cry1Ac PNCRCAPHEWNPDLDCSCRDGEKC-AHSHHFLSLDIDVCGTDLNEDLGWVWVIFKIKTQDG  
gi|539 INRCDEQHQVDMQLDAEHHHPMDCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTDG  
850 860 870 880 890 900

Cry1Ac HARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQ  
gi|539 YATLGNLELVEVGPLSGESLEREQRDNKNAELGRKRAEIDRVYLAQAQAINHLFVDYQ  
910 920 930 940 950 960

Cry1Ac YDQLQADNTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARN  
gi|539 DQQLNPEIGLAEINEASNLVESISGVYSDTLLQIPGINYEIYTELSDRLQQASYSYRSR  
970 980 990 1000 1010 1020

Cry1Ac VIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVPVEWEAEVSQEVRCVPRGYILRVYAY  
gi|539 AVQNGDFNSGLDSWNTTMDASVQQDGNMH-FLVLSHWDQVSSQLRVNPNCKYVLRVTAR  
1030 1040 1050 1060 1070

Cry1Ac KEGYGGCVTIHEIENNTDELKFSNVEEIIYPNNTVTCDYTVNQEYGGAYTSRNRGY  
gi|539 KVGGGDGYVTIRDGAHHQETLTFNAC-----DYDVN-----GTYVNDN---  
1080 1090 1100 1110

Cry1Ac NEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLEYFPETDKWVI  
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gi|539 -----SYITEEVVFPETKHMVW
1120 1130

1170 1180
Cry1Ac EIGETEGTFIVDSVELLMEE
gi|539 EVSESEGSFYIDSIEFIETQE
1140 1150

>>gi|112088045|gb|ABI06956.1| Sequence 28 from patent US (1156 aa)
initn: 2028 initl: 719 opt: 2019 Z-score: 2370.4 bits: 450.6 E(): 4.1e-123
Smith-Waterman score: 2263; 37.112% identity (63.812% similar) in 1191 aa overlap
(22-1182:59-1156)

10 20 30 40 50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|112 LASDPNAALQNMNYKDYLMQMTDEDYTDSYINPSLSISGRDAVQTALTVVGRILGALGVFP
30 40 50 60 70 80

60 70 80 90 100 110
Cry1Ac SEFVPGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLY
gi|112 SGQI--VSFYQFLNLTWLPVNDTAIWEAFMRQVEELVQIITEFARNQALARLQGLGDSF
90 100 110 120 130 140

120 130 140 150 160 170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|112 NVYQRSLQNLADRNDTRNLSVVRQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNL
150 160 170 180 190 200

180 190 200 210 220 230
Cry1Ac HLSVLRDVSVFQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWI
gi|112 HLLLLKDALFEGEGWFTQGEISTYYDRQLELTAKYTYNCETWYNTGLDRLRGTNTESWL
210 220 230 240 250 260

240 250 260 270 280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLENFD--GSFR--G
gi|112 RYHQFRREMTLVVLDVVALFPYDVRLYPTGNSNPQLTREVTYDPIVFNPPANVGLCRRWG
270 280 290 300 310 320

290 300 310 320 330
Cry1Ac SA----QGIEGS-IRSPHLMIDILNSITTYTDAH--RGEY--YWSGHQIMASPVGFSGPE
gi|112 TNPYNTFSELENAFIRPPHLFDRLNSLTISSNRFPVSSNFMFDYWSGHTLRRSYLNSAVQ
330 340 350 360 370 380

340 350 360 370 380 390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY
gi|112 ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRASFPVPGGLFN-
390 400 410 420 430

400 410 420 430 440 450
Cry1Ac GTSSNLPASAVYRKSQGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA

gi|112 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
440 450 460 470 480 490

460 470 480 490 500 510
Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN
gi|112 GSVPTYVWTRDRVDLNMNTITPNRITQLPLVKASAPVSGTTVLKPGPGFTGGGILRRRTNGT
500 510 520 530 540 550

520 530 540 550 560
Cry1Ac NIQNRGYIEVPIHFPTSTSTRYRVRVRYASVTPIHLNVNWNSSI----FSNTVP-ATATS
gi|112 ---FGTLRVTVNSPLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSGTMMNRGQELT
560 570 580 590 600

570 580 590 600 610 620
Cry1Ac LDNLQSSDFGYFES--ANAFTSSLGNI-VGVRNFGTAGVVIDRFEFIPVTATLEAEAYNL
gi|112 YESFVTSEFTTNQSDLPFTFTQAEENLILAEVSTGSEYFIDRIEIIIPVNPAREAEEDL
610 620 630 640 650 660

630 640 650 660 670 680
Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRL
gi|112 EAAKAVANLFTTRTD-GLQVNVTDYQVDAQANLVSCLSDEQYGHDKMLLEAVRAAKRL
670 680 690 700 710 720

690 700 710 720 730 740
Cry1Ac SDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQK
gi|112 SRERNLLQDPDFNTINSTEENGWASNGVTIISGEGPFFKGRALQLASA-RENYPTYIYQK
730 740 750 760 770 780

750 760 770 780 790 800
Cry1Ac IDESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGE
gi|112 VDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVVHLVKNVDPNL---VSDTYSDGSCSG
790 800 810 820 830 840

810 820 830 840 850 860
Cry1Ac PNRCAHLEWNPDLDCSCRDEKCA-AHSHHFLSDIDVGCTDLNEDLGVVWVIFKIQTQDG
gi|112 INRCDEHQHVDMLDAEHHPMDCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTDG
850 860 870 880 890 900

870 880 890 900 910 920
Cry1Ac HARLGNLEFLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQ
gi|112 YATLGNLELVEVGPLSGESLEREQRDQNAKWNALGRKRAEIDRVYLAQAQAINHLFVDVQ
910 920 930 940 950 960

930 940 950 960 970 980
Cry1Ac YDQLQADNTIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLDARN
gi|112 DQQLNPEIGLAEINEASNLVESISGVYSDTLQIPGINYEIYTELSDRLQQAASYLYTSRN
970 980 990 1000 1010 1020

990 1000 1010 1020 1030 1040
Cry1Ac VIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVPEWEAEVSVQEVRCVCPGRGYILRVYAT



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Cry1Ac KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAY
gi|150 TKWRNKLTQLRTETQAIYTRAKALDNLFDAQDSHLKIGATFAAIVAARKIVQSIREAY
920 930 940 950 960 970

950 960 970 980 990 1000
Cry1Ac LPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNN
gi|150 MSWLQSDVPLNYPIFTELNDRVQRAFQLYDVQNVVRNGRFLNGVLDWIVTSDVKVQEGNG
980 990 1000 1010 1020 1030

1010 1020 1030 1040 1050 1060
Cry1Ac QRSVLVVPWEAEVQSEVVRVCPGRGYILRVTAKEGYGECVTHIEIENNTDELKFSNCV
gi|150 N-NVLVLSGWDAQVLQCLNLYQNRGYILRVTAKEGLGEGYITITDEEGNTDQLTFGSC-
1040 1050 1060 1070 1080 1090

1070 1080 1090 1100 1110 1120
Cry1Ac EEIYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPN
gi|150 -ENIDSSNS-----FVST-----
1100

1130 1140 1150 1160 1170 1180
Cry1Ac CEFNRGRYDYTPPLVGVYVTKELYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|150 -----GYITKELEFFPDDTDQIQIEIGETEGTFQVESVELFLMENLC
1110 1120 1130 1140

>>gi|71792200|emb|CAJ21127.1| unnamed protein product [B (1154 aa)
initn: 1809 initl: 441 opt: 1979 Z-score: 2323.3 bits: 441.8 E(): 1.7e-120
Smith-Waterman score: 2128; 36.522% identity (62.479% similar) in 1202 aa overlap
(20-1182:57-1154)

10 20 30 40
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|717 YPLASEQNGVLQNMNYKEYLQTYDGYTGSLINPNLSINTRDVLQGITIVGRVLG---F
30 40 50 60 70 80

50 60 70 80 90 100
Cry1Ac LLSEFVPGAG----FVLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLE
gi|717 LG---VPFAGQLVTFYTFLLNQLWPTNNAVWEAFMAQVEELIDQRISDQVVRNALDDLT
90 100 110 120 130 140

110 120 130 140 150 160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALTTAIPLFAV----QNYQVP
gi|717 GLHDIYNEYLAALEEWLDRP-NGA-RANLAFQRFENLHTAFVTRMPSFGTGPQSORDAVA
150 160 170 180 190

170 180 190 200 210
Cry1Ac LLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYN---DLTRLIGNYTDHAVRWYNT
gi|717 LLTVYAQAANLHLLKDAEIIYGARWGLQSQINLYFNAQQDRTRI---YTNHCVATYNR
200 210 220 230 240 250

220 230 240 250 260 270

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Cry1Ac GLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL
gi|717 GLEDLKGNTESWYNYHQFRREMTLMAMDVLALFPYINVRQYPNGANPOLREIYTDPPVV
260 270 280 290 300 310

280 290 300 310 320
Cry1Ac ENF---DGSFR--GSA----QGIEGS-IRSPHLMIDLNSITITYTDAHRGEY-----YW
gi|717 FNPPANQGLCRRWGNPNYMTFSGLENAFIRPPHLDRLNLSLTI--NSHRFPISSNFMDYW
320 330 340 350 360 370

330 340 350 360 370 380
Cry1Ac SGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN
gi|717 AGHTLRRSYMNSAVQ---EDSYGAIPTTRVTINPGVNGNHIESTAVDFRSGLVGIY
380 390 400 410 420

390 400 410 420 430
Cry1Ac N-QQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSHVSM
gi|717 GVHRASFVPGGLFN-GTIS--PANAGCRN-LHDTRDVLPLEENNGSP---SHRSHVTF
430 440 450 460 470 480

440 450 460 470 480 490
Cry1Ac --FRSGFSSSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNLFLNGS-VISGPG
gi|717 LSFQTNQAGSLANGGSVPLYVWARQDIDFNNTITANRITQLPLVKAFEIAAGTTIVKGGP
490 500 510 520 530 540

500 510 520 530 540 550
Cry1Ac FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNWGNSSIFS
gi|717 FTGGDILRRTSTGT---LGTIRVNVNSPLTQ-RYRVFRYASTVDFDFVSRGGTTVNN
550 560 570 580 590

560 570 580 590 600 610
Cry1Ac NTVPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEPVPT
gi|717 FRFPRTMSRGQESRYESYVTSEFTTPTFTQSQDFIRTSIQGLSGNGEVYLDRIEIIIPVN
600 610 620 630 640 650

620 630 640 650 660 670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDEFCLDEKRELS
gi|717 PAREAEEDLEAAKAVASLFTTRTD-GLQVNVTDYQVDQAANLVSLSDSEQYGHDKMMLL
660 670 680 690 700 710

680 690 700 710 720 730
Cry1Ac EKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDE
gi|717 EAVRAAKRLSRERNLLQDPDFNEINSIEENGWKASNGVTISEGGPPFKGRAIQLASA-RE
720 730 740 750 760 770

740 750 760 770 780 790
Cry1Ac CYPYTYLQKIDESKLFATRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSA
gi|717 NYPTIYIYQKVDASVLKPYTRYRLDGFVKSSQDLEIDLHKKVHLVKNVDPDNL---VSD
780 790 800 810 820

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      800      810      820      830      840      850
Cry1Ac QSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC-AHSHHFLSLDIDVGCETDLNE--DLGV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 TYSDGSCSGINRCDEQHQQVDMQLDAEHHHPMCCEAAETHFSSYIDTG--DLNPSVDQGI
      830      840      850      860      870      880

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      860      870      880      890      900      910
Cry1Ac WVIFIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 WVVLKVRTTDGYATLGNLELVEVGSLSGESLEREKRENAEWAELGRKRAETERVYQAAK
      890      900      910      920      930      940

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      920      930      940      950      960      970
Cry1Ac ESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAEIFEELLEGRI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 RAINHLFVDYDQQQLNLEVLGLAEINEVSNLVEIPSVSVDTVLQIPGVNYEYIYELSNRL
      950      960      970      980      990      1000

```

```

      980      990      1000      1010      1020      1030
Cry1Ac FTAFSLYDARNVIKNGDFNNGLSQWNVKGHVDVEEQNNQRSVLVPEWEAEVSEQVRRVCP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 QQASYLYMSRNAVQNGDFNNGLSQWNVKGHVDVEEQNNQRSVLVPEWEAEVSEQVRRVCP
      1010      1020      1030      1040      1050      1060

```

```

      1040      1050      1060      1070      1080      1090
Cry1Ac GRGYILRVTAKEYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 NCKYVLRVTRARKVGSQDGYVTIRNGAHHHETLIFNAC-----DYDIN----
      1070      1080      1090      1100

```

```

      1100      1110      1120      1130      1140      1150
Cry1Ac GGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRNPFCEFNRYRDTYPLPVGYVTKEL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 -GTYVNTNT-----YITKEV
      1110      1120

```

```

      1160      1170      1180
Cry1Ac EYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 VFYPHTEHTWVEVSESEGAFYIDSIELIETQE
      1130      1140      1150

```

```

>>gi|62288329|gb|AAx78440.1| crystal protein Cry9Ed1 [Ba (1154 aa)
  initn: 1809 initl: 441 opt: 1979 Z-score: 2323.3 bits: 441.8 E(): 1.7e-120
Smith-Waterman score: 2128; 36.522% identity (62.479% similar) in 1202 aa overlap
(20-1182:57-1154)

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```

      10      20      30      40
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 YPLASEQNGVLQNMNYKEYLQTYDGDYTGSLINPNLSINTRDVLQGTGIVTRVGLG---F
      30      40      50      60      70      80

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      50      60      70      80      90      100
Cry1Ac LLSEFVPGAG---FVLGLVDIIWIGIFGPSQWDAFLVQIEQLINRIIEEFARNQAIISRL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 LG---VPFAGQLVTFYTFLLNQLWPTNNAVWEAFMAQVEELIDQRISDQVVRNALDDLT
      90      100      110      120      130      140

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```

      110      120      130      140      150      160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALT'TAIPLFAV---QNYQVP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 GLHDYYNEYLAALAEWLDRP-NGA-RANLAFQRFENLHTAFVTRMPSFGTGPQSQRDAVA
      150      160      170      180      190

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      170      180      190      200      210
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYN--DLTRLIGNYTDHAVRWYNT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 LLTVYAQAANLHLLKDAEYGARWGLQSQINLYFNAQQDRTRI---YTNHCVATYNR
      200      210      220      230      240      250

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      220      230      240      250      260      270
Cry1Ac GLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 GLEDLKGNTESWYNYHQFREMTLMAMDVLFPPYVNRQYPNGANPQLTREIYTPDPV
      260      270      280      290      300      310

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      280      290      300      310      320
Cry1Ac ENF---DGSFR--GSA-----QGIEGS-IRSPHMDILNSITTYTDAHRGEY-----YW
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 FNPANQGLCRRWGNPNPYMTFSGLENAFIRPPHLDRLNSLTI--NSHRFPISSNFMDY
      320      330      340      350      360      370

```

```

      330      340      350      360      370      380
Cry1Ac SGHQIMASVPVSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSLTLYRRPFNIGIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 AGHTLRRSYMNNNAVQ-----EDSYGAIPTTRVTINPGVNGTNIHIESTAVDFRSLVGIY
      380      390      400      410      420

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      390      400      410      420      430
Cry1Ac N-QQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSM
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 GVHRASFVPGGLFN-GTIS--PANAGCRN-LHDTRDVLPLEENNGSP---SHRLSHVTF
      430      440      450      460      470      480

```

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      440      450      460      470      480      490
Cry1Ac --FRSGFNSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 LSFQTNQAGSLANGGSVPLYVWARQDIDFNNTITANRITQLPLVKAFEIAAGTTIVKGP
      490      500      510      520      530      540

```

```

      500      510      520      530      540      550
Cry1Ac FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 FTGGDILRRTSTGT---LGTIRVNVNSPLTQ-RYRVRFRYASTVDFDFVSRGGTTVNN
      550      560      570      580      590

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```

      560      570      580      590      600      610
Cry1Ac NTVPATATSLDNLQSSDF--GYFESANAFTSSLGNI-VGVRNFSGTAGVIDRFEFIPVT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 FRFPRMRSRQGESRYESYVTFSEFTTFFFTQSQDFIRTSIQLSGNGEVYLDRIEIIIPV
      600      610      620      630      640      650

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      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622 PAREAEEDLEAAKKAVALFTRTRD-GLQVNVTDYQVDAQANLVSCLSDQEQYGHDKMLL
      660      670      680      690      700      710

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      680      690      700      710      720      730
Cry1Ac  EKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  EAVRAAKRLSRERNLLQDPDFNEINSIEENGWKAASNGVTISEGGFFFKGRALQLASA-RE
      720      730      740      750      760      770

      740      750      760      770      780      790
Cry1Ac  CYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLWPLSA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  NYPTYIYQKVDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVVHLVKNVDPNL----VSD
      780      790      800      810      820

      800      810      820      830      840      850
Cry1Ac  QSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKC-AHSHHFSLDIDVGCTDLNE--DLGV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  TYSDGSCSGINRCDEQHQVDMQLDAEHHFMDCCCAAETHFSSYIDTG--DLNPSVDQGI
      830      840      850      860      870      880

      860      870      880      890      900      910
Cry1Ac  WVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  WVVLKVRITDGYATLGNLELVVSGESLEREKRENAEWAELGRKRAETERVYQAAK
      890      900      910      920      930      940

      920      930      940      950      960      970
Cry1Ac  ESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNAEIFELEGRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  RAINHLFVDYDQQLNLEVLAEINEVSNLVESIPSVSVDTVLQIPGVNVEIYTELSNRL
      950      960      970      980      990      1000

      980      990      1000      1010      1020      1030
Cry1Ac  FTAFLSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSLVLPVEWAEVSEQVVRVCP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  QQASYLYMSRNAVQNGDFNGLDSWNATTDATVQ-QDGMHFLVLVSHWDAQVSQLRVQP
      1010      1020      1030      1040      1050      1060

      1040      1050      1060      1070      1080      1090
Cry1Ac  GRGYILRVITAYKEGYGEGCVTIIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  NCKYVLRVTARKVSGDGYVTIRNGAHHHETLIFNAC-----DYDIN----
      1070      1080      1090      1100

      1100      1110      1120      1130      1140      1150
Cry1Ac  GGAYTSRNRNGYNEAPSVPADYASVYEEKSYTDGRENPECFNRGRYRDYTPLVGVYTKEL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  -CTYVNT-----YITKEV
      1110      1120

      1160      1170      1180
Cry1Ac  EYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|622  VFYPHTEHTWVEVSESEGAFYIDSIELIETQE
      1130      1140      1150

```

```

>>gi|45593719|gb|AAS68357.1| insecticidal protein Cry9Ec (1154 aa)
  initn: 1866  initl: 444  opt: 1963  Z-score: 2304.4  bits: 438.4  E(): 2e-119
Smith-Waterman score: 2101; 36.386% identity (61.615% similar) in 1201 aa overlap
(20-1182:57-1154)

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```

      10      20      30      40
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  YPLTDDPNAGLQNMNYKEYLQTYDGDYTGSLINPPLSINTRDVLQGTG---INIVGRVLGF
      30      40      50      60      70      80

      50      60      70      80      90      100
Cry1Ac  LLESEFVPGAG----FVLGLVDIIWGI FGPSSQWDAFLVQIEQLINQRIEEFARNQAI SRLE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  LG---VPFAGQLVTFYTFLLNQLWPTNNNAVWEAFMAQIEELIDQRRISEQVVRNALDALT
      90      100      110      120      130      140

      110      120      130      140      150      160
Cry1Ac  GLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALTTAIPLFAV---QNYQVP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  GIHDYYNEYLAALEEWLERP-NGA-RANLAFQRFENLHQLFVSPFSGSPGSESDAVA
      150      160      170      180      190

      170      180      190      200      210      220
Cry1Ac  LLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGNYTDHARWYNTGLE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  LLTVYAQAANLHLLLLKDAEIIYGARWGLNQGQINLYFNAQQDRTQIYTNHCVATYNRGLE
      200      210      220      230      240      250

      230      240      250      260      270      280
Cry1Ac  RVWGPDSDRDIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  NLRGTNTESWYNYHQFREMFTLMDLVALFPYINLRQYPNGANPQLTREIYTDPVVFPN
      260      270      280      290      300      310

      290      300      310      320
Cry1Ac  DGS-----FRGSA----QGI EGS-IRSPHLMIDLNSITITYDAHRGEY-----YWSGH
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  PANQGLCCRWRNNPYMTFSELENTFIRPPHFLDRLNSLTI--NSHRFPISSNFMDYWAGH
      320      330      340      350      360      370

      330      340      350      360      370      380
Cry1Ac  QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSSLTYRRPFNIGINN-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  TLRRSYMNSAVQEDS--YG---ATTSTRVTINTGVNGTNRRESTAVDFRSGLLVGVY
      380      390      400      410      420      430

      390      400      410      420      430      440
Cry1Ac  QQLSVLDGTFEYAGTSSNPLSAVYRKSGLTVDLSEIPPQNNVPPRQGFSHRSLSHVSMFR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  HRASFVPGGLFN-GTIS--PANAGCRN-LHDTRDELPLEENNGSP----SHRSLSHVT-FL
      440      450      460      470      480

      450      460      470      480      490
Cry1Ac  SGFSNSVSIIRA---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLPNGS-VISGPGF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  SFLTDQAGSIRNSGAVLYVWARQDIDLNNTITANRITQLPLVKASEIAAGTIVVRGPGF
      490      500      510      520      530      540

      500      510      520      530      540
Cry1Ac  TGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|455  TGGDILRRTSAGT---LGTIRVNVNSPLTQ-RYRVRFRYASTTDFNFFVIRGGTIVNPF

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gi|382 TVDSLTELPPEDNSVPPREGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLTN
410 420 430 440 450 460

Cry1Ac IIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPST
470 480 490 500 510 520

gi|382 TIDPERINQIPLVKGFRVWGGTTSVITGPGFTGGDILRRNTFGDFVS---LQVNNINSPI
470 480 490 500 510

Cry1Ac STRYRVRVRYASVTPIHNLNVNWNSSI----FSNTVPATATSL--DNLQSSDFGYFESA
530 540 550 560 570 580

gi|382 Q-RYRLRFRYASSRDARVIVLTGAASTGVGGQVSNMPLQKMEIGENLTSRTFRYTD
520 530 540 550 560 570

Cry1Ac NAFTSSLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNAL
590 600 610 620 630

gi|382 NPFSSFRANPDIIGISEQPLFGAGSISGGELYDKIEIILADATFEAESDLERAQKAVNAL
580 590 600 610 620 630

Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDS
640 650 660 670 680 690

gi|382 FTSSNQIGLKTVDYHIDQVSNLVE
640 650 660

>>gi|3986086|dbj|BAA34908.1| Cry9 like protein [Bacillus (1150 aa)
initn: 1812 initl: 450 opt: 1945 Z-score: 2283.2 bits: 434.4 E(): 3e-118
Smith-Waterman score: 2080; 34.866% identity (62.375% similar) in 1196 aa overlap
(20-1182:57-1150)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
10 20 30 40

gi|398 YPLASDPNAAFQNMNYKEYLQTYDGYTGSLINPNLSINPRDVLQTG---INIVGRILGF
30 40 50 60 70 80

Cry1Ac LLESEFVPGV---FVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIARLE
50 60 70 80 90 100

gi|398 LG---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDLT
90 100 110 120 130 140

Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT'AIPLFAV---QNYQVPL
110 120 130 140 150 160

gi|398 GLHDYEEYLAALEEWLERP-NGARANLVQRFENLHTAFVTRMPSFGTGPQSQRDAVAL
150 160 170 180 190

Cry1Ac LSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
170 180 190 200 210 220

gi|398 LTVYAQAANLHLLLLKDAEIIYGARWGLQQGQINLYFNAQQERTRIYTNHCVEYTYNRGLED
200 210 220 230 240 250

Cry1Ac VWGPDSDRWIRYNQFRRELTTLVLDIVLFFPNYDSRTYPIRTVSQLTREIYTNPVLENF-
230 240 250 260 270 280

gi|398 VRGTNTESWLNHYHRFREMTLMAMDVLALFPFYNVQYPPNGANPQLTREIYTDPIVYNPP
260 270 280 290 300 310

Cry1Ac --DGSFR-----GSAQGIIEGS-IRSPHMLDILNSITI---YTDahrgey--YWSGHQ
290 300 310 320

gi|398 ANQGCRRWGNPNYTFSELENAFIRPPHLFERNLRLTISRNRYPAPTNSFLDYWSGHT
320 330 340 350 360 370

Cry1Ac IMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPF-NIGINNQQ
330 340 350 360 370 380

gi|398 LQSQHA--NNPTTYETSQYQITSNT--RLFNNTN-GA-RAIDSRA--RNFGLNYANLYG
380 390 400 410 420 430

Cry1Ac LSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDLDEIPPQNNVPPRQGFSHRSLSHVSMFRSG
390 400 410 420 430 440

gi|398 VSSLN--IPPTGVMSITNAANTCRQDLTTEELPLENNF-----NLLSHVTFLRFN
440 450 460 470 480

Cry1Ac FSNSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGG
450 460 470 480 490 500

gi|398 TTQGGPLATLGFVPTVYVWTRDVFDTNTITADRITQLPWWKASEIGGGTTVVKGPFTGG
490 500 510 520 530 540

Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVP
510 520 530 540 550 560

gi|398 DILRRDGGAVGTIRANVNAPL----TQQYRIRLRYASTTSFVVNL-FVNNSAAGFTLP
550 560 570 580 590

Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLE
570 580 590 600 610

gi|398 STMAQNGSLTYESFNTLEVHTIRFSQSDTTLRLNIFPSISGQEVVVDKLEIVPINPTRE
600 610 620 630 640 650

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVK
620 630 640 650 660 670

gi|398 AEEDELEDAKAVASLFTTRTRD-GLQVNVTDYQVDQAAANLVSCLSDEQYGHDKMLLEAVR
660 670 680 690 700 710

Cry1Ac HAKRLSDERNLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPT
680 690 700 710 720 730

gi|398 AAKRLSRERNLQDPPFNEINSTEENGWAKASNGVTISEGGPFFKGRALQLASA-RENYPT
720 730 740 750 760 770

Cry1Ac YLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAKHETVNVVPGTSSLWPLSAQSPI
740 750 760 770 780 790

gi|398 YIYQKVDASTLKPTRYKLDGQVSSQDLEIDLIIHHKVVHLVKNVDPNL---VSDTYS
780 790 800 810 820

Cry1Ac GKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHFSLDIDVGCCTDLNEDLGVWVIFKI
800 810 820 830 840 850





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          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFSTSSLGNIVGVRN--FSGTAG--VIIDRFEFIPVTATLE
gi|539 STMAQNGSLTYESFNTLEVTHTIRFSQSDTTLRLNIFPISISGQEVYVVKLEIVPINPTRE
          600      610      620      630      640      650
          620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
gi|539 AEEDLEDAKAVASLFTRTRD--GLQVNVTDYQVDQANLVSLDSEQYGHDKKMLLEAVR
          660      670      680      690      700      710
          680      690      700      710      720      730
Cry1Ac HAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPT
gi|539 AAKRLSRERNLLQDDPFNEINSTEENGWKASNGVTISEGGPPFKGRALQLASA--RENYPT
          720      730      740      750      760      770
          740      750      760      770      780      790
Cry1Ac YLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSAQSPI
gi|539 YIYQKVDASTLKPYPTRYKLDGFGVQSSQDLEIDLHKKVHLVKNVPDNL---VSDTYS
          780      790      800      810      820
          800      810      820      830      840      850
Cry1Ac GKCGEPNRCAPHLEWNPDLDCSCRDEKEC-AHSHHFLSDIDVGCDDLNEGLGVVWIFKI
gi|539 GSCSGINRCEEQHQVQVLDLAEHDHPKDCCEAAQTHEFSSYIHTGDLNASVDQGIWVVLQV
          830      840      850      860      870      880
          860      870      880      890      900      910
Cry1Ac KTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDAL
gi|539 RTTDDYATLGNLELVEVGLSGLSGLERERQDNNAKWNNEVGRKRAETDRIYQDAKQAINHL
          890      900      910      920      930      940
          920      930      940      950      960      970
Cry1Ac FVNSQYDQLQADNTIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSL
gi|539 FVDYQDQQLSPEVGMADIIDAQNLIASISDVYSDAVLQIPGINYEMYTELSNRLQQASYL
          950      960      970      980      990      1000
          980      990      1000      1010      1020      1030
Cry1Ac YDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLPVPEWAEVSVQEVVCPGRGYIL
gi|539 YTSRNVVQNGDFNSGLDSWNAATTDVAVQDGNMH--FLVLSHWDAQVSQQFRVQPNCKVYL
          1010      1020      1030      1040      1050      1060
          1040      1050      1060      1070      1080      1090
Cry1Ac RVTAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEQEYGGAYTS
gi|539 RVTAKKVGNGDGYVTIQDGAHRETLTTFNAC-----DYDVN-----GTHVN
          1070      1080      1090      1100
          1100      1110      1120      1130      1140      1150
Cry1Ac RNRGYNEAPSPVADYASVYEEKSYTDGRENPCEFNRGYRDTPLVPGVYVTKLEYFPEP
gi|539 DN-----SYITKELVFYPKT
          1110      1120

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          1160      1170      1180
Cry1Ac DKVWIEIGETEGTFIVDSVELLME
gi|539 EHMWVEVSETEGTFYIDSIEFIETQE
          1130      1140      1150
>>gi|33731259|gb|AAQ37322.1| Sequence 74 from patent US (1150 aa)
  initn: 1812 init1: 450 opt: 1945 Z-score: 2283.2 bits: 434.4 E(): 3e-118
Smith-Waterman score: 2080; 34.866% identity (62.375% similar) in 1196 aa overlap
(20-1182:57-1150)
          10      20      30      40
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|337 YPLASDPNAAFQNMNYKEYLQTYDGDYTGSLINPNLSINPRDVLQGTG---INIVGRILGF
          30      40      50      60      70      80
          50      60      70      80      90      100
Cry1Ac LLSEFVPGAG---FVLGLVDIIWGFGPSQWDAPLQIEQLINQRIEEFARNQAISRLE
gi|337 LG---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDLT
          90      100      110      120      130      140
          110      120      130      140      150      160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPL
gi|337 GLHDYEEYLAALAEWLERP--NGARANLVTQRFENLHTAFVTRMPSFGTGPQSQRDAVAL
          150      160      170      180      190
          170      180      190      200      210      220
Cry1Ac LSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|337 LTVYAQAANLHLLLLKDAEYGARWGLQQGQINLYFNAQQERTRIYTNHCVTYNRGLED
          200      210      220      230      240      250
          230      240      250      260      270      280
Cry1Ac VWGPDSDRWIRYQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPNVLENF-
gi|337 VRGTNTESWLNHYRFRREMTLMAMDVLVLPFYVNRQYPNGANPQLTREIYTDPIVYNPP
          260      270      280      290      300      310
          290      300      310      320
Cry1Ac --DGSFR-----GSAQGIEGS-IRSPHMLDILNSITI----YTDHRGEY--YWSGHQ
gi|337 ANQGICRRWGNPNYNTFSELENAFIRPPHLFERLNRLTISRNRYPAPTNTSFLDYWSGHT
          320      330      340      350      360      370
          330      340      350      360      370      380
Cry1Ac IMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPF--NIGINNQ
gi|337 LQSQHA--NNPTTYETSYGQITSNT---RLFNFTN--GA-RAIDSRA--RNFGLNYANLYG
          380      390      400      410      420      430
          390      400      410      420      430      440
Cry1Ac LSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSG
gi|337 VSSLN--IPPTVMSEITNAANTCRQDLTTEELPLENNF-----NLLSHVTFLRFN
          440      450      460      470      480

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          450      460      470      480      490      500
Cry1Ac FSNSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 TTQGGPLATLGFVPTVYVWTREDVDFNTITADRITQLPWWKASEIGGGTTVVKGGPGFTGG
          490      500      510      520      530      540
Cry1Ac
          510      520      530      540      550      560
Cry1Ac DLVRLNSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVTP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 DILRRTDGGAVGTIRANVNAPL-----TQQYRIRLRLYASTTSFVNVNL-FVNNSAAGFTLP
          550      560      570      580      590
Cry1Ac
          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEPVPTATLE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 STMAQNGSLTYESFNTLEVTHTIRFSQSDTTLRLNIFPSISGQEVVYVKLEIVPINPTRE
          600      610      620      630      640      650
Cry1Ac
          620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 AEEDLEDAKKAVALFTRTRD-GLQVNVTDYQVDQAANLVSLCSDEQYGHDKKMLLEAVR
          660      670      680      690      700      710
Cry1Ac
          680      690      700      710      720      730
Cry1Ac HAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 AAKRLSRERNLLQDPDFNEINSTEENGWKAANGVTISEGGPFKGRALQLASA-RENYPT
          720      730      740      750      760      770
Cry1Ac
          740      750      760      770      780      790
Cry1Ac YLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSAQSPI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 YIYQKVDASTLKPTRYKLDGFVQSSQDLEIDLHKKVHLVKNVPDNL---VSDTYSD
          780      790      800      810      820
Cry1Ac
          800      810      820      830      840      850
Cry1Ac GKCGEPNRCAPHLEWNPDLDCSCRDKGK-AHSHHFLSLDIDVGCTDLNEDLGWVWIFKI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 GSCSGINRCEEQHQVDVQLDAEDHPKDCCEAAQTHEFSSYIHTGDLNASVDQGIWVVLQV
          830      840      850      860      870      880
Cry1Ac
          860      870      880      890      900      910
Cry1Ac KTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKAKESVDAL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 RTTDGYATLGNLELVEVGPLSGESLEREQRDNAKWNEEVGRKRAETDRIYQDAKQAINHL
          890      900      910      920      930      940
Cry1Ac
          920      930      940      950      960      970
Cry1Ac FVNSQYDQLQADTNIAIMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 FVDYDQDQLSPEVGMADIIDAQNLIASISDVYSDAVLQIPGINYEMYTELSNRLQOASYL
          950      960      970      980      990      1000
Cry1Ac
          980      990      1000      1010      1020      1030
Cry1Ac YDARNVIKNGDFNNGLSWCNVKGVHDVVEEQNNQRSVLLVPEWAEVSEVQRVCPGRGYIL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 YTSRNVVQNGDFNSGLDSWNATTDTAQQDGNMH-FLVLSHWDAQVSSQFRVQPNCKYVL

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          1010      1020      1030      1040      1050      1060
Cry1Ac
          1040      1050      1060      1070      1080      1090
Cry1Ac RVTAYKEGYEGECVTTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 RVTAKKVGNGDGYVTIQDGAHRETTLTFNAC-----DYDVN----GTHVN
          1070      1080      1090      1100
Cry1Ac
          1100      1110      1120      1130      1140      1150
Cry1Ac RNRGYNEAPSVPADYASVYEKSYTDGRRNCPCEFNRGYRDTPLPVGVYVTKLEYFPET
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 DN-----SYITKELVFYPKT
          1110      1120
Cry1Ac
          1160      1170      1180
Cry1Ac DKVWIEIGETEGTFIVDSVELLMEE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 EHMWVEVSETEGTFYIDSIEFIETQE
          1130      1140      1150
Cry1Ac
>>gi|120431604|gb|ABM21765.1| cry9Ea3 insecticidal cryst (1150 aa)
      initn: 1812 init1: 450 opt: 1945 Z-score: 2283.2 bits: 434.4 E(): 3e-118
      Smith-Waterman score: 2079; 34.866% identity (62.291% similar) in 1196 aa overlap
      (20-1182:57-1150)
          10      20      30      40
Cry1Ac
      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
          10      20      30      40
gi|120 YPLASDPNAAFQNMNYKEYLQTYDGDYTGSLINPNLSINPRDVLQTG---INIVGRILGF
          30      40      50      60      70      80
Cry1Ac
          50      60      70      80      90      100
Cry1Ac LLSEFVPGAG---FVLGLVDIIWIFGQSDAFVQIEQLINQRIEEFARNQAISRLE
          10      20      30      40      50      60      70      80
gi|120 LG---VPFAGQLVTFYTLFLNQLWPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDL
          90      100      110      120      130      140
Cry1Ac
          110      120      130      140      150      160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPL
          10      20      30      40      50      60      70      80
gi|120 GLHDYEEYLAALEEWLERP-NGARANLVTQRFENLHTAFVTRMPSFGTGPGRDAVAL
          150      160      170      180      190
Cry1Ac
          170      180      190      200      210      220
Cry1Ac LSVVYQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
          10      20      30      40      50      60      70      80
gi|120 LTVYAQAANLHLLLLKDAEYGARWGLQGGQINLYFNAQQERTRIYTNHCVETYNRGLED
          200      210      220      230      240      250
Cry1Ac
          230      240      250      260      270      280
Cry1Ac VWGPDSDRWIRYQFRRELTTLVLDIVSLFPNYSRITYPIRTVQSLTREIYTNPVLENF-
          10      20      30      40      50      60      70      80
gi|120 VRGTNTESWLNHYHRFRREMTLMAMDVLPFPYVNRQYVNGANPQLTREIYTDPIVYVNP
          260      270      280      290      300      310
Cry1Ac
          290      300      310      320
Cry1Ac --DGSFR-----GSAQGIEGS-IRSPHLMIDLNSITI----YTDHRGEY--YWSGHQ
          10      20      30      40
gi|120 ANQICIRRWGNPNYNTFSELENAFIRPPHLFRLNRLTISRNRYPAPTDSFLDYWSGHT

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320      330      340      350      360      370
Cry1Ac  IMASPVGFSGPEFTFPLYGTGMNAAPQQRIVACLQGGVYVRTLSSTLYRRPF--NIGINNQQ
      330      340      350      360      370      380
gi|120  LQSQHA--NNPTTYETSYGQITSNT---RLFNTTN-GA-RAIDSRA--RNFGLNYANLYG
      380      390      400      410      420      430
Cry1Ac  LSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQNNVPPRGFSHRLSHVSMFRSG
      390      400      410      420      430      440
gi|120  VSSLN--IFPTGVMEITNAANTCRQDLTTTEELPLENNF-----NLLSHVTFLEFRN
      440      450      460      470      480
Cry1Ac  FSNSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGG
      450      460      470      480      490      500
gi|120  TTQGGPLATLGFVPTYVWVTRDVDFTNTITADRI TQLPWWKASEIGGTTVVKGPGFTGG
      490      500      510      520      530      540
Cry1Ac  DLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVVRYASVTPPIHLNVNWNSSIFSNVTP
      510      520      530      540      550      560
gi|120  DILRRTDGGAVGTIRANVNAPL----TQQYRIRLRYASTTSFVVNL-FVNNSAAGFTLP
      550      560      570      580      590
Cry1Ac  ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEPVPTATLE
      570      580      590      600      610
gi|120  STMAQNGSLTYESFNTLEVTHTRIRFSQDSTLRLNIFPSISGQEVVYVDKLEIVPINPTRE
      600      610      620      630      640      650
Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVK
      620      630      640      650      660      670
gi|120  AEEDLEDAKKAVASLFRTRD-GLQVNVTDYQVDQAANLVSLSDSEQYGHDKMLLEAVR
      660      670      680      690      700      710
Cry1Ac  HAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPT
      680      690      700      710      720      730
gi|120  AAKRLSRERNLLQDPDFNEINSTEENGWKASNGVTISEGGPFKGRALQLASA-RENYPT
      720      730      740      750      760      770
Cry1Ac  YLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPI
      740      750      760      770      780      790
gi|120  YIYQRVDASTLKYTRYKLDGFVQSSQDLEIDLIIHHKVVHLVKNVPDNL---VSDTYSD
      780      790      800      810      820
Cry1Ac  GKCGEPNRCAPHLEWNPDLDCSCRDEKEC-AHSHHFLSLDIDVGCTDLNEDLGVVWIFKI
      800      810      820      830      840      850
gi|120  GSCSGINRCEEQHQVDVQLDAEDHPKDCCEAAQTHEFSSYIHTGDLNASVDQGIWVVLQV
      830      840      850      860      870      880
Cry1Ac  KTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKAKESVDAL
      860      870      880      890      900      910

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gi|120  RTTDGYATLGNLELVEVGPLSGESLEREQRDQNAKWNEEVGRKRAETDRIYQDAKQAINHL
      890      900      910      920      930      940
Cry1Ac  FVNSQYDQLQADNTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFELEGRIFTAFSL
      920      930      940      950      960      970
gi|120  FVDYDQQLSPEVGMADIIDAQNLIASISDVYSDAVLQIPGINYEMYTELSNRLQQASYL
      950      960      970      980      990      1000
Cry1Ac  YDARNVIKNGDFNGLSCWNVKGHVDEEQQNQRSVLVVPEWAEVSQEVVRCVPGRGYIL
      980      990      1000      1010      1020      1030
gi|120  YTSRNVVQNGDFNSGLSDWNATD TAVQQDGNMH-FLVLSHWAQVSQQFRVQPCKYVL
      1010      1020      1030      1040      1050      1060
Cry1Ac  RVTAYKEGYEGECVTIHEIENNTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTS
      1040      1050      1060      1070      1080      1090
gi|120  RVTAKKVGNGDGYVTIQDGAHRETTLTFNAC-----DYDVN-----GTHVN
      1070      1080      1090      1100
Cry1Ac  RNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRYRDTYPLVGVYTKLEYFPET
      1100      1110      1120      1130      1140      1150
gi|120  DN-----SYITKELVFYPKT
      1110      1120
Cry1Ac  DKVWIEIGETEGTFIVDSVELLMEE
      1160      1170      1180
gi|120  EHMVVEVSETEGTFYIDSIEFIETQE
      1130      1140      1150
>>gi|21504424|gb|AAM57118.1| Sequence 74 from patent US (1150 aa)
      initn: 1812 initl: 450 opt: 1945 Z-score: 2283.2 bits: 434.4 E(): 3e-118
Smith-Waterman score: 2080; 34.866% identity (62.375% similar) in 1196 aa overlap
(20-1182:57-1150)
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      10      20      30      40
gi|215  YPLASDPNAAFQNMNYKEYLQTYDGYDTGSLINPNSINPRDLQTG---INIVGRILGF
      30      40      50      60      70      80
Cry1Ac  LLSEFVPGAG---FVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLE
      50      60      70      80      90      100
gi|215  LG---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDL
      90      100      110      120      130      140
Cry1Ac  GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPL
      110      120      130      140      150      160
gi|215  GLHDYEEYLAALEEWLERP-NGARANLVTQRFENLHTAFVTRMPSFGTGPQSQRDAVAL
      150      160      170      180      190
Cry1Ac  LSVYVQAANLHLSVLRDVSFQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
      170      180      190      200      210      220

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      . . . . .
gi|112 LLGLFDALWGSIGPSQWDLFLEQIPELLDQKIEEFARNQAIISRLLEGISLGYIYTEAPFE
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      . . . . .
gi|112 WEADPTNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVPLLSVYVQAANLHLSVLRDVS
      120     130     140     150     160     170

      190     200     210     220     230
Cry1Ac VFGQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS--RDWIRYNQFR
      . . . . .
gi|112 VFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNTGLDRL--PRTGGLRNWARFVQFR
      180     190     200     210     220     230

      240     250     260     270     280     290
Cry1Ac RELTTLVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGS-IR
      . . . . .
gi|112 RELTISVLDIISFFRNYDSRLYPIPTSSQLTREVYTDVINITYRVGSPFENIENSAIR
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac SPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVA
      . . . . .
gi|112 SPHLMDFLNNLTIDTLIRGVHYWAGHRVTSHTFG-SSQVITTPQYGITANAEPRTIAP
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac QLQGV---YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDS
      . . . . .
gi|112 STFPGLNLFYRFLSNPFFRRSENI-TPTLGINVVQGVGFI---QPNAEVLVYRSRGTVDS
      360     370     380     390     400

      420     430     440     450     460     470
Cry1Ac LDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNFIASD
      . . . . .
gi|112 LNELPIDGEN--SLVGYSHRLSHVTLTRSLYNTNITSL---PTFWTHHSATNTNTINPD
      410     420     430     440     450     460

      480     490     500     510     520     530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYR
      . . . . .
gi|112 IITQIPLVKGFRLGGGTSVIKGPFTGGDILRRNTIGEFVS---LQVNSPITQ-RYR
      470     480     490     500     510

      540     550     560     570     580
Cry1Ac VRVRYASVTPIHLLNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTS
      . . . . .
gi|112 LRFYASSRDARVIVLTGAASTGVGGQVSNMPLQKTMIEIGENLTSRTFRYTFDSNPFSP
      520     530     540     550     560     570

      590     600     610     620     630
Cry1Ac SLG-NIVGVRN---F---SGTAG-VIIDRFEFIPVATLEAE-YNLERAQKAVNALFTST
      . . . . .
gi|112 RANPDIIGISEQPLFGAGSISSELYIDKIELILADATFKRRRWSVHKASRPLHLHQAG
      580     590     600     610     620     630

      640     650     660     670     680     690

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Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREKRESEKVKHAKRSLDERNLLQDSNFKD
gi|112 LAAD
      640

>>gi|79014094|gb|ABB51653.1| crystal protein Cry28Aa [Ba (1128 aa)
      initn: 1496 initl: 541 opt: 1818 Z-score: 2133.5 bits: 406.7 E(): 6.5e-110
Smith-Waterman score: 1927; 34.660% identity (60.365% similar) in 1206 aa overlap
(22-1182:23-1128)

      10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG
      . . . . .
gi|790 MDKHKINKIGVQSTEVNSESIFFNPEVD--GSDTVAVVVSAGIVVVGITLAFASFVNPVGVV
      10      20      30      40      50

      60      70      80      90     100     110
Cry1Ac FW-LG-LVDIIWGI--FGPSQ-WDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIY
      . . . . .
gi|790 LISFGTLAPVLWPDPEEDPKKIWSQFMKHGEDLLNQTISTAVKEIALAHLNGFKDVLTY
      60      70      80      90     100     110

      120     130     140     150     160     170
Cry1Ac AESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
      . . . . .
gi|790 ERAFNDWKRNPASANTARL-VSQRFENAHFNFSVNMPLQLPTDYDLLLLSCYTEAANLHLN
      120     130     140     150     160     170

      180     190     200     210     220
Cry1Ac VLRDVSVFGQRWGFDAA-----TINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR
      . . . . .
gi|790 LLHQGVQFADQWNADQPHSPMLKSSGTYDELVVYIEKYINYCTKYHKLNLHKESEKI
      180     190     200     210     220     230

      230     240     250     260     270     280
Cry1Ac DWIRYNQFRRELTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTN--NPVLENFDGSRFG
      . . . . .
gi|790 TWDAYNTYRREMTLIVLDLVATFPFYDIRRFRGVELELTREVYTSLDPPGLNAGPIPEI
      240     250     260     270     280     290

      290     300     310     320     330     340
Cry1Ac SAQGIEGSI-RSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTM
      . . . . .
gi|790 DFSYLEDHLTRPPGLFTWLSDIELYTESVAEGDYLSG--IRESKY-YTGKQF-FTMKNIY
      300     310     320     330     340     350

      350     360     370     380     390     400
Cry1Ac GNAAPQORIVAQLGQGVYRTLSTLYRRPFN-IGINNQLSVLDGTEFAYGTSSNLPSAV
      . . . . .
gi|790 GNTNRLSKLITLLPGEFITHLSI--NRGFQTIAGINKLYSLIKVIFVFTTFKNDNE----
      360     370     380     390     400

      410     420     430     440     450
Cry1Ac YRKSQTVDSLDEIPPQNNVPPRQ-----FSHRLSHVSMF--RSGFSNSVSIIRAPM
      . . . . .
gi|790 YQKNFNVNQNQE-PQETTNYPNDYGGNSQKFKHNLSHFPLIIHKLEFAEYFHSIF---A
      410     420     430     440     450     460

      460     470     480     490     500     510

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Cry1Ac FSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRG  
 ..: : . . . . . : : : : . . . . . : : : : : : : : : : : . . . . .  
 gi|790 LGWTHNSVNSQNLISESVSTQIPLVKAYEVTNNSVIRGPGFTGGDLIELRDK-CSIKCKA  
 470 480 490 500 510 520

Cry1Ac 520 530 540 550 560 570  
 YIEVPIHFSTSTRYRVRYASVTPIHLNVNWGNSIFSNTVDPATAT-----SLDNLQ  
 . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 -----SSLKKYAISLFYAANNAIIVSIVDVGDSGAGVLLQPTFSRKGNNNFTIQDLN  
 530 540 550 560 570

Cry1Ac 580 590 600 610 620  
 SDFGYFESANAFTSSLGNIVGV--RNFSGTAGVI--IDRFEPFVPTATLEAEYNLERA  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 YKDFQYHTLLVDIELPESEEIHIHLKREDDYEEGVILLIDKLEFKPIDENYTNEMNLEKA  
 580 590 600 610 620 630

Cry1Ac 630 640 650 660 670 680  
 QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDE  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 KKAVNVLPINATN-ALKMDVTDYHIDQVANLVEICISDDLYAKEKIKLLHAKFAKQLSQA  
 640 650 660 670 680 690

Cry1Ac 690 700 710 720 730 740  
 RNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDE  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 RNLLSDPNFNLN--AENSWTANTGVTTIEGDPYKGRAIQLSAARDENFPTYLYQKIDE  
 700 710 720 730 740 750

Cry1Ac 750 760 770 780 790 800  
 SKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKC-----  
 : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 SLLKPYTRYQLRGFVEGSQDLELDLVRYGATDIVMNVPG--DLEILSYAPINPCEIEET  
 760 770 780 790 800

Cry1Ac 810 820 830 840 850  
 -----GEPNRCAPHELWNPDLDCSCRDGKCAHSHHFLSDIDVCGTDLNEDLGVVWIF  
 : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 RLDTTTCGALDRCKQSNVNSAADVR---PDQVNGDPHAFSPHIDTGTDDNRRNLGIWIF  
 810 820 830 840 850 860

Cry1Ac 860 870 880 890 900 910  
 KIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVD  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 KIATPDGYATFNGLELIELGLPLSGEALAQVQRKEQKWGKNTTQKREEAAKLYAAAKQTIN  
 870 880 890 900 910 920

Cry1Ac 920 930 940 950 960 970  
 ALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAF  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 QLFADSQGTGLRFDTEFSNLSADKLVYKIRDVYSEVLSVIPGLNYDLFMELENRIQNAI  
 930 940 950 960 970 980

Cry1Ac 980 990 1000 1010 1020 1030  
 SLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVPEWAEVSEQEVRVCPGRGY  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 DLYDARNVTNNGEFRNLANWMASSNTEVR-QIQDTSVLVLSWNAQVAQSLNVKPDHGY  
 990 1000 1010 1020 1030 1040

1040 1050 1060 1070 1080 1090  
 Cry1Ac ILRVTAYKEGEGCVTIHEIENNTDELKFSNCVVEEIEYPNNTVTNDYTVNQEEYGGAY  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 VLRVTAKKEGIGNGYVITLDCANHIDTLTFSSC-----D-----SGFT  
 1050 1060 1070 1080

Cry1Ac 1100 1110 1120 1130 1140 1150  
 TSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLEYFP  
 : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 TSSN-----ELAA-----YVTKTLEIFP  
 1090 1100

Cry1Ac 1160 1170 1180  
 ETDKVVIEIGETEGTFIVDSVELLMEE  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|790 DTDQIRIEIGETEGTFYVESVDLIRMED  
 1110 1120

>>gi|9828610|gb|AAG00235.1|AF285775\_1 parasporal inclusi (1128 aa)  
 initn: 1496 init1: 541 opt: 1810 Z-score: 2124.1 bits: 405.0 E(): 2.2e-109  
 Smith-Waterman score: 1913; 34.714% identity (60.315% similar) in 1207 aa overlap  
 (22-1182:23-1128)

10 20 30 40 50  
 Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTFLLSEFV-PGA  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 MDKHINKIGVQSTEVNSESIFFNPEVDSSTVAVVSAGIVV-VGTLTAF--ASFVNPV  
 10 20 30 40 50

60 70 80 90 100 110  
 Cry1Ac GFV-LG-LVDIIWGI--FGPSQ-WDAFLVQIEQLINQRIEERFARNQAISRLEGLSNLYQI  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 VLLISFGTLAPVLPDPEEDPKKIWSQFMKHGEDLLNQITISTAVKEIALAHLGNLHKVDLTY  
 60 70 80 90 100 110

120 130 140 150 160 170  
 Cry1Ac YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHL  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 YERAFNDWKRNPASANTARL-VSQRFENAHFNFSNMPQLQLPTYDTLLSVCYTEANLHL  
 120 130 140 150 160 170

180 190 200 210 220  
 Cry1Ac SVLRDVSVFGQRWGFDA-----TINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 NLLHQGVQFADQWADQPHSPMLKSSGTYDELLVYIEKYINCYTKTYHKGLNHLKESK  
 180 190 200 210 220 230

230 240 250 260 270 280  
 Cry1Ac RDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQTLREIYT--NPVLENFDGFSR  
 : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 ITWDAYNTYRREMTLIVLDLVATFPFYDIRRFRGVELELREVTYSLDPPGLNAGPIPE  
 240 250 260 270 280 290

290 300 310 320 330 340  
 Cry1Ac GSAQGIIEGSI-RSPHLMIDILNSITYTDAHRGEYVWSGHQIMASPVGFGSGPEFTFPLYGT  
 . : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .  
 gi|982 IDFSYLEDHLTRPPGLFTWLSDIELYTESVAEGDYLSG--IRESKY-YTGNQF-FTMKNI  
 300 310 320 330 340 350

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350      360      370      380      390      400
Cry1Ac  MGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFN-IGINNQQLSVLGDTEFAYGTSNLSLPSA
gi|982  YGNTNRLSKQLITLTLPGFEFITHLSI--NRGFQTIAGINKLYSLIQKIVFTTFKNDNE---
360      370      380      390      400

410      420      430      440      450
Cry1Ac  VYRKSGTVDSLDEIPPQNNNVPPRQG-----FSHRLSHVSMF--RSGFSNSSVSIIRAP
gi|982  -YQKNFNVNNQNE-PQETTNYPNDYGGSNSQKFKHNLSHFPLIIHQVEFAEYFHSIF---
410      420      430      440      450      460

460      470      480      490      500      510
Cry1Ac  MFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNR
gi|982  ALGWTHTNSVNSQNLISESVSTQIPLVKAYEVTNSVIRGPGFTGGDLIELRDK-CSIKCK
470      480      490      500      510      520

520      530      540      550      560
Cry1Ac  GYIEVPIHFPTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVTPATAT-----SLDNL
gi|982  A-----SSLKKYAIISLFYAANNAIIVSIVDVGDSGAGVLLQPTFSRKGNNTIQLDL
530      540      550      560      570

570      580      590      600      610      620
Cry1Ac  QSSDFGYFESANAFTSSLGNIVGV---RNFSGTAGVI--IDRFEPVPTATLEAEYNLER
gi|982  NYKDFQYHTLLVDIELPESEEIHIHLKREDDYEEGVILLIDKLEFKPKIDENYTNEMNLEK
580      590      600      610      620      630

630      640      650      660      670      680
Cry1Ac  AQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSD
gi|982  AKKAVNVLFINATN-ALKMDVTDYHIDQVANLVECSIDDLAYAKEIKLLHAIKFAKQLSQ
640      650      660      670      680      690

690      700      710      720      730      740
Cry1Ac  ERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKID
gi|982  ARNLLSDPNFNLN--AENSWTANTGVTIIEGDPLYKGRAIQLSAARDENFPPTYLYQKID
700      710      720      730      740

750      760      770      780      790      800
Cry1Ac  ESKLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKC----
gi|982  ESLLKPYTRYQLRGFVEGSQDLELDLVRYGATDIVMNVPG--DLEILSYSAPINPCEEIE
750      760      770      780      790      800

810      820      830      840      850      860
Cry1Ac  -----GEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVGCCTDLNEDLGVWVI
gi|982  TRLDTCGALDRCKQSNYVNSAADVR--PDQVNGDPHAFSFDITGTDDNRLNGIWI
810      820      830      840      850      860

860      870      880      890      900      910
Cry1Ac  FKIKTQDGHARLGNLEFLBEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKAKESV
gi|982  FKIAATPDGYATFNGLELIELGLPLSGEALAQVQRKEQKWKNTTQKREEAAKLYAAAKQTI
870      880      890      900      910      920

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920      930      940      950      960      970
Cry1Ac  DALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAIFEELEGRIFTA
gi|982  NQLFADSQGTCLRFDTEFSNLSADKLVIYKIRDVYSEVLSVIPGLNYDLFMELLENRIQNA
930      940      950      960      970      980

980      990      1000      1010      1020      1030
Cry1Ac  FSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLVPEWEAEVSQEVVRVCPGRG
gi|982  IDLYDARNVTVTNGEFPNGLANWMASSNTEVR-QIQDTSVLVSSWNAQVAQSLNVKPDHG
990      1000      1010      1020      1030      1040

1040      1050      1060      1070      1080      1090
Cry1Ac  YILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIPNNTVTCNDYTVNQEEYGG
gi|982  YVLRVTAKEGEGYGVYVITLDCANHIDTLTFSSC-----D-----SGF
1050      1060      1070

1100      1110      1120      1130      1140      1150
Cry1Ac  YTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKELEYF
gi|982  TTSSN-----ELAA-----YVTKTLEIF
1090

1160      1170      1180
Cry1Ac  PETDKVWIEIGETEGTFIVDSVELLMEE
gi|982  PDTDQIRIEIGETEGTFYVESVDLIRMED
1100      1110      1120

>>gi|114439356|gb|ABI74753.1| Cry1Ab-like toxin [uncultu (373 aa)
initn: 1796 init1: 1580 opt: 1800 Z-score: 2119.4 bits: 402.5 E(): 3.9e-109
Smith-Waterman score: 1800; 75.926% identity (87.302% similar) in 378 aa overlap
(238-611:1-373)

210      220      230      240      250      260
Cry1Ac  TDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQ
gi|114  RDMTVIVLDIVSLFPNYDSRTYPIRTVSQ
10 20 30

270      280      290      300      310      320
Cry1Ac  TREIYTNVPLENFDGSGFRGSAQIEGSIRSPHMLDILNSITIYTDahrgeyywshqima
gi|114  TREIYTNVPLENFDGSGFRGSAQIEGSIRSPHMLDILNSITIYTDahrgeyywshqima
40 50 60 70 80 90

330      340      350      360      370      380
Cry1Ac  SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVL
gi|114  SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVL
100 110 120 130 140 150

390      400      410      420      430      440
Cry1Ac  DGTEFAYGTSSNLSAVYRKSGTVDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSFGS
gi|114  DGTEFAYGTSSNLSAVYRKSGTVDSLDEIPPQNNNVPPRQGFSHRLSHVSMFRSFGS
160 170 180 190 200 210

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400      410      420      430      440      450
Cry1Ac GTSSNLPASVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
gi|594 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
440      450      460      470      480      490

460      470      480      490      500      510
Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN
gi|594 GSVPTYVWTRRDVLDLNNITTPNRITQLPLVKASAPVSGTTVLKGPFGTGGGILRRTTNGT
500      510      520      530      540      550

520      530      540      550      560      570
Cry1Ac NIQNRGYIEVPIHFSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTVPATATSLDNLQ
gi|594 ----FGTLRVTVNSPLTQ-QYRLRVRFASTGNFNSIRVLRGGVSGIDVRLGSTMNRGQELT
560      570      580      590      600

580      590      600      610      620
Cry1Ac SSSF-----GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYIN
gi|594 YESFPTREFTTTGPFNPPFTTQAQEBILTVNAEGVSTGGEYIIDRIEIVPVNPAREAEED
610      620      630      640      650      660

630      640      650      660      670      680
Cry1Ac LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELESEKVKHAKR
gi|594 LEAAKAVASLFTTRTRD-GLQVNVTDYQVDQAANLVSCLSDQYGHDKMLLEAVRAAKR
670      680      690      700      710      720

690      700      710      720      730      740
Cry1Ac LSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQ
gi|594 LSRERNLLQDPDFNTINSTEENGWKASNGVTISEGGPFKGRALQLASA-RENYPTYIYQ
730      740      750      760      770      780

750      760      770      780      790      800
Cry1Ac KIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVNPGTGSWLPLSAQSPIGKCG
gi|594 KVDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVVHLVKNVPDNL---VSDTYSYDGGSCS
790      800      810      820      830      840

810      820      830      840      850      860
Cry1Ac EPNRCAPHLEWNPDLDCSCRDEKGC-AHSHHFSLDIDVGCITDLNEDLGVVWVIFKIKTQD
gi|594 GINRCDEQHQVDMQLDAEHHMDCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTD
850      860      870      880      890      900

870      880      890      900      910      920
Cry1Ac GHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNS
gi|594 GYATLGNLELVEVGPLSGESLEREQRDNAKWAELGRKRAEIDRVYLAQAINHLFVDY
910      920      930      940      950      960

930      940      950      960      970      980
Cry1Ac QYDQLQADNTIAMIHAADRKRVHSIREAYLPELSVIPGVNAAIFELEGRIFTAFSLYDAR
gi|594 QDQQLNPBGLAEINEASNLVESISGVYDILLQIPGNIYEIYELSDRLQQAQSYLYTSR
970      980      990      1000      1010      1020

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990      1000      1010      1020      1030      1040
Cry1Ac NVIKNGDFNNGLSQVNVKGVHDVVEEQNNQRSLVLPVEWAEVSVQEVVCPGRGYILLRVTA
gi|594 NAVQNGDFNSGLDSWNTTMDASVQQDGNMH-FLVLSHWDAQVSVQQLRVNPNCKYVLRVTA
1030      1040      1050      1060      1070

1050      1060      1070      1080      1090      1100
Cry1Ac YKEGYGEGCVTTIHEIENNTDELKFSNCVEEIYPNNVTVCNDYTVNQEEYGGAYTSRNRG
gi|594 RKVGGGDGYVTTIRDGAHQETLTFNAC-----DYDVN-----GTYVNDN--
1080      1090      1100      1110

1110      1120      1130      1140      1150      1160
Cry1Ac YNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGVYTKLELYFPETDKVM
gi|594 -----SYITEEVVFPETKHMW
1120      1130

1170      1180
Cry1Ac IEIGETEGTFIVDSVELLMEE
gi|594 VEVSESEGSFYIDSIEFIETQE
1140      1150

>>gi|13619537|emb|CAC36453.1| unnamed protein product [B (1157 aa)
initn: 2011 init1: 719 opt: 1724 Z-score: 2022.5 bits: 386.2 E(): 9.9e-104
Smith-Waterman score: 2241; 36.829% identity (63.507% similar) in 1192 aa overlap
(22-1182:59-1157)

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|136 LASDPNAALQNMNYKDYLMQMTDEDYDTSYINPSLSISGRDAVQ TALTVVGRILGALGVFP
30      40      50      60      70      80

60      70      80      90      100      110
Cry1Ac SEFVPGAGFVLGLVDIIWGIQFQPSQWDAFLVQIEQLINQRIEFARNQAIISRLEGLSNLY
gi|136 SQGI--VSFYQFLNLTLPVNDTAVIWEAFMRQVEELVNVQITFARNQALARLQGLGDSF
90      100      110      120      130      140

120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|136 NVYQRSLOQNLADNRDTRNLSVVRAQFIALDLDFVNAIPLFAVNGQVPLLSVYAQAVNL
150      160      170      180      190      200

180      190      200      210      220      230
Cry1Ac HLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWI
gi|136 HLLLLKDALFGEWGFQGEISTYYDRQLELTAKYTNVYETWYNTGLDRLRGTNTESWL
210      220      230      240      250      260

240      250      260      270      280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD---GSFR--G
gi|136 RYHQFRREMTLVVLDVVALFPYDVRLYPTGSPNQLTREYVYDPIVFNPPANVGLCRRWG
270      280      290      300      310      320

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          290      300      310      320      330
Cry1Ac SA----QGIEGS-IRSPHLMIDLNSITIIYTDAA--RGEY--YWGHQIMASPVGFSGPE
gi|136 TNPYNTFSELENAFIRPPHLDRLNLSLTISSNRFVSSNFMFYWSGHGTLRRSYLNDSSAVQ
          330      340      350      360      370      380

          340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQRORIVAQLG-QGVYRTLSSSTLYRRPFNIGINN-QQLSVLDGTEFAY
gi|136 ED--SYGLITTT----RATINPGVDGTNRIESTAVDFRSALIGIYGVNRFVPPGGLFN-
          390      400      410      420      430

          400      410      420      430      440      450
Cry1Ac GTSSNLPsAVYRKSgtVDSLDEIPQNNVPPRQGFShRLSHVSMFRSGFSNssVSIIRA
gi|136 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
          440      450      460      470      480      490

          460      470      480      490      500      510
Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLNGS-VISGPGFTGGDLVRLNssGN
gi|136 GSVPTFYVWTRRDVDLNNITIPNRITQLPLVKASAPVSGTTVLKGPFGTGGGILRRTTNGT
          500      510      520      530      540      550

          520      530      540      550      560      570
Cry1Ac NIQNRGYIEVPIHFpSTSTRYRVRVRYASVTPiHLNVNwGNSSIFsNTVpATATSLDNLQ
gi|136 ----FGTLRVTVNSPLTQ-QYRLRVRFASGTGNFSIRVLRGGVSiGDVRLGStMNRGQELT
          560      570      580      590      600

          580      590      600      610      620
Cry1Ac SSDF-----GYFESANAFtSSLgNI-VGVRNfSGTAGVIIDRFfIPVtATLEAEYn
gi|136 YESFFtREfTTTGpFPNPPfTfTQAQEILtVNAEGVStGGEYyIDRIEiVpVNPAREAEED
          610      620      630      640      650      660

          630      640      650      660      670      680
Cry1Ac LERAQKAVNALfTSTnQLGLKtNVTdYHIDQVSNLvtYLSdEFCLdEKRElSEKVKHAKR
gi|136 LEAAKkAVASLfTRTRD-GLQVnVtDYQVDQAANLVsCLSDeQYGHdKMKLLeAVRAAKR
          670      680      690      700      710      720

          690      700      710      720      730      740
Cry1Ac LSDERNLLQDSnFKDINRqPERGwGGStGITIqGGDdVfKEnYvTLsGTFdECYpTYLYQ
gi|136 LSRERNLLQDPDFnTINStEENGkASNGVtISeGGpFFKGRALQlASa-RENYpTYIYQ
          730      740      750      760      770      780

          750      760      770      780      790      800
Cry1Ac KIDESKLKAfTRYQLRGYIEDsQDLEIYSIRYNAKHETVnVPGtSLWpLSAQSpIGKCG
gi|136 KVdASvLKpYTRyRLDgFVKSSQDLEIDLIHHHKVHLVKNVpDNL---VSDtYSDGScS
          790      800      810      820      830      840

          810      820      830      840      850      860
Cry1Ac EPNRCAPHLEWNPDLDCScRDGEKc-AHSHHFSLDIDVGCtDLNEdLGVWvIFKIKtQD
gi|136 GINRCDEQHqVDMQLDAEHHPMDCCeAAQTHEfSSyINTGDlnASvDQGIWvVLKvRTTD

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          850      860      870      880      890      900
Cry1Ac GHARLGNLFLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNS
gi|136 GYATLGNLELVEVGPLSGESLEREQRDNakWNAELGRKRAEIDRVYLAakQAINHLFVDY
          910      920      930      940      950      960

          930      940      950      960      970      980
Cry1Ac QYDQLQADtNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIfeELEGRIftAFSLyDAR
gi|136 QDQQLNPEIGLAEINEASNLVESISGVYSdTLlQIPGINyEiYTELSdRLQqASyLYTSR
          970      980      990      1000      1010      1020

          990      1000      1010      1020      1030      1040
Cry1Ac NVIKNGDFNngLscWnVKGHVDVEEQNNQRsVLVpVEWAEVsqEVrVcPGRGYILRVtA
gi|136 NAVQNGDFNSGLDSWNTTMDASVQDGNMH-FLVLSHWDAQVsqQLRVNPNCKyVLRVtA
          1030      1040      1050      1060      1070

          1050      1060      1070      1080      1090      1100
Cry1Ac YKEGYGEGCVtIHEIENNTDELKfSNcVEEEIYPnNTVtCNDYtVnQBEYGGAYTSRNRG
gi|136 RKVGGDGyVtTIRdGAHQETLTFNAC-----DYDVN----GTyVNDN--
          1080      1090      1100      1110

          1110      1120      1130      1140      1150      1160
Cry1Ac YNEAPSVpADYASVYEEKsYtDGRRENpCFNrgYRDYtPLpVgYvTKLEyFPETDKVW
gi|136 -----SYITEEVVfYPETKHMW
          1120      1130

          1170      1180
Cry1Ac IEIGETEGTFIVDSVellLMEE
gi|136 VEVSESGSFYIDSIefIETQe
          1140      1150

>>gi|6064160|emb|CAB58495.1| unnamed protein product [un (1157 aa)
  initn: 2011 init1: 719 opt: 1724 Z-score: 2022.5 bits: 386.2 E(): 9.9e-104
  Smith-Waterman score: 2241; 36.829% identity (63.507% similar) in 1192 aa overlap
  (22-1182:59-1157)

          10      20      30      40      50
Cry1Ac CMQAMDNPNINeCIPYnCLSNPEVEVLGGERIETGYTPIDISLStQfLL
gi|606 LASDPNAALQNMNYKDYlQMTDEdYtDSYINpSLSiSGRDAVQTAItVvGRILGALGVpF
          30      40      50      60      70      80

          60      70      80      90      100      110
Cry1Ac SEfVpGAGfVLGLVDIiWGIgFgSQWDAFLVQIEQLINQRIEEFARNQAIsrLEGLSNLY
gi|606 SQQI--VSfYQfLLNtLWPVNDtAIWEAFMRQVEELVnQQITeFARNQALARLQGLGDSf
          90      100      110      120      130      140

          120      130      140      150      160      170
Cry1Ac QIYAESfREWEADpTNPALREEMRIQfNDMNsalTtAIpLFAVQNYQVpLLSVYVQAANL
gi|606 NVYQRSLQNWlADRNdTRnLSVvRAQfIALDLDFVNAIPLFAVNGQVpLLSVYAQAVNL

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150      160      170      180      190      200
Cry1Ac  HLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
gi|606  HLLLLKDALFEGEGWFTQGEISTYYDRQLELTAKYTNYCETWYNTGLDRLRGTNTESWL
210      220      230      240      250      260
Cry1Ac  RYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVPLENFD--GSFR--G
gi|606  RYHQFREM TLVVLDVVALFPYDVRLYPTGSNPQLTREVIYDFIVFNPPANVGLCRRWG
270      280      290      300      310      320
Cry1Ac  SA----QGIEGS-IRSPHLM DILNSIT IYTDAAH--RGEY--YWSGHQIMASPVGFSGPE
gi|606  TNPYNTFSELENAFIRPPHLDRLNSLTISSNRFVSSNFM DYWSGHTLRRSYLNDSAVQ
330      340      350      360      370      380
Cry1Ac  FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSSTLYRRPFNIGINN-QQLSVLDGTEFAY
gi|606  ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRSFVPGGLFN-
390      400      410      420      430
Cry1Ac  GTSSNLP SAVA YRKS GTVDSLDEIPPQNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRA
gi|606  GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
440      450
Cry1Ac  ---PMF S WIHRS AEFN NIIASDSITQIPAVKGNFLFN GS-VISGPGFTGGDLVRLN SSGN
gi|606  GSVPTYVWTRRDVLDLNNITITPNRITQLPLVKASAPVSGTTVLKGPFGFTGGGILRRRTTNGT
500      510      520      530      540      550
Cry1Ac  NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVN WGNSSIFSNTPATATSLDNLQ
gi|606  ----FGTLRVTVNSPLTQ-QYRLRVRFASTGNF SIRVLRGGVSI G DVRLGSTMNRGQELT
560      570      580      590      600
Cry1Ac  SSDF-----GYFESANAF TSSLGNI-VGVRNFSGTAGVIIDRF EIPVTATLEAEY N
gi|606  YESFFTREFTTTGPFNPPFTTQAQEILTVNAEGVSTGGEYYIDRIEIVPVN PAREAEED
610      620      630      640      650      660
Cry1Ac  LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKR
gi|606  LEAAKAVASLFTTRTRD-GLQVNVTDYQVDQAAANLV SCLSDEQYGHDKMLLEAVRAAKR
670      680      690      700      710      720
Cry1Ac  LSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL SGTDFDECYPTIYLYQ
gi|606  L-----
690      700      710      720      730      740
Cry1Ac  L-----
gi|606  L-----

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gi|606  LSRERNLLQDPDFNTINSTEENGWKASNGVTISEGGPFFKGRALQLASA-RENYPTYIYQ
730      740      750      760      770      780
Cry1Ac  KIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQSPIGKCG
790      800
gi|606  KVDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVLVKNVPDNL----VSDTYS DGSCS
810      820      830      840
Cry1Ac  EPNRCAPHLEWNPDLDCSCRDGEKC-AHSHHFSLDIDVGCTDLNEDLGWVVIKIKTQD
850      860
gi|606  GINRCDEQH QVMDQLDAEHHPMCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTD
870      880      890      900
Cry1Ac  GHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNS
910      920
gi|606  GYATLGNLELVEVGPLSGESLEREQRDNAKWAELGRKRAEIDRVYLAQAINHLFVDY
930      940      950      960
Cry1Ac  QYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNAIFEELEGRIFTAFSLYDAR
970      980
gi|606  QDQQLNPEI GLAEINEASNLVESISGVYSDTLLQIPGINYEIYTELSDRLQQASYLTSR
990      1000      1010      1020
Cry1Ac  NVIKNGDFNGLSCWNVKGHV DVEEQNNQRSVLVVPEWAEVSVQEVVRCVCPGRGYILRVTA
1030      1040
gi|606  NAVQNGDFNSGLDSWNTTMDASVQDGNMH-FLVLSHWDAQVSQLRVNPNCKYVLRVTA
1050      1060      1070
Cry1Ac  YKEGYGEGCVTIHEIENNTDELKFSNCV EEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRG
1080      1090      1100      1110
gi|606  RKVGGGDGYVTTIRDGAHQETLTFNAC-----DYDVN----GTYVNDN--
1120      1130
Cry1Ac  YNEAPSVPADYASVYEEKSYTDGRRENPCFN RGYRDTPLPVGYVTKLEYFPETDKVW
1140      1150
gi|606  -----SYITEEVVFPETKHMW
1160      1170
Cry1Ac  IEIGETEGTFIVDSVELLMEE
1180
gi|606  VEVSESEGSFYIDSIEFIETQE
1190      1200
>>gi|547556|emb|CAA85764.1| unnamed protein product [Bac (1157 aa)
initn: 2011 init1: 719 opt: 1724 Z-score: 2022.5 bits: 386.2 E(): 9.9e-104
Smith-Waterman score: 2241; 36.829% identity (63.507% similar) in 1192 aa overlap
(22-1182:59-1157)
1210      1220      1230      1240      1250
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
1260      1270

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gi|547 LASDPNAALQNMNYKDYLMQMTDEDYDTSYINPSLSISGRDAVQTALTVVGRILGALGVFP
30      40      50      60      70      80

          60      70      80      90      100     110
Cry1Ac SEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 SGQI--VSFYQLLNTLWPNVDTAIWEAFMRQVEELVNQITTEFARNQALARLQGLGDSF
90      100     110     120     130     140

          120    130    140    150    160    170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 NVYQRSLOLWDLADRNDTRNLSVVRQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNL
150     160     170     180     190     200

          180    190    200    210    220    230
Cry1Ac HLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 HLLLLKDALSLFGEWGFQGEISTYYDRQLELTAKYTNYCETWYNTGLDRLRGTNTESWL
210     220     230     240     250     260

          240    250    260    270    280
Cry1Ac RYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLENFD---GSFR--G
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 RYHQFRREMTLVVLDVVALFPYDVRLYPTGSNPQLTREVTYDPIVFNPPANVGLCRRWG
270     280     290     300     310     320

          290    300    310    320    330
Cry1Ac SA-----QGIEGS-IRSPHLMIDILNSITYTDAH--RGEY--YWSGHQIMASPVGFSGPE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 TNPYNTFSELENAFIRPPHLDRLNLSLTISSNRFVSSNFMFYWSGHTLRRSYLNDSSAVQ
330     340     350     360     370     380

          340    350    360    370    380    390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRFVPPGGLFN-
390     400     410     420     430

          400    410    420    430    440    450
Cry1Ac GTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
440     450     460     470     480     490

          460    470    480    490    500    510
Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 GSVPTYVWTRRDVLDLNTITPNRITQLPLVKASAPVSGTTVLKGPFGFTGGGILLRRTTNGT
500     510     520     530     540     550

          520    530    540    550    560    570
Cry1Ac NIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNTVPATATSLDNLQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 ----FGTLRVTVNSPLTQ-QYRLRVRFASSTGNFIRVLRGGVSIQDVLRLGSTMNRGQELT
560     570     580     590     600

          580    590    600    610    620
Cry1Ac SSDF-----GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYN

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: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 YESFFTRREFTTTGPFNPPFTTQAQEILTVNAEGVSTGGEYYIDRLEIVPNPAREAEED
610     620     630     640     650     660

          630    640    650    660    670    680
Cry1Ac LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 LEAAKAVASLFTTRTRD-GLQVNVTDYQVDQAANLVSCLSDQYGHDKMLLEAVRAAKR
670     680     690     700     710     720

          690    700    710    720    730    740
Cry1Ac LSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 LSRERNLLQDDPFTNTINSTEENGWKASNGVTISEGGPFKGRALQLASA-RENYPTYIYQ
730     740     750     760     770     780

          750    760    770    780    790    800
Cry1Ac KIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKGC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 KVDASVLKPYTRYRLDGFVKSSQDLEIDLIIHHKVVHLVKNVPDNL----VSDTYSDGSCS
790     800     810     820     830     840

          810    820    830    840    850    860
Cry1Ac EPNRCAPHLEWNPDLDCSCRDGKCA-AHSHHFLSLDIDVCGCTDLNEDLGVVWVIFKIKTQD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 GINRCDEQHQVMDQLDAEHHPMDCCEAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTD
850     860     870     880     890     900

          870    880    890    900    910    920
Cry1Ac GHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 GYATLGNLELVEVGPLSGESLEREQRDNAKWNAELGRKRAEIDRVYLAQAQAINHLFVDY
910     920     930     940     950     960

          930    940    950    960    970    980
Cry1Ac QYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDAR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 DQQLNPEIGLAEINEASNLVESISGVYSDTLLQIPGINYEIYTELSDRLQOQASYLYTSR
970     980     990    1000    1010    1020

          990    1000    1010    1020    1030    1040
Cry1Ac NVIKNGDFNNGLSQWNVKGVHVDVEEQNNQSVLVPPEWAEVSVQEVVPCPRGYILRVTA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 NAVQNGDFNSGLDSWNTTMDASVQDGNMH-FLVLSHWDAQVSVQQLRVNPNCKYVLRVTA
1030    1040    1050    1060    1070

          1050    1060    1070    1080    1090    1100
Cry1Ac YKEGYGEGCVTIIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 RKVGGGDGVYTIIRDGAHQETLTFNAC-----DYDVN-----GTYYVNDN--
1080    1090    1100

          1110    1120    1130    1140    1150    1160
Cry1Ac YNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRDYRTPLPVGYVTKLELYFPETDKWV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|547 -----SYITEEVVFPETKHMW
1120    1130

1170    1180

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1050      1060      1070      1080      1090      1100
Cry1Ac YKEGYEGECVTTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272 RKVGGGDGYVVTIRDGAHQHQTETLFNAC-----DYDVN----GTYVNDN--
1080      1090      1100      1110

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1110      1120      1130      1140      1150      1160
Cry1Ac YNEAPSVPADYASVYEEKSYTDGRRNPCEFNRGYRDYTPLPVGYVTKELEYFPETDKVW
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272 -----SYITEEVVFPETKHMW
1120      1130

```

```

1170      1180
Cry1Ac IEIGETEGTFIVDSVELLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272 VEVSESEGSFYIDSIEFIETQE
1140      1150

```

```

>>gi|6064240|emb|CAB58501.1| unnamed protein product [un (1157 aa)
  initn: 2009 initl: 717 opt: 1722 Z-score: 2020.1 bits: 385.8 E(): 1.3e-103
  Smith-Waterman score: 2239; 36.829% identity (63.507% similar) in 1192 aa overlap
(22-1182:59-1157)

```

```

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 LASDPNAALQNMNYKDYLMQMTDEDYTDYSINPSLSISGRDAVQALTAVVGRILGALGVPF
30      40      50      60      70      80

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60      70      80      90      100      110
Cry1Ac SEFVPGAGFVLGLVDIIWGI FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 SGQI--VSFYQFLNLTLPVNDTAWFAFMQRQVEELVNQIIEFARNQALARLQGLGDSF
90      100      110      120      130      140

```

```

120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALITTAIPLFAVQNYQVPLLSVYVQAANL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 NVYQRSLQNLWLRNDRNTRNLSVVRQAFIALDLDFVNAIPLFAVNGQQVPLLSVYVQAANL
150      160      170      180      190      200

```

```

180      190      200      210      220      230
Cry1Ac HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 HLLLLKDALSLFGEWGFQGEISTYYDRQLELPAKYTYNCTWYNTGLDRLRGTNTESWL
210      220      230      240      250      260

```

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240      250      260      270      280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFND--GSFR--G
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 RYHQFRREMTLVVLDVVALFPYVDVRLYPTGSNPQLTREVTYDPIVFNPPANVGLCRRWG
270      280      290      300      310      320

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290      300      310      320      330
Cry1Ac SA----QGIEGS-IRSPHLMIDLNSITTYTDAH--RGEY--YWSGHQIMASPVGSGPE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 TNPYNTFSELENAFIRPPHLDRLNLSLTISSNRFPVSNFMDYWSGHTLRRSYLNSAVQ
330      340      350      360      370      380

```

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340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRASVFPGLFN-
390      400      410      420      430

```

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400      410      420      430      440      450
Cry1Ac GTSSNLPSAVYRKSGTVDLSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSFGFSNSSVSIIRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
440      450      460      470      480      490

```

```

460      470      480      490      500      510
Cry1Ac ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 GSVPTYVWTRRDVLDLNTITPNRITQLPLVKASAPVSGTTVLKGPFTGGGILRRITNGT
500      510      520      530      540      550

```

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520      530      540      550      560      570
Cry1Ac NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 ---FGTLRVTVNSPLTQ-QYRLRVRFASGTGNFSIRVLRGGVSIQDVRGSLTMRGQELT
560      570      580      590      600

```

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580      590      600      610      620
Cry1Ac SSDLF-----GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLAEAYN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 YESFFTREFTTTGFNPPFTTQAQELITVNAEGVSTGGEYIIDRIEIVPVNFAEAEED
610      620      630      640      650      660

```

```

630      640      650      660      670      680
Cry1Ac LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 LEAAKKAVASLPTTRTRD-GLQVNVTDYQVDQAANLVSCLSDEQYGHDKMLLEAVRAAKR
670      680      690      700      710      720

```

```

690      700      710      720      730      740
Cry1Ac LSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 LSRERNLLQDPPDFNTINSTENGWKAASNGVTISEGGPFKGRALQLASA-RENYPTYIYQ
730      740      750      760      770      780

```

```

750      760      770      780      790      800
Cry1Ac KIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 KVDASVLPKYTRYRLDGFVKSSQDLEIDLHKKVHLVKNVPDNL---VSDTYSDGSCS
790      800      810      820      830      840

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810      820      830      840      850      860
Cry1Ac EPNRCAPHLEWNPDLDCSCRDGKCA-AHSHHFSLDIDVGCTDLNEDLGVVIFKIKTQD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 GINRCDEQHVDMLDAAEHHPMDCCCAAQTHEFSSYINTGDLNASVDQGIWVVLKVRTTD
850      860      870      880      890      900

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870      880      890      900      910      920
Cry1Ac GHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVVKEAKESVDALFVNS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|606 GYATLGNLELVEVGPLSGESLEREQRDNAKWNAELGRKRAEIDRVVLAQAQAINHLFVDY
910      920      930      940      950      960

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          930      940      950      960      970      980
Cry1Ac QYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAFEELEGRIFTAFSLYDAR
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|606 QDQQLNPEIGLAEINEASNLVESISGVYSDTLQLQIPGINYEIYTELSRDLQQAASYLYTSR
          970      980      990      1000     1010     1020

          990      1000     1010     1020     1030     1040
Cry1Ac NVIKNGDFNNGLSCWNVKGHVDVEEQNNQSRVSVVPEWEAEVSQEVVRCVGRGYILRVTA
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|606 NAVQNGDFNSGLDSWNTTMDASVQDQGNMH-FLVLSHWDQAQVSQLRVNPNCKYVLRVTA
          1030     1040     1050     1060     1070

          1050     1060     1070     1080     1090     1100
Cry1Ac YKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRG
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|606 RKVGGGDGYVTTIRDGAHQHTLTFNAC-----DYDVN----GTYVNDN--
          1080     1090     1100                       1110

          1110     1120     1130     1140     1150     1160
Cry1Ac YNEAPSVPADYASVYEEKSYTDGRENPCFNRGRYRDTPLPVGVVTKLEYFPETDKVW
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|606 -----SYITEEVVFPETKHMW
          1120     1130

          1170     1180
Cry1Ac IEIGETEGTFIVDSVELLMEE
: . . . . . : . . . . . :
gi|606 VEVSESEGSFYIDSIEFIETQE
          1140     1150

>>gi|22122188|dbj|BAC07226.1| cry8 [Bacillus thuringiensis (1144 aa)
  initn: 1655 initl: 540 opt: 1719 Z-score: 2016.6 bits: 385.1 E(): 2.1e-103
Smith-Waterman score: 2322; 37.531% identity (64.527% similar) in 1215 aa overlap
(8-1182:39-1144)

          10      20      30
Cry1Ac          CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGY
: . . . . . : . . . . . : . . . . .
gi|221 YEILDASSSTSVDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPEL--FGNPETFISS
          10      20      30      40      50      60

          40      50      60      70      80      90
Cry1Ac TPIDISLSLT-QFLLSEFVPGAGFVLGLVDIIWGFGPSQ---WDAFLVQIEQLINQRI
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 STVQTGIGIVGQVLGALGVFPAGQIASFYFVIGQLWPSSTVSVWEMIMKQVEDLIDQKI
          70      80      90      100     110     120

          100     110     120     130     140     150
Cry1Ac EEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 TDSVRKTALAGLQGLGDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFVAKIPSF
          130     140     150     160     170     180

          160     170     180     190     200     210
Cry1Ac AVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAV
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 AISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTPEIISTFVDRQVTRTAQVSDYCV
          190     200     210     220     230     240

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          220      230      240      250      260      270
Cry1Ac RWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLVDIVSLFPNYSRTYPIRTVSQLTREIY
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 KWYNTGLDKLKGTTNAASWLKYHQFREMTLLVLDLVALFPNYDTRTYPIETTAQLTREYV
          250     260     270     280     290     300

          280      290      300      310
Cry1Ac TNPVLENFD--GSF--RGSAQG-----IEGS-IRSPHMLDILNSITITYTDA----HRG
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 TDPVFNRETSGGFCRRWLSNDSISFSEVESAVIRSPHLFDILSEIEFVYTRAGLPLNNT
          310     320     330     340     350     360

          320      330      340      350      360      370
Cry1Ac EY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRP
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 EYLEYVWVGHSIKYKNTNASSALER--NYGTITSNKKIYYDLANKDIFQVRSGLADLANYY
          370     380     390     400     410     420

          380      390      400      410      420
Cry1Ac FNI-GINNQQLSVLD---GTEFAYGTSSNLPSAVYRK--SGTVSDLEIIPPQNNVPPRQG
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 AQVYGVVYASFLLDKNTGSGVSGGFTYSKPHTTMQVCTQNYNTIDEIIPPENE--PLSRG
          430     440     450     460     470     480

          430      440      450      460      470      480
Cry1Ac FSHRLSHVSMFRSGFSNSVSIIRA---PMFSWIHRSAEFNIIASDSITQIPAVKGNFL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 YSHRLSHITSY--SFSKNASSPARYGNLVPFAWTHRSADVNTVTVYSDKITQIPVVKAHTL
          490     500     510     520     530     540

          490      500     510     520     530     540
Cry1Ac FNGS-VISGPGFTGGDLVRLNNGSNNIQNRGYIEVPIHPSTSTRYRVRVRYASVTPIHIL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 VSGTTVIKGPGFTGGNILKRTSSGP----LAYTSVSVKSP--LSQRVRIYASTTNLRL
          550     560     570     580     590     600

          550      560     570     580     590     600
Cry1Ac NVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT--SSLGN--IVGVRNFSGTAGV
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 FVTISGTRIYSINVNKTMNKGDLLTFNTFDLATIGTAFVSNYSDSLTVGADSFASGGEV
          600     610     620     630     640     650

          610      620     630     640     650     660
Cry1Ac IIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVITYLSD
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 YVDKFELIPVNATFEAEEDLDVAKKAVK-----NLVECLSD
          660     670     680

          670      680     690     700     710     720
Cry1Ac EFCLEDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKE
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 ELYPNKRLWDAVKEAKRLVQARNLLQDTGFNRIN--GENGWGTSTGIEVABGDVLFKD
          700     710     720     730     740

          730      740     750     760     770
Cry1Ac NYVTLSGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHET
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|221 RSLRLTSAREIDTETYPTYLYQQIDESLKPTRYKLGKGFIGSSQDLEIKLIRHRANQIV

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Smith-Waterman score: 1776; 48.226% identity (73.548% similar) in 620 aa overlap (5-617:1-605)

Sequence alignment for Cry1Ac vs gi|151. Includes residue numbers 10-60, 70-120, 130-180, 190-240, 250-290, 300-350, 360-410, 420-470, 480-530, 540-590. Shows high identity between the two sequences.

Sequence alignment for Cry1Ac vs gi|341. Includes residue numbers 530-580, 600-650, 590-600, 10-50, 60-110, 120-170, 180-230, 240-290, 300-350, 360-410, 420-470, 480-530. Shows lower identity compared to gi|151.

>>gi|3410669|gb|AAC31091.1|I90729 Sequence 4 from patent (725 aa)
initn: 2225 initl: 886 opt: 1657 Z-score: 1946.5 bits: 371.4 E(): 1.7e-99
Smith-Waterman score: 2275; 50.135% identity (73.514% similar) in 740 aa overlap (36-764:3-725)

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gi|341 PPEDESVPPIYIGYSHQCHVGFGRNTNVEFSPNFARVVFWSWTHRSATPTNTIDPDRITQ
      390      400      410      420      430      440
Cry1Ac 480      490      500      510      520      530
IPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTS-TRYRVRVR
gi|341 IPSVKASSLRNSTVVSVPFTGGDIVRMGAHQIYAXDLSMNV---RPSVALSRYLIRLR
      450      460      470      480      490
Cry1Ac 540      550      560      570      580      590
YASVTPIHNLNWNWGNSSIFSNTPVATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVR
gi|341 YACRGSNNIVIH--GPSIRFVSLPSTMSNDEPLTYQSPRYASITPITRPIYNMFLNLSIS
      500      510      520      530      540      550
Cry1Ac 600      610      620      630      640      650
NFSGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
gi|341 RISGVQNLFDRIEFIPVDANFEAERDLERAQKAVNALFTSTNQXGLKXDVTDYHIDQVS
      560      570      580      590      600      610
Cry1Ac 660      670      680      690      700      710
NLVITYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQ
gi|341 NLVXCLSDXFLDEKRELSKVKHAKRLSDEXNLLQDXNFTGINRQVDRGRGSDTITIQ
      620      630      640      650      660      670
Cry1Ac 720      730      740      750      760      770
GGDDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYQIRGYIEDSQDLEIYSIRYN
gi|341 GGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLPXTRYELRGYIEDSQ
      680      690      700      710      720
Cry1Ac 780      790      800      810      820      830
AKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFS

>>gi|48880|emb|CAA41425.1| crystal protein [Bacillus thu (1151 aa)
  initn: 1636 initl: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97
Smith-Waterman score: 1912; 33.469% identity (60.163% similar) in 1225 aa overlap
(5-1177:26-1151)

Cry1Ac          10          20          30
CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
gi|488 MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSQCNSSILN--WINIIGDAAKE
      10      20      30      40      50
Cry1Ac 40      50      60      70      80      90
TGYPIDISLSLTQFLLSEFVPG-AGFVLGLVD-IIWGFPGSQWDAFLVQIEQLINQRI
gi|488 A---VSIGTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQISDLSICDLLSIIIDLRV
      60      70      80      90      100     110
Cry1Ac 100     110     120     130     140
EEFARNQAI SRLGLSNLYQIYAESFREWEADPTNPALREEMRIQF---NDMNSALT--
gi|488 SQSVLNDGIADFNQSVLLYRNYLEALDSWKNP-NSASAEELRTRFRDIADSEFDRILTRG
      120     130     140     150     160     170

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Cry1Ac 150     160     170     180     190     200
--TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWG-FDAATINSRYNDLTRL
gi|488 SLTNGGSLARQNAQILLLPSFASAAFFHLLLRDADTRYGTNWLGNATPFINYQSKLVEL
      180     190     200     210     220     230
Cry1Ac 210     220     230     240     250     260
IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPI
gi|488 IELYTDYCVHWYNRGPNELRQRGTSATAWLEFPHRYRREMTLMVLDIVASFSSLDITNYPI
      240     250     260     270     280     290
Cry1Ac 270     280     290     300     310
RTVSQLTREIYTNPLENFDGSGFRGSA-----QGIEGSIRSPHMLDILNSITIYT
gi|488 ETDFQLSRVIYTDPIGFVHRSSLRGSEWFSFVNRFNSDLENAIPNPRPSWFLNMIIST
      300     310     320     330     340     350
Cry1Ac 320     330     340     350     360
DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGV
gi|488 GSLTLFVSPSTDRARV-WYGSRDRISP---ANSQFITELISGQHTTATQ---TILGRNI
      360     370     380     390     400
Cry1Ac 370     380     390     400     410
YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSGT---VDSLDE-I
gi|488 FRVDSQACNLNDTTYGVN-RAVFIHDASE---GSQRSVYEGYIRTTGIDNPRVQINITYL
      410     420     430     440     450     460
Cry1Ac 420     430     440     450     460     470
PPQNNNVPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|488 PGENSIDIPTPEDYTHILSTTINLTGGLRQVASNRRSSLV---MYGWTBKSLARNNTINPD
      470     480     490     500     510
Cry1Ac 480     490     500     510     520     530
SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|488 RITQIPLTKVDTRGTGVSYVNDPGFIGGALLQRTDHGSLGLVLR--VQFPLHL---RQYQR
      520     530     540     550     560     570
Cry1Ac 540     550     560     570     580     590
VRVRYASVTPIHNLNWNWGNSSIFSNTPVATATSLDNLQSSDFGY--FESANAFTSSLGNI
gi|488 IRVRYASTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIRPTASPDQI
      580     590     600     610     620     630
Cry1Ac 600     610     620     630     640
-VGVRNFSGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|488 RLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLFRTRD-GLQVNVKDYQ
      640     650     660     670     680     690
Cry1Ac 650     660     670     680     690     700
IDQVSNLVITYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|488 VDQANLVSCLSDQYGYDKMMLLEAVRAAKRLSRERNLLQDPDFNTINSTEENGWKASN

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700      710      720      730      740      750
Cry1Ac  710      720      730      740      750      760
GITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIY
gi|488  GVTISEGGFFYKGRAIQLASA-RENYPTYIYQKVDASELKPYTRYRLDGFVKSSQDLEID
760      770      780      790      800      810

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```

770      780      790      800      810      820
Cry1Ac  S1RYNAKHETVNVPGTGS1WPLSAQSP1GKCGEPNRCAPHLEWNPDLDCSCRDGEKC--A
gi|488  LIHHHKVHLVKNVDPNL---VSDTYPDDSCSGINRCQEQQMVAQLTEHHHPMDCCEA
820      830      840      850      860

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830      840      850      860      870      880
Cry1Ac  HSHHFLSLDIDVGCDDLNE1DGLVWV1FKIKTQDGHARLGNLEFL1EEKPLVGEALARVKRA
gi|488  AQTHEFSSYIDTGD1LNS1VDQGIW1A1FKVRTTDGYATLGNLE1LVEV1G1PLSGESLEREQRD
870      880      890      900      910      920

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890      900      910      920      930      940
Cry1Ac  EKKWRDKREKLEWETN1VYKEAKESVDALFVNSQYDQLQADTN1AMIHAADKRVHSIREA
gi|488  NTKWSAELGRKRAETDRVYQDAKQ1SINHLFVDYQDQQLNPE1GMAD1MDAQNLVASISDV
930      940      950      960      970      980

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```

950      960      970      980      990      1000
Cry1Ac  YLPELSVIPGVNAA1FEELEGRIF1TAFSLYDARNV1KNGDFNGLSCWNVKG1HVDVEEQN
gi|488  YSDAVLQIPGINYE1YTELSNR1LQQA1SYLYTSRN1AVQNGDFNGLSD1SWNATAGASVQQDG
990      1000      1010      1020      1030      1040

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1010     1020     1030     1040     1050     1060
Cry1Ac  NQRSVLVPEWEAEV1SQEVRV1C1PGRGY1LLRV1TAYKEGYEGCV1T1HEIENNTDELKFSNC
gi|488  NTH-FLVLSHWDAQV1SQFRV1QP1NCKY1VLRV1TAEKVG1GDGYV1T1R1DDAHTTETLTFNAC
1050     1060     1070     1080     1090     1100

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1070     1080     1090     1100     1110     1120
Cry1Ac  VEEEIYPNNTV1TCNDY1TVNQE1YGGAY1TSRNR1GYNEAP1SVPADYASV1YEEKSYTDGRREN
gi|488  -----DYDIN-----GT1YVTDNT-----
1110

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1130     1140     1150     1160     1170     1180
Cry1Ac  PCEFNRGRYRDY1TPLPVGYV1TKELEYF1PETDKVW1EIGETEGF1VIDSV1ELL1MEE
gi|488  -----YLTKEV1V1FHPET1QHMW1VEVNETEGAF1H1DS1EF
1120     1130     1140     1150

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>>gi|33731257|gb|AAQ37320.1| Sequence 70 from patent US (1156 aa)  
 initn: 1512 initl: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97  
 Smith-Waterman score: 1916; 33.415% identity (60.163% similar) in 1230 aa overlap  
 (5-1182:26-1156)

```

10      20      30
Cry1Ac  CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
gi|337  MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSNCQSSILN--WINIIGDAAKE

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```

10      20      30      40      50
Cry1Ac  40      50      60      70      80      90
TGYPIDISLSLTQFL1LSEFV1PG-AGFV1LGLVD-1I1W1G1F1G1P1S1Q1W1D1A1F1L1V1Q1E1Q1L1N1Q1R1I
gi|337  A----V1S1G1T1T1V1S1L1T1A1P1S1L1T1G1L1S1I1V1D1L1G1K1V1L1G1G1S1G1Q1S1D1L1S1I1C1D1L1S1I1D1L1R1V
60      70      80      90      100     110

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100     110     120     130     140
Cry1Ac  EEFARNQAI1SRLEGL1SNLYQ1IYAES1FREWEAD1PTNPALREEMRIQF---NDMNSALT--
gi|337  SQSVLNDGIAD1FNGSV1LLYRN1YLEAL1D1SWNKNP-NSASAEELR1TRFRIAD1SEFDR1LLTRG
120     130     140     150     160     170

```

```

150     160     170     180     190     200
Cry1Ac  --TA1PLFAVQNYQV1LLSV1YVQAANL1HLSV1LRDVS1VFGQRWG-FDAAT1NSRYNDL1TRL
gi|337  SL1TNGG1SLARQNAQ1LLL1P1SFASAA1FFH1LLLR1D1ATRYGT1N1W1G1L1Y1N1A1T1P1F1I1N1Y1Q1S1K1L1V1E1L
180     190     200     210     220     230

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210     220     230     240     250     260
Cry1Ac  IGN1YTD1HAVRWYNT1GLE--RVW1G1P1D1SRDW1IRYNQ1FRREL1TL1VLD1IV1S1L1FP1NYD1SR1TY1P1I
gi|337  IEL1YTD1CVH1WYNR1G1F1NELR1QRGT1SATAW1LEF1HRYR1REMT1LMV1LD1IV1AS1F1S1S1LD1IT1NY1P1I
240     250     260     270     280     290

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270     280     290     300     310
Cry1Ac  RTV1S1QL1TRE1Y1TNP1VLE1N1F1D1G1S1FR1G1SA-----Q1G1E1G1S1I1R1S1P1H1L1M1D1I1L1N1S1I1T1Y1T
gi|337  ET1D1F1Q1L1SRV1I1Y1T1D1P1I1G1F1V1HR1S1SL1RG1ES1W1F1S1F1V1N1R1A1N1F1S1D1L1E1N1A1I1P1N1P1R1P1S1W1F1L1N1M1I1S1T
300     310     320     330     340     350

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320     330     340     350     360
Cry1Ac  DA-----HR1GEY1Y1W1SG1HQ1I1MAS1P1V1G1F1S1G1P1E1F1T1P1L1Y1G1T1M1G1N1A1P1Q1R1I1V1A1Q1L1G1Q1G1V
gi|337  G1S1L1T1L1P1V1S1P1S1T1D1R1A1R1V-WY1G1S1R1D1R1I1S1P---ANS1Q1F1I1T1E1L1S1G1H1T1T1A1T1Q---T1I1L1G1R1N1I
360     370     380     390     400

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370     380     390     400     410
Cry1Ac  YR1T1L1S1T1L1Y1R1R1P1F1N1I1G1N1N1Q1L1S1V1L1D1G1T1E1F1A1Y1G1T1S1N1L1P1S1A1V1Y1R1K1S1G1T---V1D1S1L1D1E1I
gi|337  F1R1V1D1S1Q1A1C1N1L1N1D1T1T1Y1G1V-NRAV1FY1H1D1A1S1E---GS1Q1R1S1V1E1G1Y1I1R1T1T1G1D1N1P1R1V1Q1N1T1Y1L
410     420     430     440     450     460

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```

420     430     440     450     460     470
Cry1Ac  P1Q1N1N1V1P1R1Q1G1F1S1H1R1L1S1H1V1S1M1F1R1S1G1F---SN1S1V1S1I1R1A1P1M1F1S1W1I1H1R1S1A1E1F1N1N1I1A1S1D
gi|337  P1G1E1N1S1D1I1P1T1P1E1D1Y1T1H1L1S1T1T1I1N1L1T1G1L1R1Q1V1A1S1N1R1R1S1S1L1V---M1Y1G1W1T1H1K1S1L1A1R1N1T1I1N1P1D
470     480     490     500     510

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480     490     500     510     520     530
Cry1Ac  S1I1T1Q1I1P1A1V1K1G1N1F1L1F1N1G-SV1S1G1P1G1F1T1G1G1D1L1V1R1L1N1S1S1G1N1I1Q1N1R1G1Y1E1V1P1I1H1F1P1S1T1R1Y1R
gi|337  R1I1T1Q1I1P1L1T1K1V1D1T1R1G1T1G1V1S1Y1V1N1D1P1G1F1I1G1A1L1L1Q1R1T1D1H1G1S1L1G1V1L1R--V1Q1F1L1H1L---R1Q1Y1R
520     530     540     550     560     570

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540     550     560     570     580     590
Cry1Ac  V1R1V1R1Y1A1S1V1T1P1I1H1L1N1W1N1G1N1S1I1F1S1N1T1V1P1A1T1A1T1S1L1D1N1L1Q1S1D1F1G1Y--F1E1S1A1N1A1F1T1S1S1L1G1N1I
gi|337  M1N1Q1N1K1H1G1I1I1G1A1S1N1C1G1C1A1S1D1D1V1A1K1Y1P1L1A1N1P1Y1S1S1A1L1N1L1N1S1C1Q1N1S1S1I1L1N--W1I1N1I1G1D1A1A1K1E

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gi|337 IRVRYASTTNIRLSVN-GSFGTISQNLPSMRLGEDLRYGSFAIREFNISIRPTASPDQI
      580      590      600      610      620      630
      600      610      620      630      640
Cry1Ac -VGVRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYH
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 RLTIIEPSFIRQEVVVDRIEFIPVNPTRREAKEDLEAAKAVASLFRTRTD-GLQVNVKDYQ
      640      650      660      670      680      690
      650      660      670      680      690      700
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 VDQAAANLVCSLDEQYGYDKKMLLEAVRAAKRLSRERNLLQDPDFNTINSTENGWKASN
      700      710      720      730      740      750
      710      720      730      740      750      760
Cry1Ac GITIQQGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 GVTISEGGPFYKGRAIQLASA-RENYPTYIYQKVDASELKPTRYRLDGFVKSSQDLEID
      760      770      780      790      800      810
      770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNPVGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC--A
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 LIHHHKVHLVKNVPDN---LVSDTYPDDSCSGINRCQEQMVNAQLETEHHHPMDCCEA
      820      830      840      850      860
      830      840      850      860      870      880
Cry1Ac HSHHFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 AQTHEFSSYIDTGDNLSSVDQGIWAIFKVRTTGDYATLGNLELVEVGPLSGESLREQRD
      870      880      890      900      910      920
      890      900      910      920      930      940
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 NTKWSAELGRKRAETDRVYQDAKQSIINHLFVDYQDQQLNPEIGMADIMDAQNLVASISDV
      930      940      950      960      970      980
      950      960      970      980      990      1000
Cry1Ac YLPELSVIPGVNAAFEELRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 YSDAVLQIPGINYEIYTELSNRLQQASYLYTSRNAVQNGDFNGLSDSNWATAGASVQQDG
      990      1000      1010      1020      1030      1040
      1010      1020      1030      1040      1050      1060
Cry1Ac NQRSVLVPEWAEVSEVVRVCPGRGYILRVTAAYKEGYEGECVTHIEIENNTDELKFSNC
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 NTH-FLVLSHWDAQVQQFRVQPNCKYVLRVTAEKVGGGDYVTRDAHTTETLTFNAC
      1050      1060      1070      1080      1090      1100
      1070      1080      1090      1100      1110      1120
Cry1Ac VEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRREN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 -----DYDIN-----GTYYVDNT-----
      1110
      1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

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      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 -----YLTKEVVVHPETQHMVVEVNETEGAFHIDSIEFVETEK
      1120      1130      1140      1150
>>gi|53970040|gb|AAV19133.1| Sequence 70 from patent US (1156 aa)
      initn: 1512 initl: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97
      Smith-Waterman score: 1916; 33.415% identity (60.163% similar) in 1230 aa overlap
      (5-1182:26-1156)
      10      20      30
Cry1Ac CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
      10      20      30      40      50
gi|539 MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSNCSQNSILN--WINIIGDAAKE
      10      20      30      40      50
      40      50      60      70      80      90
Cry1Ac TGYPIDISLSLTQPLLSEFVPG-AGFVLGLVD-IIWGIFGPSQWDAFLVQIEQLINQRI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 A---VSI GTTIVSLITAPSLTGLISIVYDLIGKVLGSSGQSISDLSICDLLSIIDLVR
      60      70      80      90      100      110
      100      110      120      130      140
Cry1Ac EEFARNAQISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQF---NDMNSALT--
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 SQSVLNDGIADFNGLVLRNYLEALDSWNKNP-NSASAEELRTRFRIDSEFDRLLTRG
      120      130      140      150      160      170
      150      160      170      180      190      200
Cry1Ac --TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWG-FDAATINSRYNDLTRL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 SLTNGGSLARQNAQILLPSFASAAFFHLLLRDATTRYGTNWGLYNATPFINYQSKLVEL
      180      190      200      210      220      230
      210      220      230      240      250      260
Cry1Ac IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYQFRRELTTLVLDIVSLFPNYSRTYPI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 IELYTDYCVHWYNRGFNLRQRGTSATAWLEFHRYPREMTLMVLDIVASFSSLDITNYPI
      240      250      260      270      280      290
      270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPLENFDGSGFRGSA-----QGIEGSIIRPHLMDILNSITIIYT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 ETDQFLSRVIYTDPIGFVHRSSLRGSEWFSFVNRAFSDLENAIPNPRPSWFLNMIIST
      300      310      320      330      340      350
      320      330      340      350      360
Cry1Ac DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 GSLTLVPSPSTDRARV-WYGSRDRIISP---ANSQFITELISQHTTATQ----TLLGRNI
      360      370      380      390      400
      370      380      390      400      410
Cry1Ac YRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKSGT----VDSLDE-I
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 FRVDSQACNLNDTTYGVN-RAVFYHDASE---GSQRSVYEGYIRTGTGIDNPRVQNTIYL
      410      420      430      440      450      460
      420      430      440      450      460
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNIIASD

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Cry1Ac DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQV
gi|215 GSLTLVPVSPSTRARV-WYGSRRDRISP---ANSQFITELISGQHTTATQ---TILGRNI
      360      370      380      390      400
      370      380      390      400      410
Cry1Ac YRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQT---VDSLDE-I
gi|215 FRVDSQACNLNDTTYGVN-RAVIFYHDASE---GSQRSVYEGYIRTTGIDNPRVQNIITYL
      410      420      430      440      450      460
      420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGSFHRLSHVMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNIIASD
gi|215 PGENS DIPTPEDYTHILSTTINLTGGLRQVASNRRSSLV---MYGWTHKSLARNNTINPD
      470      480      490      500      510
      480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
gi|215 RITQIPLTKVDTRGTGVSYVNDPGFIGGALLQRTDHDGSLGVLR--VQFPLHL---RQQYR
      520      530      540      550      560      570
      540      550      560      570      580      590
Cry1Ac VRRVRYASVTPPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI
gi|215 IRVRYASTTNIRLSVN-GSFGTISQNLPSMTRLGEDLRYGSAIFREFNISIRPTASPDQI
      580      590      600      610      620      630
      600      610      620      630      640
Cry1Ac -VGVRFNSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|215 RLTIPEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKKAVALSFLTRTRD-GLQVNVKDYQ
      640      650      660      670      680      690
      650      660      670      680      690      700
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|215 VDQAAANLVSCLSDEQYGDYKMLLEAVRAAKRLSRERNLLQDPDPNTINSTEENGWKASN
      700      710      720      730      740      750
      710      720      730      740      750      760
Cry1Ac GITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLKAFTRYQLRGYIEDSQDLEIY
gi|215 GVTISEGGPFYKGRAIQLASA-RENYPTYIYQKVDASELKPTRYRLDGFVKSSQDLEID
      760      770      780      790      800      810
      770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGLSLWPLSAQSPIGKCGEPNRCAPHELWNPDLDCSCRDGEK--A
gi|215 LIHHKHVHLVKNVDPN---LVSDTYPDDSCSGINRCQEQQMVNAQLETEHHHPMDCCEA
      820      830      840      850      860
      830      840      850      860      870      880
Cry1Ac HSHHFSLDIDVGCITDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
gi|215 AQTHEFSSYIDTGDNLSSVDQGIWAIKVRVTTDGYATLGNLELVEVGPLSGESLEREQRD
      870      880      890      900      910      920

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      890      900      910      920      930      940
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREA
gi|215 NTKWSAELGRKRAETDRVYQDAKQSNHFLFVDYQDQQLNPEIGMADIMDAQNLVASISDV
      930      940      950      960      970      980
      950      960      970      980      990      1000
Cry1Ac YLPELSVIPGVNAAFEELLEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQN
gi|215 YSDAVLQIPGINYEIYTELSNRLQQASYLYTSRNAVQNGDFNNGLSWVNVKGVHVDVEEQN
      990      1000      1010      1020      1030      1040
      1010      1020      1030      1040      1050      1060
Cry1Ac NQRSVLVVPWEAEVSVQEVVPCPRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNC
gi|215 NTH-FLVLSHWDAQVQQFRVQPNCKYVLRVTAEKVGGDGYVTIRDDAHTTETLTFNAC
      1050      1060      1070      1080      1090      1100
      1070      1080      1090      1100      1110      1120
Cry1Ac VEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGREN
gi|215 -----DYDIN----GTYYVDNT-----
      1110
      1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGRYDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|215 -----YLTKEVVHPETQHMWVEVNETEGAFHIDSIEFVETEK
      1120      1130      1140      1150
>>gi|15105606|gb|AAE66200.1| Sequence 10 from patent US (1156 aa)
initn: 1512 initl: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97
Smith-Waterman score: 1916; 33.415% identity (60.163% similar) in 1230 aa overlap
(5-1182:26-1156)
      10      20      30
Cry1Ac CMQAMDNNP-----NINECIPYCNLSNPEVEVLGGERIE
gi|151 MNQKNGHGIIGASNCGCASDDVAKYPLANNPYSSALNLSNCSQNSILN--WINIIGDAAKE
      10      20      30      40      50
      40      50      60      70      80      90
Cry1Ac TGYTPIDISLSLTQFLLSEFVPG-AGFVLGLVD-IIWGFPGPSQWDAFLVQIEQLINQRI
gi|151 A----VSI GTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQSISDLSICDLLSIIDLRV
      60      70      80      90      100      110
      100      110      120      130      140
Cry1Ac EEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN PALREEMRIQF---NDMNSALT--
gi|151 SQSVLNDGIADFNQSVLLYRNYLEALDSWKNP-NSASAEELRTRFRIADSEFDLILTRG
      120      130      140      150      160      170
      150      160      170      180      190      200
Cry1Ac --TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWG-FDAATINSRYNDLTRL
gi|151 SLTNGGSLARQNAQIILLPSFASAAFFHLLLLLRDATRYGTNWGLYNATPFINYQSKLVEL
      180      190      200      210      220      230

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210      220      230      240      250      260
Cry1Ac  IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRRELTLTVLIDIVSLFPNYDSRTYPI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  IELYTDYCVHWYNRGFMNLRQRTSATAWLEFHRYRREMTLMVLDIVASFSSLDITNYPI
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac  RTVSQLTREIYTNPVLENFDGSRFGSA-----QGIEGSIRSPHMLDILNSITIYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  ETDQFSLRVIIYTDPIGVFVHRSSLRGESWFSFVNRRANFSDLENAIPNRPFSWFLNMIIST
300      310      320      330      340      350

320      330      340      350      360
Cry1Ac  DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  GSLTLPVSPSTDRARV-WYGSRRDRISP---ANSQFITEISGQHTTATQ---TILGRNI
360      370      380      390      400

370      380      390      400      410
Cry1Ac  YRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQT---VDSLDE-I
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  FRVDSQACNLNDTTYGVN-RAVIFYHDASE---GSQRSVYEGYIRTTGIDNPRVQNIINTYL
410      420      430      440      450      460

420      430      440      450      460      470
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFVSIHRSAEFNIIIASD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  PGENSIDPTPEDYTHILSTTINLTGGLRQVANSRRSSLV---MYGWTHKSLARNNTINPD
470      480      490      500      510

480      490      500      510      520      530
Cry1Ac  SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIQNRGYIEVP IHPSTSTRYR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  RITQIPLTKVDTRGTGVSIVNDPGFIGGALLQRTDHGSLGVLR--VQFPLHL---RQQYR
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VRVRYASVTPPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  IRVRYASTTNIIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNISIRPTASPDQI
580      590      600      610      620      630

600      610      620      630      640
Cry1Ac  -VGVNRFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  RLTIIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKKAVALSFTRTRD-GLQVNVKDYQ
640      650      660      670      680      690

650      660      670      680      690      700
Cry1Ac  IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  VDQAANLVSCLSDEQYGYDKMLLEAVRAAKRLSRERNLLQDPDFNTINSTEENGWKASN
700      710      720      730      740      750

710      720      730      740      750      760
Cry1Ac  GITIQGGDDVFKENVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  GVTISEGGFFYKGRAIQLASA-RENYPTYIYQKVDASBLKPYTRYRLDGFVKSSQDLEID
760      770      780      790      800      810

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770      780      790      800      810      820
Cry1Ac  SIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEK--A
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  LIHHKHVHLVKNVDPN---LVSDTYPDDSCSGINRCQQEQMVNAQLETEHHHPMDCCEA
820      830      840      850      860

830      840      850      860      870      880
Cry1Ac  HSHHFLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  AQTHEFSSYIDTGDNLSSVDQGIWAFKVRTTDDGYATLGNLELVEVGPLSGESLEREQRD
870      880      890      900      910      920

890      900      910      920      930      940
Cry1Ac  EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  NTKWSAELGRKRAETDRVYQDAKQSNHILFVDYQDQQLNPEIGMADIMDAQNLVASISDV
930      940      950      960      970      980

950      960      970      980      990      1000
Cry1Ac  YLPELSVIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  YSDAVLQIPGINYEIYTELSNRLQQASYLYTSRNVAQNGDFNGLSDWNAQSVQQDG
990      1000      1010      1020      1030      1040

1010      1020      1030      1040      1050      1060
Cry1Ac  NQRSVLVPEWEAEVVSQEVRCVGRGYILRVTAKEGYGEGCVTIEIENNTDELKFSNC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  NTH-FLVLSHWDAQVVSQFRVQPNCKYVLRVTAEKVGGDGYVTIRDDAHTTETLTFNAC
1050      1060      1070      1080      1090      1100

1070      1080      1090      1100      1110      1120
Cry1Ac  VEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPVSPADYASVVEEKSYYTDGRREN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  -----DYDIN-----GYVTDNT-----
1110

1130      1140      1150      1160      1170      1180
Cry1Ac  PCEFNRGRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|151  -----YLTKEVVFHPETQHMWVEVNETEGAFHIDSIEFVETEK
1120      1130      1140      1150

>>gi|53984836|gb|AAV26512.1| Sequence 10 from patent US (1156 aa)
initn: 1512 initl: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97
Smith-Waterman score: 1916; 33.415% identity (60.163% similar) in 1230 aa overlap
(5-1182:26-1156)

10      20      30
Cry1Ac  CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539  MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSQCNSSILN--WINIIGDAAKE
10      20      30      40      50

40      50      60      70      80      90
Cry1Ac  TGYPIDISLSLTQFLLEFVPG-AGFVLGLVD-IIWGIFGSPQWDAFLVQIEQLINQRI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539  A---VSIQTTIVSLITAPSLTGLISIVYDLIGKVLGGSSGQISDLSICDLLSIDLVR
60      70      80      90      100      110

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          100      110      120      130      140
Cry1Ac EEFARNQAISRLEGLSNLYQIYAESFRWEADPTNPAALREEMRIQF---NDMNSALT--
gi|539 SQSVLNDGIADFNGSVLLYRNYLEALDSWNKNP-NSASAEELRTRFRDIADSEFDRILYTRG
          120      130      140      150      160      170

          150      160      170      180      190      200
Cry1Ac --TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWG-FDAATINSRYNDLTRL
gi|539 SLTNGGSLARQNAQILLSPFASAAFFHLLLRDATRYGTNGLYNATPFINYSKQLVEL
          180      190      200      210      220      230

          210      220      230      240      250      260
Cry1Ac IGSYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|539 IELYTDYCVHWYNRGPNELRQRGTSATAWLEFHRVRRMTMLVLDIVASFSSLDITNYPI
          240      250      260      270      280      290

          270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPVLENFDGSGFRGSA-----QGIEGSIRSPHLMIDLNSITIIYT
gi|539 ETDFQLSRVIYTDPIGFVHRSSLRGESWFSFVNANRANFSDLENAIPNPRPSWFLNMIIST
          300      310      320      330      340      350

          320      330      340      350      360
Cry1Ac DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
gi|539 GSLTLVPVSPSTRARV-WYGSRRDRISP---ANSQFITEISGQHTTATQ---TILGRNI
          360      370      380      390      400

          370      380      390      400      410
Cry1Ac YRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQT---VDSLDE-I
gi|539 FRVDSQACNLNDTTYGVN-RAVPHYDASE---GSQRSVYEGYIRTTGIDNPRVQNTIYTL
          410      420      430      440      450      460

          420      430      440      450      460      470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNII IASD
gi|539 PGENSIDIPTPEDYTHILSTTINLTGGLRQVASNRRSSLV---MYGWTHTKSLARNNTINPD
          470      480      490      500      510

          480      490      500      510      520      530
Cry1Ac SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYR
gi|539 RITQIPLTKVDTRGTGVSVNDPGFIGGALLQRTDHGSLGVLR--VQFPLHL---RQQYR
          520      530      540      550      560      570

          540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI
gi|539 IRVRYASTTNIIRLSVN-GSFGTISQNLPSMTMLRGLDRLYGSFAIREFNISIRPTASPDQI
          580      590      600      610      620      630

          600      610      620      630      640
Cry1Ac -VGVRNFGSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|539 RLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLFTTRTRD-GLQVNVKDYQ

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          640      650      660      670      680      690
Cry1Ac IDQVSNLVTYLSDSEFCLEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|539 VDQAANLVSCLSDEQYGYDKMMLLEAVRAAKRLSRERNLLQDPDFNTINSTENGWKASN
          700      710      720      730      740      750

          710      720      730      740      750      760
Cry1Ac GITIQQGDDVFKENYVTLTSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQLEIY
gi|539 GVTISEGGPFYKGRAIQLASA-RENYPTYIYQKVDASELKPYPTRYRLDGFVKSSQDLEID
          760      770      780      790      800      810

          770      780      790      800      810      820
Cry1Ac SIRYNAKHETVNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKGC--A
gi|539 LIHHHKVHLVKNVDPN---LVSDTYPDDSCSGINRCQEQQMVAQLETEHHHPMDCCEA
          820      830      840      850      860

          830      840      850      860      870      880
Cry1Ac HSHSHFSLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
gi|539 AQTHEFSSYIDTGDNLSSVDQGIWAIKVRVTTDGYATLGNLELVEVGLSGLSGLEREQRD
          870      880      890      900      910      920

          890      900      910      920      930      940
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIAHADKRVHSIREA
gi|539 NTKWSAELGRKRAETDRVYQDAKQSIHHLFVVDYQDQQLNPEIGMADIMDAQNVLVASISDV
          930      940      950      960      970      980

          950      960      970      980      990      1000
Cry1Ac YLPELSVIPGVNAEIFEELGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGVHVDVEEQN
gi|539 YSDAVLQIPGINYEIYTELSNRLQQAASYLYTSRNAVQNGDFNNGLDSWNTAGASVQQDG
          990      1000      1010      1020      1030      1040

          1010      1020      1030      1040      1050      1060
Cry1Ac NQRSVLVVPEWEAEVQEVVRCVCGRYILRVTAKEGYGEGCVTTHEIENNTDELKFSNC
gi|539 NTH-FLVLSHWDAQVSVQFRVQPNCKYVLRVTAEKVGGDGYVTIRDDAHTTTLTFNAC
          1050      1060      1070      1080      1090      1100

          1070      1080      1090      1100      1110      1120
Cry1Ac VEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVPADYASVYEEKSYTDGREN
gi|539 -----DYDIN-----GTYYVDNT-----
          1110

          1130      1140      1150      1160      1170      1180
Cry1Ac PCFENRGRYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|539 -----YLTKEVVFHPETQHMWVVEVNETEGAFHIDSIEFVETEK
          1120      1130      1140      1150

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>>gi|40271|emb|CAA41122.1| delta-endotoxin CryIG protoxi (1156 aa)
initn: 1512 init1: 470 opt: 1619 Z-score: 1898.6 bits: 363.3 E(): 7.8e-97

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Smith-Waterman score: 1916; 33.415% identity (60.163% similar) in 1230 aa overlap (5-1182:26-1156)

Sequence alignment for Cry1Ac (1-1182) and gi|402 (5-1156). The alignment shows high identity between the two sequences, with gaps indicated by dashes. Residue positions are marked at intervals of 10.

Sequence alignment for Cry1Ac (510-1156) and gi|402 (510-1156). This section shows the alignment of the C-terminal region of the protein, with residue positions marked at intervals of 10.

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Cry1Ac VEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRREN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 -----DYDIN-----GTYVTDNT-----
      1110

      1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGRYRDYTPLVPGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 -----YLTKEVVFPETQHMWVEVNETEGAFHIDSIEFVETEK
      1120      1130      1140      1150

>>gi|162767653|emb|CAP58830.1| unnamed protein product [ (604 aa)
  initn: 1899 init1: 1301 opt: 1610 Z-score: 1892.2 bits: 361.1 E(): 1.8e-96
Smith-Waterman score: 1907; 51.282% identity (74.199% similar) in 624 aa overlap
(10-624:6-604)

      10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 MAEINNQNQCVPYNCLSNPKEIILGEEERLETGNTVADISLGLINFLYSNFVPGGGF
      10      20      30      40      50

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 IVGLLELIWGFIGPSQWDFLAQIEQLISQRIEEFARNQAISRLEGLSNLYKVYVRAFSD
      60      70      80      90      100     110

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 WEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEVALLSVYVQAANLHLSILRDVS
      120     130     140     150     160     170

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRREL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 VFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGLRRLEGRFLSDWIVYNRFRQL
      180     190     200     210     220     230

      250     260     270     280     290
Cry1Ac TLTVLDIVLSLFPNYSRTYPIRTVSQLTREIYTN-PVL-ENFD--GSFRGSAQGIEGSIR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 TISVLDIVAFFPNYDIRTYPIQTATQLTREVYLDLDFINENLSPAASYPTFSAESAIR
      240     250     260     270     280     290

      300     310     320     330     340     350
Cry1Ac SPHLMIDILNSITTYTDAHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 SPHLVDFLNSFTIYTDLARYAYWGGHLVNSFRTGTTNLRISPLYGREGNTERPVTITA
      300     310     320     330     340     350

      360     370     380     390     400     410
Cry1Ac QLQGQVYRTRLSSTLYRRPFNIGINNQQ-LSVLDGTFAYGTSNLSAVYRKSGTVDSLD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 SPSVPIFRTRLS-----YITGLDNSNPVAGIEGVEF----QNTISRSIYRKSGPIDSF
      360     370     380     390     400

      420     430     440     450     460     470

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Cry1Ac EIPPQNNVPPRQGFHSHLHVSMFRSGFSSSSVSIIRAPMFSWIHRSAEFNNIIASDSI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 ELPPQDASVSPAIGYSHRLCHAT-FLERISGPRIA---GTVFVSWTHRSASPTNEVSPSRI
      410      420      430      440      450      460

      480     490     500     510     520     530
Cry1Ac TQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI--HFPSTSTRYR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 TQIPWVKAHTLASGASVIKGPFTGGDILTRNSMGE---LGTLRVTFTRGRLPQS---YY
      470     480     490     500     510

      540     550     560     570     580     590
Cry1Ac VVRVYASVTPIHNLVNVGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 IRFRYASVANRSGTFRYSQPPSYGISFPKTMUDGEPLTSRSFAH---TTLFTPIITFSAQ
      520     530     540     550     560     570

      600     610     620     630     640     650
Cry1Ac GVRNFGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 EEFDLYIQSGVYIDRIEFIPVTATFEAEYDLER
      580     590     600

      660     670     680     690     700     710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI

>>gi|162767651|emb|CAP58829.1| unnamed protein product [ (726 aa)
  initn: 1899 init1: 1301 opt: 1610 Z-score: 1891.0 bits: 361.2 E(): 2.1e-96
Smith-Waterman score: 1907; 51.282% identity (74.199% similar) in 624 aa overlap
(10-624:128-726)

      10      20      30
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 KSTASLPVARRSSRLGNVSNNGGRIRCEINNQNQCVPYNCLSNPKEIILGEEERLETGNTV
      100     110     120     130     140     150

      40      50      60      70      80      90
Cry1Ac IDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 ADISLGLINFLYSNFVPGGGFIVGLLELIWGFIGPSQWDFLAQIEQLISQRIEEFARNQ
      160     170     180     190     200     210

      100     110     120     130     140     150
Cry1Ac AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 AISRLEGLSNLYKVYVRAFSDWEKDPTNPALREEMRIQFNDMNSALITAIPLFRVQNYEV
      220     230     240     250     260     270

      160     170     180     190     200     210
Cry1Ac PLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 ALLSVYVQAANLHLSILRDVSVFGERWGYDTATINNRYSDLTSLIHVYTNHCVDTYNQGL
      280     290     300     310     320     330

      220     230     240     250     260     270
Cry1Ac ERVWVGPDSDRWIRYNQFRRELTLTVLDIVLSLFPNYSRTYPIRTVSQLTREIYTN-PVL-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 RRLEGRFLSDWIVYNRFRRLTISVLDIVAFFPNYDIRTYPIQTATQLTREVYLDLDFIN

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340      350      360      370      380      390
Cry1Ac 280      290      300      310      320      330
ENFD--GSFRGSAQGIIEGSIIRSPHLMIDLNSITIIYDHAHRGEYYWSGHQIMASPVGFSGP
gi|162 ENLSPAASYPTFSAAESAIIRSPHLVDFLNSFTIYDLSLARAYWGGHLVNSFRTGTTN
400      410      420      430      440      450

340      350      360      370      380      390
Cry1Ac EFTFFPLYGTMGNAAPQQRIVAQLGQGVYRRTLSSTLYRRPFNIGINNOQ--LSVLDGTEFAY
gi|162 LIRSPLYGREGNTERPVITITASPSVPIFRTLS-----YITGLDNSNPFVAGIEGVEF--
460      470      480      490      500

400      410      420      430      440      450
Cry1Ac GTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLHSVMSFRSGFSNSSVSIIRA
gi|162 --QNTISRSIYRKSGPIDSFSELPPQDASVSPAIGYSHRSLCHAT--FLERISGPRIA---G
510      520      530      540      550      560

460      470      480      490      500      510
Cry1Ac PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQ
gi|162 TVFSWTHRSASPTNEVSPSRIITQIPWVKAHTLAGASVIKGGPFTGGDILTRNSMGE---
570      580      590      600      610

520      530      540      550      560      570
Cry1Ac NRGYIEVPI--HFPSTSTRYRVRVRYASVTPIHLMNVNWNSSIFSNTPATATSLDNLQS
gi|162 -LGTLRVFTTGRLPQS---YYIRFRYASVANRSGTFRYSQPPSYGISFPKTM DAGEPLTS
620      630      640      650      660      670

580      590      600      610      620      630
Cry1Ac SDFGYFESANAFTS--SLGNIVGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVN
gi|162 RSPAH---TTLFTPIITFSRAQEEFDLYIQSGVYIDRIEFIPVTATFEAEYDLER
680      690      700      710      720

640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLQ

>>gi|49035989|gb|AAT48690.1| Cry8X [Bacillus thuringiens (1174 aa)
  inith: 1393 inittl: 489 opt: 1601 Z-score: 1877.3 bits: 359.3 E(): 1.2e-95
  Smith-Waterman score: 2266; 36.834% identity (64.378% similar) in 1238 aa overlap
  (6-1179:23-1171)

          10      20      30
Cry1Ac      CMQAMDNN--PNINECIPYNCLSNPEVEVLGGERIETGYTP--
gi|490 MSPNNQNEYEIIDMAPSTSVTNDNSNRYPFANE--PTNALQNNYK--DYLRMSEGYSPEY
          10      20      30      40      50

          40      50      60      70      80
Cry1Ac -----IDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGFGPSQ--WDAFLVQIE
gi|490 LTSLSPPSYQFGTVDKIISIIISLLNSAAGIPGLDFFTGLLQFILDFFAPEDPWAEIMELVE
          60      70      80      90      100      110

          90      100      110      120      130      140

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Cry1Ac QLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEM-RIQFNDMNSA
gi|490 QLLDQKITVATREKALAE LRGLINGLVYQQSLESWLENPN--ATRASIVREQYVALELD
          120      130      140      150      160      170

          150      160      170      180      190      200
Cry1Ac LTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLI
gi|490 FVTSISSFAIAGQEVPLLA VYAQAANLHLLLRDVSIFGEEWGLTVNEVNTFYIRQMTYT
          180      190      200      210      220      230

          210      220      230      240      250      260
Cry1Ac GNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTV
gi|490 TEYSDYCVRIYNTGLNKLKGSASSWVDYNRFRREMNLLVLDI IALFPPNYDVRYPMETT
          240      250      260      270      280      290

          270      280      290      300      310
Cry1Ac SOLTREIYTNP-VLENFDG-----SFRGSAQGIIEGSIIRSPHLMIDLNSITIIYTD-AH
gi|490 TELTRVVYTDPIVDFDERKGVASTHSWTAIAPSFSSIESLRRRPLFTWLDQLTIFSKRIS
          300      310      320      330      340      350

          320      330      340      350      360
Cry1Ac RGEYY--WSGHQIMASPVGFSGPEFTFPLYGTMGNA--PQQRIVAQLGQ--GVYRRTLS-
gi|490 QPSVFINSWAGHKIST---FRTQKTDILINTHGDITNPN IKEFVVVDTKKVEDIYQTIAY
          360      370      380      390      400      410

          370      380      390      400      410
Cry1Ac -STLYRRPFNI--GINNQQLSVLDGTEFAYGTSSNLPSAVYRKSG--GTVDSLD----EIP
gi|490 PHAVANEVYFLGVPKVDNFMVP---AGGSANSAHTLIFSDSTGGRLESITKNSEAEELP
          420      430      440      450      460

          420      430      440      450      460      470
Cry1Ac PQNN--NVP-PRQ-GFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDS
gi|490 PTESLSDTPQPQVTVYSHRLDYATI I KANKSYGSGYI---PLLGWTHRSVDRNNTIYPNK
          470      480      490      500      510      520

          480      490      500      510      520      530
Cry1Ac ITQIPAVKG-NFL--FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRY
gi|490 ITQIPAVKAFSYTESFNVNIAGPGFTGGDLISLG---HLEN---IYMKLVNPNPQ-KF
          530      540      550      560      570

          540      550      560      570      580
Cry1Ac RVRVRYASVTPIHLMN-----NWNSSIFSNTPATATSLDNLQSSDFGYFESANAFT--S
gi|490 RVRIRYAASTTSLYQITGLSNLAQSDRFEQTY--SNENENMLMFEFNQYVELRNIFSVDA
          580      590      600      610      620      630

          590      600      610      620      630      640
Cry1Ac SLGN-IVGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|490 PLENHQVSIQNYQNGFVVIDRIEFIPVNATYEAQDLDLSAKKAVNTLFTNTKD--GLRPG
          640      650      660      670      680      690

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510      520      530      540      550      560
Cry1Ac  SGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS--VTPIHL-NVNWGNSSIFSNTVPATAT
gi|161  --DRI---GSCHEFQMIPE-SQRFRIRIRYASNETSYISLYGLNQSGLTKFNQTY--SNK
      560      570      580      590      600
Cry1Ac  SLDNLQSSDFGYFE-----SANAFSTSSLGNI-VGVNRFSGTAGVIIDRFEPVVTATLEA
gi|161  NENDLTYNDFKYIEYPRVISVNA-SSNIQRLSIGIQ--TNTNLFILDRIEFPVDETYEA
      610      620      630      640      650      660
Cry1Ac  EYNLEAQAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKH
gi|161  ETDLEAAKAVNALFTNTKD-GLQPGVTDYEVNQAANLVECLSDDLYPNEKRLFLDAVRE
      670      680      690      700      710      720
Cry1Ac  AKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD--ECY
gi|161  AKRLSEARNLLQDDPFQEI--GENGWASTGIEVIEGDVAFKGRYLRLPGAREIDTETY
      730      740      750      760      770      780
Cry1Ac  PTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQS
gi|161  PTYLYQKVEEGVLKPYTRYRLRGFVGGSSQGLEIYITIRHQTNRIKVNPPD--DLLP--DVP
      790      800      810      820      830
Cry1Ac  PIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVCTDLNEDLGVWVIFK
gi|161  PVNNDGRINRCSEQKYVNSRLEVENRSGE-----AHEFSIPIDTGELDYENAGIWWGFK
      840      850      860      870      880      890
Cry1Ac  IKTDQGHARLGNLFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDA
gi|161  ITDPEGYATLGNLLEVEEGPLSGDALERLQKEEQWKIQMTRRREEDDRRYMASKQAVDR
      900      910      920      930      940      950
Cry1Ac  LFNVSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVPGVNAAIFFEELEGRIFTAFS
gi|161  LYADYDQQLNPNVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFTELTDRLQQAAG
      960      970      980      990      1000      1010
Cry1Ac  LYDARNVIKNGDFNNGLSWVKGHVDVEEQNNQRSVLVPEWEAEVSEQVRCVCPGRGYI
gi|161  LYDQRNAIPNGDYRNELSNWNTTSGVNVQ-QINHTSVLVIPNWNEQVSKFTVQPNQRVY
      1020      1030      1040      1050      1060      1070
Cry1Ac  LRVTAAYKEGYEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTICNDYTVNQEEYGGAYT
gi|161  LRVTARKEGVNGYVSIIRDGGNQSETLTFSA-----SDYDTNGM-YDTQAS

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1080      1090      1100      1110
Cry1Ac  SRNRGYNEAPSPVADYASVYEEKSYTDGRRENPCFENRGRDYTPLPVGVYVTKLEYFPE
gi|161  NTN-GYNTN-----SVYMIK-----PA-ISRKTVDLSSV-----Y---
      1120      1130      1140
Cry1Ac  TDKVWIEIGETEGTFIVDSVELLLMEE
gi|161  -NQMWIEISETEGTFYIESVELIVDVE
      1150      1160
>>gi|436835|gb|AAA21118.1| CryIII delta-endotoxin (1169 aa)
initn: 1779 init1: 801 opt: 1584 Z-score: 1857.3 bits: 355.6 E(): 1.6e-94
Smith-Waterman score: 2461; 39.531% identity (65.745% similar) in 1194 aa overlap
(22-1179:59-1166)
      10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|436  FANEPTNALQNMDYKDYLKMSAGNVSEYPGSPEVFLSEQDAVKAA---IDIVGKLLTGLG
      30      40      50      60      70      80
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNL
gi|436  VPFVGPVIVSLYQLDIDLWPSKQKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
      90      100      110      120      130      140
Cry1Ac  YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
gi|436  YQLYLTALEEWKENPNRSRALRDVRNRFELDSLFTQYMPFRVTNFEVFPFLTVYTMAN
      150      160      170      180      190      200
Cry1Ac  LHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
gi|436  LHLLLLRDASIFGEEWGLSTSTINNYNRQMKLTAEYSDHCVKWYETGLAKLKGSSAKQW
      210      220      230      240      250      260
Cry1Ac  IRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLENFD---GSFRG
gi|436  IDYNQFRREMTLTVLDVVALFSNYDTRTYPLATTAQLTREVYTDLP-LGAVDVPNIGSWYD
      270      280      290      300      310      320
Cry1Ac  SAQGI---EGSIRSPHLMIDILNSTIYTD----AHRGEYWSGHQIMASVPGVSGPEF
gi|436  KAPSFSEIEKAAIRPPHFVDYITGLTVYTKRSFTSDRYMRYWAGHQISYKHIGTSSST-F
      330      340      350      360      370      380
Cry1Ac  TFFLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRFPNIGINNQQLSVLD
gi|436  T-QMYGTQNLQSTSNF-DFTNYDIYKTLNNGAVLLDIVPGYTYTF-FGMPETEFFMVN

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390      400      410      420      430      440
Cry1Ac  GTEFAYGTSSNLPASVYRKSQVDSLDEIPPQNNVPPRQGFVSHRSHVSMFRSGFSNS
gi|436  QLNNTKTLTYKPAKDIIDRTRDSELELPPETSGQPNYESYSHRIGHITFI---YSSST
      450      460      470      480      490
Cry1Ac  VSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNS
gi|436  STYV--PVFSWTHRSADLNTVTKSGEITQIPGGKSTIGRNTYIIKGRGYTGGDLVALT-
      500      510      520      530      540      550
Cry1Ac  SGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS--VTPIHL-NVNWGNSIFSENTVPATAT
gi|436  --DRI---GSCEFQMIFFE-SQFRIRIRYASNETSYISLYGLNQSGLTKFNQTY--SNK
      560      570      580      590      600
Cry1Ac  SLDNLQSSDFGYFE----SANAFSTSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEA
gi|436  NENDLTYNDFKYIEYPRVISVNA-SSNIQRLSIGIQ--TNTNLFILDRIEFIPVDETYEA
      610      620      630      640      650      660
Cry1Ac  EYNLEERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKH
gi|436  ETDLEAAKAVNALFTNTKD-GLQPGVTDYEVNQAAANLVECLSDDLYPNEKRLFLDAVRE
      670      680      690      700      710      720
Cry1Ac  AKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFFD--ECY
gi|436  AKRLSEARNLLQDPDFQEI--GENGWASTGIEVIEGDVAFKGRYLRLPGAREIDTETY
      730      740      750      760      770      780
Cry1Ac  PTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSWPLSAQS
gi|436  PTYLYQKVEEGVLKPYTRYRLRGFVGSQGLEIYTIHQTNRIKVNVPD--DLLP--DVP
      790      800      810      820      830
Cry1Ac  PIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGTDLNEDLGVWVIFK
gi|436  PVNNDGRINRCSEQKYVNSRLEVENRSGE----AHEFSIPIDTGELDYENAGIWVGFK
      840      850      860      870      880      890
Cry1Ac  IKTDQGHARLGNLFLLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDA
gi|436  ITDPEGYATLGNLLEVEEGPLSGDALERLQKEEQQWKIQMTRRREEDRRRYMASQAVDR
      900      910      920      930      940      950
Cry1Ac  LFNVSQYDQLQADTNLAMIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFS
gi|436  LFNVSQYDQLQADTNLAMIHAADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFS

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gi|436  LYADYQDQQLNPNVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFTELTDRLQQAAG
      960      970      980      990      1000      1010
Cry1Ac  LYDARNVIKNGDFNGLSCWNVKGHVDEEQNNQSVLVVPEWEAEVSEQEVRVCPGRGYI
gi|436  LYDQRNAIPNGDYRNELSNWNTTSGVNVQ-QINHSTVLVLPNWNQVSVQKFTVQPNQRYV
      1020      1030      1040      1050      1060      1070
Cry1Ac  LRVTAKEGEGYEGCVTIHEIENNTDELKFSNVCVEEIIYPNNTVTCNDYTVNQEEYGGAYT
gi|436  LRVTARKEGVNGYVSIIRDGGNQSELTLSA-----SDYDTNGM-YDTQAS
      1080      1090      1100      1110
Cry1Ac  SRNRYNEAPSPADYASVYEEKSYTDGRRNCPCEFNRGRDYTPPLVGYVTKLEYPFE
gi|436  NTN-GYNTN-----SVYMIK-----PA-ISRKTVDISSV-----Y---
      1120      1130      1140
Cry1Ac  TDKVWIEIGETEGTFIVDSVELLLMEE
gi|436  -NQMWIEISSETEGTFYIESVELIVDVE
      1150      1160
>>gi|58700647|gb|AAW81032.1| Cry8 [Bacillus thuringiensis (739 aa)
initn: 971 initl: 489 opt: 1579 Z-score: 1854.3 bits: 354.4 E(): 2.3e-94
Smith-Waterman score: 1624; 40.025% identity (66.540% similar) in 792 aa overlap
(407-1179:20-736)
      380      390      400      410      420      430
Cry1Ac  IGINNQLSVLDGTEFAYGTSSNLPASVYRKSQVDSLDEIPPQNN--NVP-PRQ-GFSH
gi|587  GSANSAHTLIFSDSTGGRLESITKNSEAEPLPPTESLSDTPQPNQVITYSH
      10      20      30      40
Cry1Ac  RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFL--FNG
gi|587  RLDYATIIKANKSYSGYI---PLLGWTHRSVDRNNTIYPNKITQIPAVKAFSYTESFNV
      50      60      70      80      90      100
Cry1Ac  SVISGPGFTGGDLVRLNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNV--
gi|587  NVIAGPFTGGDLISLG---HLEN---IYMKLNVPNPQ-KFRVRIRYAASTTSYLAQITG
      110      120      130      140      150
Cry1Ac  --NWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAF--SSLGN-IVGVRNFSGTAGV
gi|587  LSNLAQSDRFEQTY--SNENENMLMFENFYVELRNIFSVADAPLENHQVSIQNYQGNGFV
      160      170      180      190      200      210
Cry1Ac  IIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS

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170      180      190      200      210      220
Cry1Ac ANLHLSVLRDVSFVQQRWGFDAATI-NSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|337 ANLHLLLLLADAEKYGARWGLRESQIGNLYFNELQTRTRDYTNHCVNAYNNGLAGLRGTS
180      190      200      210      220      230

230      240      250      260      270      280
Cry1Ac RDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV-LENFDGSF--
gi|337 ESWLKYHQFRREATLMAMDIALFPYINTRRYPIAVNPQLTREVYTDPLGVPSESSLFP
240      250      260      270      280      290

290      300      310      320
Cry1Ac -----RGSQAQ---GIEGSI-RSPHLMIDLNSITIYTDA---HRGEYY---WSGHQIM
gi|337 ELRCLRWQETSAMTFNSLENAISSPHLFDITINNLMITYGSPSVHLTNQLIEGWIGHSVT
300      310      320      330      340      350

330      340      350      360      370      380
Cry1Ac ASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSV
gi|337 SLLA-SGP--TTVLRNRYGSTTSIVNYFSFNDRDQVYQINT---RSHTGLGFQNAPLFG
360      370      380      390      400

390      400      410      420      430      440
Cry1Ac LDGTEF-AYGTSSNLPASVYRKSQVDSLDEIPPQNNVPPRQGFVSHRSLHV-SMFRSGF
gi|337 ITRAQFYPPGGTYSVTORNALTCQNYNSIDELPSLDNPEPISRSYSHRSHITSYLHRVL
410      420      430      440      450      460

450      460      470      480      490      500
Cry1Ac SNSSVSIIRA--PMFSWIHRSAEFNIIASDSITQIPAVKGNFLNFGS-VISGPGFTGGD
gi|337 TIDGINIYSGNLPTVWTHRDVLDLNTITADRITQLPLVKSFEIPAGTIVVRGPGFTGGD
470      480      490      500      510      520

510      520      530      540      550      560
Cry1Ac LVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTPVA
gi|337 LLRRTGVGT---FGTIRVRRTPAPLTQ-RYRIRFRFASTNLFIRGIRVQDRQVNYFDQFR
530      540      550      560      570

570      580      590      600      610
Cry1Ac TATSLDNLQSSDFGYFESANAFT-SSLGNIVGV--RNFSGTAGVIDRFEFIPVTATLEA
gi|337 TMNRGDELRYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIPVNPAREA
580      590      600      610      620      630

620      630      640      650      660      670
Cry1Ac EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKH
gi|337 KEDLEAAKAVASLFTTRTD-GLQVNVKDYQVDQAANLVSCLSDBEQYGYDKMLLEAVRA
640      650      660      670      680      690

680      690      700      710      720      730
Cry1Ac AKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTY
gi|337 AKRLSREERNLLQDPDFNTINSTEENGWKASNGVTISEGGPFYKGRALQLASA-RENYPTY
700      710      720      730      740      750

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740      750      760      770      780      790
Cry1Ac LYQKIDESLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIG
gi|337 IYQKVDASELKPYTRYRSDFVKSSQDLEIDLHKKVHLVKNVDPN---LVSDTYPPD
760      770      780      790      800      810

800      810      820      830      840      850
Cry1Ac KCGEPNRCAPHLEWNPDLDCSCRDEKGC--AHSHHFSLDIDVGCITDLNEDLGWVWIFKI
gi|337 SCSGINRCQQQMVNAQLETHEHHHPMCCEAAQTHEFSSYIDTGLNNSVDQGIWAIFKV
820      830      840      850      860      870

860      870      880      890      900      910
Cry1Ac KTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDAL
gi|337 RTTDGYATLGNLELVVGVPLSGESLEREQRDNTKWSAELGRKRAETDRVYQDAKQSIHNL
880      890      900      910      920      930

920      930      940      950      960      970
Cry1Ac FVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAFELEGRIFTAFSL
gi|337 FVDYDQDQLNPEIGMADIMDAQNLVASISDVYSDAVLQIPGINYEIYTELSNRLQOQASYL
940      950      960      970      980      990

980      990      1000      1010      1020      1030
Cry1Ac YDARNVIKNGDFNNGLSNWNKGVHDVVEEQNNQRSVLPVPEWAEVSEVRRVCPGRGYIL
gi|337 YTSRNVQNGDFNNGLSDWNATAGASVQQDGNTH-FLVLSHDAQVSSQFRVQPNCKYVL
1000      1010      1020      1030      1040      1050

1040      1050      1060      1070      1080      1090
Cry1Ac RVTAYKEGYEGECVTHIEIENNTDELKFSNCEVEEYIPNNTVTCNDYTVNQEEYGGAYTS
gi|337 RVTAEKVGGGDYVTTIRDAHHTETLTFNAC-----DYDIN---GTYVT
1060      1070      1080      1090

1100      1110      1120      1130      1140      1150
Cry1Ac RNRGYNEAPSVPADYASVYEEKSYTDGRENPCEPNRGYRDYTPLPVGVVTELEYPFET
gi|337 DNT-----YLTKEVIFYSHS
1100

1160      1170      1180
Cry1Ac DKVWIEIGETEGTFIVDSVELLMEE
gi|337 EHMWVEVNETEGAFHIDSIIEFVETEK
1110      1120      1130

>>gi|53970043|gb|AAV19136.1| Sequence 76 from patent US (1134 aa)
initn: 1802 initl: 470 opt: 1543 Z-score: 1809.1 bits: 346.7 E(): 7.6e-92
Smith-Waterman score: 2258; 36.498% identity (62.848% similar) in 1222 aa overlap
(5-1182:1-1134)

10      20      30      40      50
Cry1Ac CMQAMNPNINECIPYNCLSNPEVEVLGGER--IETGY-TPIDISLSLTQFLLESEFVPG
gi|539 MDNPNINECIPYNCLSNPEVEVLGGERGNVRTGLQGTGIDIVAVVVGALGG---PV
10      20      30      40      50

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60 70 80 90 100 110  
Cry1Ac AGFVLGLVDIIWGFGPSQ---WDAFLVQIEQLINQRIIEEFARNQAI SRL EGLSNLYQI  
gi|539 GGILTFGLSTLFGFLWPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQNYNQ  
60 70 80 90 100 110

120 130 140 150 160  
Cry1Ac YAESFREWADPTNPALREEMRIQ-FNDMNSALTTAIPFAV---QNYQVPLLSVYVQA  
gi|539 YLIAKKEWEERPNG--VRANLVLQRFEILHALFVSSMPSFGSGPGSQRFOAQLLVVYAQA  
120 130 140 150 160 170

170 180 190 200 210 220  
Cry1Ac ANLHLSVLRDVSFVGRWGFDAATI-NSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS  
gi|539 ANLHLLLLADAEEKYGARWGLRESQIGNLYFNELQTRTRDYTNHCVNAYNNGLAGLRGTS  
180 190 200 210 220 230

230 240 250 260 270 280  
Cry1Ac RDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV-LENFDGSF--  
gi|539 ESWLKYHQFRREATLMAMDLIALFPYYNTRRYIAVNPQLTREVYTDPLGVPSEESSLFP  
240 250 260 270 280 290

290 300 310 320 330 340 350  
Cry1Ac -----RGSQAQ---GIEGSI-RSPHLM DILNSIT IYTD A---HRGEYY---WSGHQIM  
gi|539 ELRCLRWQETSAMTFSNLENAI ISSPHLFD TINNLM IYTG SFSVHL TNQLIEGWIGHSVT  
300 310 320 330 340 350

330 340 350 360 370 380  
Cry1Ac ASPVFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSV  
gi|539 SLLA-SGP--TTVLRNRYGSTTSIVNYFSFNDRDQVYQINT---RSHTGLGFQNAFLFG  
360 370 380 390 400

390 400 410 420 430 440 450 460  
Cry1Ac LDGTEF-AYGTSNNLPSAVYRKS GTVDSLDEIPPQNNVPPRQGF SHRLSHV-SMFRSGF  
gi|539 ITRAQFYPPGGTYSVTQRNALTCEQNYNSIDELPSLDPNEPISRSYSHRLSHITSYLHRVL  
410 420 430 440 450 460

450 460 470 480 490 500 510 520  
Cry1Ac SNSSVSIIRA--PMFSWIHRSAEFNNI IASDSITQIPAVKGNFLFN GS-VISGPGFTGGD  
gi|539 TIDGINIYSGNLPTVYVWTHRDVLDLNTITADRITQLPLVKFSFEIPAGTTVVRGPGFTGGD  
470 480 490 500 510 520

510 520 530 540 550 560  
Cry1Ac LVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPA  
gi|539 ILRRITGVGT---FGTIRVRTTAPLTQ-RYRIRFRFASTTNLFIGIRVGDQVNYVDFGR  
530 540 550 560 570

570 580 590 600 610  
Cry1Ac TATSLDNLQSSDFGYFESANAFT-SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEA  
gi|539 TMNRGDELRYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREA

580 590 600 610 620 630  
Cry1Ac EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKH  
gi|539 KEDLEAAKAVASLFRTRD-GLQVNVKDYQVDQAANLVSCLSDEQYGYDKMLLEAVRA  
640 650 660 670 680 690

680 690 700 710 720 730  
Cry1Ac AKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTY  
gi|539 AKRLSRERNLLQDPDFNTINSTEENGWKASNGVTISEGGPFYKGRALQLASA-RENYPTY  
700 710 720 730 740 750

740 750 760 770 780 790  
Cry1Ac LYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPIG  
gi|539 IYQKVDASELKPYTRYRSDGFKSSQDLEIDLH H K V H L V K N V P D N --- L V S D T Y P D D  
760 770 780 790 800 810

800 810 820 830 840 850  
Cry1Ac KCGEPNRCAPHLEWNPDLDCSCRDEKCC--AHSHHFSLDIDVGC TDLNEDLGVVWVFKI  
gi|539 SCSGINRCQQQMVNAQLETEHHHPMDCCEAAQT H E F S S Y I D T G D L N S S V D Q G I W A I F K V  
820 830 840 850 860 870

860 870 880 890 900 910  
Cry1Ac KTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDAL  
gi|539 RTTDGYATLGNLELVEVGPLSGESLEREQRDNTKWSAELGRKRAETDRVYQDAKQSIHNL  
880 890 900 910 920 930

920 930 940 950 960 970  
Cry1Ac FVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFSL  
gi|539 FVDYDQQLNPEIGMADIMDAQNLVASISDVYSDAVLQIPGINYEIYTELSNRLQQASYL  
940 950 960 970 980 990

980 990 1000 1010 1020 1030  
Cry1Ac YDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLPVPEWEAEVSQEVVRCVCPGRGYIL  
gi|539 YTSRNAVQNGDFNNGLDSWNA TAGASVQDGNTH-FLVLSHWDAAQVQQFRVQPNCCKYVL  
1000 1010 1020 1030 1040 1050

1040 1050 1060 1070 1080 1090  
Cry1Ac RVTAYKEGYEGCVTIHEIENNTDELKFSNCEVEEYIPNNTVTCNDYTVNQEEYGGAYS  
gi|539 RVTAEKVGGDGYVTTIRDGAHHTETLTFNAC-----DYDIN-----GTYVT  
1060 1070 1080 1090

1100 1110 1120 1130 1140 1150  
Cry1Ac RNRGNEAPSVPADYASVYEEKSYTDGRENPECFNRGRDYTPLPVGVVTKLEYFPET  
gi|539 DNT-----YLTKEVIFYSHT  
1100

1160 1170 1180  
Cry1Ac DKVWIEIGETEGTFIVDSVELLMEE  
.....



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gi|215 1060 1070 1080 1090
RVTAEKVGGGDYVTRDGAHHTETLTFNAC-----DYDIN----GTVVT
1060 1070 1080 1090

Cry1Ac 1100 1110 1120 1130 1140 1150
RNRGYNEAPSPADYASVYEEKSYTDGRENPCFENRGRYDTPPLVGVYTKLEYFPET
:
gi|215 -----YLTKEVIFYSHT
1100

Cry1Ac 1160 1170 1180
DKVWVIEIGETEGTFIVDSVELLLMEE
.....:
gi|215 EHMWVEVNETEGAFHIDSIEFVETEK
1110 1120 1130

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>>gi|1334252|emb|CAA52927.1| delta-endotoxin [Bacillus t (1144 aa)  
 initn: 1628 initl: 470 opt: 1543 Z-score: 1809.0 bits: 346.7 E(): 7.6e-92  
 Smith-Waterman score: 2070; 34.830% identity (62.261% similar) in 1203 aa overlap  
 (30-1182:29-1144)

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Cry1Ac 10 20 30 40 50
CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSL-TQFLLESEFVPGA-
:
gi|133 VFELKTCIWHAAFFLTKLSSYKDYLMSEGDYIDSYINPGNVRTGLQGTGIDIVAVVVGAL
10 20 30 40 50

Cry1Ac 60 70 80 90 100
----GFVLGLVDIIWGFGPSQ----WDAFLVQIEQLINQRIEEFARNQAI SRLEGLSN
:
gi|133 GGPVGGILTGFLSTLFGFLWPSNDQAVWEAFIEQMEELIEQRISDQVVRTALDDLTGIQN
60 70 80 90 100 110

Cry1Ac 110 120 130 140 150 160
LYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALTTAIPFAV---QNYQVPLLVS
:
gi|133 YYNQYLIALKEWEERP--GVRANLVLRFEILHALFVSSMPSFGSGPGSQRFQAQLLVV
120 130 140 150 160 170

Cry1Ac 170 180 190 200 210 220
YVQANLHLSVLRDVSVFGQRWGFDAATI-NSRYNDLTRLIGNYTDHAVRWYNTGLERVW
:
gi|133 YAQANLHLLLLADAKEYGARWGLRESQIGNLYFNELQTRTRDYTNHCVNAYNGLAGLR
180 190 200 210 220 230

Cry1Ac 230 240 250 260 270 280
GPDSDRWIRYNQFRRELTTLVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPV-LENFDG
:
gi|133 GTSAESWLKYHQFRREATLMAMDLIALFPYNTTRYPIAVNPQLTREVYTDPLGVPSEES
240 250 260 270 280 290

Cry1Ac 290 300 310 320
SF-----RGSAG--GIEGSI-RSPHLMIDLNSITTYTDA---HRGEYY---WSG
:
gi|133 SLFPELRLRWOQETSAMTFSNLENALISSPHLFDITNNLMIYTGFSVHLTNQLIEGWIG
300 310 320 330 340 350

Cry1Ac 330 340 350 360 370 380
HQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVALQLGQGVYRTLSTLYRPFNIGINNQ

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gi|133 360 370 380 390 400 410
HSVTSSLLA-SGP--TTVLRNRYGSTTSIVNYSFNDRDVYQINT---RSHTGLGFQNA
360 370 380 390 400 410

Cry1Ac 390 400 410 420 430 440
QLSVLDGTEF--AYGTSSNLPASAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHV-SMF
:
gi|133 PLFGITRAQFYPPGGTYSVTQRNALTCEQNYNSIDELPSLDPNEPISRSYSHRLSHITSYL
420 430 440 450 460 470

Cry1Ac 450 460 470 480 490
RSGFNSSSVSIIRA--PMFSWIHRSAEFNNI IASDSITQIPAVKGNFLFNGS-VISGPGF
:
gi|133 HRVLTIDGINIYSGNLPTYVWTHRVDLNTITADRITQLPLVKSFEIPAGTIVVVRGPGF
480 490 500 510 520 530

Cry1Ac 500 510 520 530 540 550
TGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSN
:
gi|133 TGGDILRRTGVT---FGTIRVRTTAPLTQ-RYRIRFRFASTTNLFIGIRVGDQVNYF
540 550 560 570 580

Cry1Ac 560 570 580 590 600 610
TVPATATSLDNLQSSDFGYFESANAFT-SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTA
:
gi|133 DFGRTMNRGDELRYESFATREFTTDFNFRQPQELISVFANAFSAGQEVYFDRIEIIIPVNP
590 600 610 620 630 640

Cry1Ac 620 630 640 650 660 670
TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSE
:
gi|133 AREAKEDLEAAKAVASLFRTRD-GLQVNVKDYQVDQAANLVSCLSDEQYGYDKKMLLE
650 660 670 680 690 700

Cry1Ac 680 690 700 710 720 730
KVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTFDEC
:
gi|133 AVRAAKRLSRERNLLQDPDFNTINSTEENGWKASNGVTISEGGPFYKGRALQLASA-REN
710 720 730 740 750 760

Cry1Ac 740 750 760 770 780 790
YPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVVPGT--GSLWPLS
:
gi|133 YPTYIYQKVDASELKPYPTRYRSDGFVKSSQDLEIDLIIHHKHVHLVKNVPDNLVSDTYPPD
770 780 790 800 810 820

Cry1Ac 800 810 820 830 840 850
AQSPIGKCGEPNRCAPHLEW--NPDLDCSCRDGKCAHSHHFFSLDIDVGCITDLNEDLVG
:
gi|133 SCSGINRCQEQMVNAQLETEHHHPMDC-CE-----AAQTHEFSSYIDTGDNLSSVDQGI
830 840 850 860 870

Cry1Ac 860 870 880 890 900 910
WVIFKIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAK
:
gi|133 WAFKVRTTDGYATLGNLELVEVGPLSGESLEREQRDNTKWSAELGRKRAETDRVYQDAK
880 890 900 910 920 930

Cry1Ac 920 930 940 950 960 970

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Cry1Ac  ESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRI
gi|133  QSINHLFVDYQDQLNPEIGMADIMDAQNLVASISDVYSDAVLQIPGINYEIYTELSNRL
      940      950      960      970      980      990

      980      990      1000      1010      1020      1030
Cry1Ac  FTAFLSYDARNVIKNGDFNNGLSWNVKGVHDVVEEQNNQSRVLLVPEWEAEVSEQVRVCP
gi|133  QQASYLYTSRNAVQNGDFNNGLSWNVKGVHDVVEEQNNQSRVLLVPEWEAEVSEQVRVCP
      1000      1010      1020      1030      1040      1050

      1040      1050      1060      1070      1080      1090
Cry1Ac  GRGYILRVTAAYKEGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEY
gi|133  NCKYVLRVTAAYKEGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEY
      1060      1070      1080      1090

      1100      1110      1120      1130      1140      1150
Cry1Ac  GGAYTSRNRGYNEAPVSPADYASVYEEKSYTDGRRENPCFNRGRYDYTPLPVGVYTKEL
gi|133  -GTYYTDNT-----YLTKEV
      1100                                  1110

      1160      1170      1180
Cry1Ac  EYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|133  IFYSHTEHMWVEVNETEGAFHIDSIEFVETEK
      1120      1130      1140

>>gi|2102642|dbj|BAA19948.1| cry9Da1 [Bacillus thuringie (1169 aa)
  in1tn: 1823 in1tl: 442 opt: 1536 Z-score: 1800.6 bits: 345.2 E(): 2.2e-91
Smith-Waterman score: 2106; 34.917% identity (62.250% similar) in 1200 aa overlap
(20-1182:57-1169)

      10      20      30      40
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|210  YPLTDDPNAGLQNMNYKEYLQTYGGDYTDPLINPNLSVSGKDVIVQGINIVGRLLSFFGF
      30      40      50      60      70      80

      50      60      70      80      90      100
Cry1Ac  -LLSEFVPGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLS
gi|210  PFSSQWVTVYTY---LLNSLWPDDENSVWDAFMERVEELIDQKISEAVKGRALDDLTLGLQ
      90      100      110      120      130      140

      110      120      130      140      150      160
Cry1Ac  NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPLLSV
gi|210  YNYNLYVEALDEWLNRP-NGARASLVSQRFNILDSLFTQFMPSFGSGPGSQNYATILLPV
      150      160      170      180      190      200

      170      180      190      200      210      220
Cry1Ac  YVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG
gi|210  YAQAANLHLLLDKADIIYGARWGLNQTQIDQFHSRQSLTQTYTNHCVTAYNDGLAELRG
      210      220      230      240      250      260

      230      240      250      260      270

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Cry1Ac  PDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYP IRTVSQTLREIYTNPV---LEN-
gi|210  TTAESWFKYNQYRREMTLTAMDVLVFPYINLRQYDPDGNPQLTREYVYTDPIAFDPLEQP
      270      280      290      300      310      320

      280      290      300      310      320
Cry1Ac  -----FDGSFRG--SAQGI EGS-IRSPHLM DILNSIT IYTD AHRGEY YWSGHQIMA
gi|210  TTQLCRSWYINPAFRNHLNFSVLENSLIRPPHLFERLSNLQILVNYQTNGSAWRGSRVRF
      330      340      350      360      370      380

      330      340      350      360      370      380
Cry1Ac  SPVFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRP----FNIGINNQ
gi|210  HYLHSSIIQEK--SYGLLSD--PVGANIN VQNNDIYQIISQVSNFASPVGSYSVWDTNF
      390      400      410      420      430

      390      400      410      420      430      440
Cry1Ac  QLSVLDGTEFAYGTSSNLP SAVYRKSGT VDSLDEIPPQNNVPPRQGF SHRLSHVSMFRS
gi|210  YLSSGQVSGISGYTQQGIPAVCLQQRNSTDELPSLNPEGDII---RNYSHRLSHITQYRF
      440      450      460      470      480      490

      450      460      470      480      490
Cry1Ac  GFSNS-SVSIIRA--PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFT
gi|210  QATQSGSPSTVSANLPTCVWTHRDVLDNTITANQITQLPLVKAYELSSGATVVKGPGFT
      500      510      520      530      540      550

      500      510      520      530      540      550
Cry1Ac  GGDVLRNLSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSI--FS
gi|210  GGDVIRRTNTGG---FGAIRVSVTGPLTQ-RYRIRFRYASTIDPFFVTRGGTTINFR
      560      570      580      590      600      610

      560      570      580      590      600      610
Cry1Ac  NTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRFNSGTAGVIIDRFEFIPVTAT
gi|210  FTRTMNRGQESRYESYRTVEFTTPFNFTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNP
      620      630      640      650      660      670

      620      630      640      650      660      670
Cry1Ac  LEAEYNLERAQKAV-NALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSE
gi|210  REAEEDLEAAKKAARQNLFRTRD-GLQVNVTDYQVDQAANVLSCLSDQYGHDKMLLE
      680      690      700      710      720

      680      690      700      710      720      730
Cry1Ac  KVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDEC
gi|210  AVRAAKRLSRENRLLQDDPFNTINSTEENGWKASNGVTISEGGPPFKGRALQLASA-REN
      730      740      750      760      770      780

      740      750      760      770      780      790
Cry1Ac  YPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQ
gi|210  YPTYIYQKVDASVLKPYTRYRLDGFVKSSQDLEIDLIIHYHKVHLVKNVDPNL---VSDT
      790      800      810      820      830      840

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      800      810      820      830      840      850
Cry1Ac SPIGKCGEPNRCAPHLEWNPDLDCSCRDKGEC--AHSHHFLSLDIDVGCTDLNEDLGVVW
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 YSDGSCSGMNRCEEQQMVNAQLETEHHHPMDCCEAAQTHEFSSYINTGDLNASVDQGIWV
      850      860      870      880      890      900

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      860      870      880      890      900      910
Cry1Ac IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKES
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 VLKVRTTDGYATLGNLELVEVGPLSGESLEREQRDNAKWNAELGRKRAEIDRVYLAQQA
      910      920      930      940      950      960

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      920      930      940      950      960      970
Cry1Ac VDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPESVIPGVNAAIFEELEGRIFT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 INHLFVDYDQQLNPEIGLAEINEASNLVESISGVYSDTLLQIPGINYIETELSDRLQQ
      970      980      990      1000      1010      1020

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      980      990      1000      1010      1020      1030
Cry1Ac AFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQSRVSVLVPWEAEVVSQEVRCVCPGR
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 ASYLYTSRNVQNGDFNSGLDSWNTTDDASVQDGNMH-FLVLSHWDAQVSQLRVNPNPC
      1030      1040      1050      1060      1070      1080

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      1040      1050      1060      1070      1080      1090
Cry1Ac GYILRVYAYKEGYEGCVTIHEIENNTDELKFSNVCVEEIIYPNNTVTCDYTVNQEEYGG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 KYVLRVTARKVGGDGYVTIRDAHGHQETLTFNAC-----DYDVN-----G
      1090      1100      1110      1120

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      1100      1110      1120      1130      1140      1150
Cry1Ac AYTSTRNGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGRDYRDTPLVGYVTKLEY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 TVVNDN-----SYITEEVVVF
      1130

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      1160      1170      1180
Cry1Ac FPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|210 YPETKHMWVEVSESESGSFYIDSIEFIETQE
      1140      1150      1160

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>>gi|3991198|gb|AAC84625.1|AR001048 Sequence 2 from pate (1169 aa)
  initn: 1823 initl: 442 opt: 1536 Z-score: 1800.6 bits: 345.2 E(): 2.2e-91
Smith-Waterman score: 2106; 34.917% identity (62.250% similar) in 1200 aa overlap
(20-1182:57-1169)

```

```

      10      20      30      40
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 YPLTDDPNAGLQNMNYKEYLQTYGGDYTDPLINPNLSVSGKDVIQVGINIVGRLLSFFGF
      30      40      50      60      70      80

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      50      60      70      80      90      100
Cry1Ac -LLSEFVPGAGVFLGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 PFSSQWVTVYTY--LLNSLWPDDENSVWDAFMERVEELIDQKISEAVKGRALDDLTGLQ
      90      100      110      120      130      140

```

```

      110      120      130      140      150      160
Cry1Ac NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT'AIPLFAV---QNYQVPLLSV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 YNYNLYVEALDEWLNRP-NGARASLVSRFNILDSLFTQFMPSPGSGPQNYATILLPV
      150      160      170      180      190      200

```

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      170      180      190      200      210      220
Cry1Ac YVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 YAQAANLHLLLLKDADIYGARWGLNQTDIDQFHSRQSLTQTYTINHCVTAYNDGLAELRG
      210      220      230      240      250      260

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      230      240      250      260      270
Cry1Ac PDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPV---LEN-
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 TTAESWFKYNQYRREMTLTAMDVLALFPYVYVNLRYQYDPDGTNPQLTREVYTDPIAFDPLEQP
      270      280      290      300      310      320

```

```

      280      290      300      310      320
Cry1Ac -----FDGSFRG--SAQGIEGS-IRSPHLMIDLNSITTYTDAHRGEYYWSGHQIMA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 TTQLCRSWYINPAFRNHLNFSVLENSLIRPPHLFERLSNLQILVNYQTNGSAWRGSRVRY
      330      340      350      360      370      380

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      330      340      350      360      370      380
Cry1Ac SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRP---FNIGINNQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 HYLHSSIIQEK--SYGLLSD--PVGANINVQNNDIYQIISQVSNFASPVGSSYSVWDTNF
      390      400      410      420      430

```

```

      390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 YLSSGQVSGISGYTQQGIPAVCLQQRNSTDELPSLNPEGDII---RNYSHRLSHI'QYRF
      440      450      460      470      480      490

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      450      460      470      480      490
Cry1Ac GFSNS-SVSIIRA--PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 QATQSGSPSTVSNALPTCVWVTHRDVLDNTITANQITQLPLVKAYELSSGATVVKGPGFT
      500      510      520      530      540      550

```

```

      500      510      520      530      540      550
Cry1Ac GGDVLRNLSSGNNIQRNYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSII--FS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 GGDVIRRTNTGG---FGAIRVSVTGPLTQ-RYRIRFRYASTIDPFFVTRGGTTINNFR
      560      570      580      590      600      610

```

```

      560      570      580      590      600      610
Cry1Ac NTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEPFIPVTAT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 FTRTMNRGQESRYESYRTVEFTTPFNFTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNP
      620      630      640      650      660      670

```

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      620      630      640      650      660      670
Cry1Ac LEAEYNLERAQKAV-NALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDFECLDEKRELSE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|399 REAEEDLEAAKKAARQLNLFTRTRD-GLQVNVTDYQVDQAAANLVSCLSDBQYGHDKKMLLE
      680      690      700      710      720

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gi|622 HDKMKLMEAVRAAKRLSRERNLLQDPDFNEINSTENEGWKASNGIIIEGGFFPKGRVLQ
730 740 750 760 770 780

Cry1Ac LSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTG
730 740 750 760 770 780

gi|622 LASA-RENYPTYIYQKVDASVLKPYTRYRLDGFVKSSDLEIDLQHVKHLVKNVDPNL
790 800 810 820 830 840

Cry1Ac SLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC-AHSHHFLSLDIDVGTDLN
790 800 810 820 830 840

gi|622 ----VSDTYPDGSCRGVNRCDEQHQVDVQIDTEHHPMDCCEAAQTHEFSSYINTGDLNSS
850 860 870 880 890

Cry1Ac EDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIV
850 860 870 880 890 900

gi|622 VDQGIWVVLKVRTADGYATLGNLELVEVGPLSGESLEREQRDNKAWNAELGRERAETDRV
900 910 920 930 940 950

Cry1Ac YKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIPGVNAAIFEE
910 920 930 940 950 960

gi|622 YLAQAQAINHLFVDYDQQLNPEIGLAEINEASNLVESITGVYSYDVTLQIPGISYIETYE
960 970 980 990 1000 1010

Cry1Ac LEGRIFTAFSLYDARNVIKNGDFNNGLSWCNVKGVHDVEEQNQRSVLPVPEWEAEVQSQE
970 980 990 1000 1010 1020

gi|622 LSDRLQASLYTSRNVQNGDFDGLDSWNATTDASVQDQGNMH-FLVLSHWDAQVTQQ
1020 1030 1040 1050 1060 1070

Cry1Ac VRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCDNDYTV
1030 1040 1050 1060 1070 1080

gi|622 LRVNPNCKYVLRVTARKVGGDGYVTIRDGAHHRRETLTFNAC-----DYDV
1080 1090 1100 1110 1120

Cry1Ac NQEEYGGAYTSRNRGYNEAPSPADYASVYEKSYTDGRRNPCEFNRGYRDYTPLPVGY
1090 1100 1110 1120 1130 1140

gi|622 N-----GTYYVNDNT-----Y
1130

Cry1Ac VTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1150 1160 1170 1180

gi|622 ITKEVVFYPHTEHTWVEVSESEGFYIDSIELIETQE
1140 1150 1160

>>gi|71792198|emb|CAJ21126.1| unnamed protein product [B (1169 aa)
initn: 1790 initl: 432 opt: 1523 Z-score: 1785.3 bits: 342.3 E(): 1.6e-90
Smith-Waterman score: 2159; 35.791% identity (62.386% similar) in 1207 aa overlap
(20-1182:57-1169)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
10 20 30 40

gi|717 YPLTDDPNAGLQNMNYKEYLQMYGGDYTDPLINPNLSVSGKDKVIQVGINIVGRLLSFFGF
30 40 50 60 70 80

Cry1Ac -LLSEFVPGAGFVLGLVDI IWGIFGSPQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLS
50 60 70 80 90 100

gi|717 PFSSQWVTVYTY---LLNSLWPDDENSVWDAFMKRIEELIDQKISEAVKGRALDELDTGLQ
90 100 110 120 130 140

Cry1Ac NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPLLSV
110 120 130 140 150 160

gi|717 DNYNLYVEALDEWLNRP-NGARASLVSQRFNILDSLFTQFMPSPFGSGPSONYSTILLPV
150 160 170 180 190 200

Cry1Ac YVQAANLHLSVLRDVSVFGQWGFDAATIN---SRYNDLTRLIGNYTDHAVRWYNTGLER
170 180 190 200 210 220

gi|717 YAQAANLHLLLLKADDIYGARWLNQTDQFHSRQOSLTR---TYTNHCVTYNDGLAE
210 220 230 240 250

Cry1Ac VWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLENF-
230 240 250 260 270 280

gi|717 LRGTSVESWLKYHQYRREMTVTAMDVLVLPFYNNVRQYPNGANPQLTREVYTDPIVFNPP
260 270 280 290 300 310

Cry1Ac ---DGSFRGSAQGI EGS-----IRSPHLM DILNSIT IYTD AHRGEY-----
290 300 310

gi|717 EPPSGAFCESPFYNIRAARERLTFSQLENAIIRPPLRFERFQALGIYTG EARLNQNSAPT N
320 330 340 350 360 370

Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQGVYR--TLSS TLYRRPF N
320 330 340 350 360 370

gi|717 YWIGHFIRNTRLGDSSTTIIT--NYGTTNRLTN--FIPPTTSDVYQINSISSNLASALST
380 390 400 410 420 430

Cry1Ac I-GINNQQLSVLDGTEFAY-GTSSNLPSAVYRKS GTVDSLDEIPPQNNVPPRQGF SHRL
380 390 400 410 420 430

gi|717 LFGVTRAQFHYGSGI IWSYVQGNVLPQC---HQNYNSIEELPNQSD E-PTVRSYS HRL
440 450 460 470 480 490

Cry1Ac SHVSMFRSG--FSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFN GS-V
440 450 460 470 480 490

gi|717 SHITSFNFSVQLNPNVIVSLGNMPVYVWTHRSVDLNNITSDRITQLPAVKASTLGAGAI V
500 510 520 530 540 550

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNWNWG N
500 510 520 530 540 550

gi|717 VKGPGFTGGDVI RRTSVGD---FGTIRVSVT-GSLTQQYRIRFRYASTIDDFDFVIRGG
560 570 580 590 600

560 570 580 590 600



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420      430      440      450      460      470
Cry1Ac PPQNN--NVP-PRQ-GFSHRLSHVSMFRSGFSNSVSIIRAPMFWIHRSAEFNNIIASD
gi|153 PPTESLSDTPQPQNQVYTYSHRLDYATIHKANKSYGSGYI---PLLGWTHRSVDRQQTIYQ
470      480      490      500      510      520

480      490      500      510      520      530
Cry1Ac SITQIPAVKG-NFL--FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHFPSTSTR
gi|153 KITQIPAVKAFSFTESFNVNVIAGPGFTGGDLISL---GHLEN---IYMKLNVPNPQ-K
530      540      550      560      570

480      550      560      570      580
Cry1Ac YRVRVRYASVTP IHLNV----NWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT--
gi|153 FRVRIRYAASTTSYLQITGLSNLAQSDRFEQTY--SNENENMLMFENFYVELRNIFSV
580      590      600      610      620      630

590      600      610      620      630      640
Cry1Ac SSLGN-IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNLGLK
gi|153 APLENHQVSIQNYQNGFVVIDRIFIPVNTATYDAE-----NEAVNTTFTEGRN-ALQK
640      650      660      670      680

650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER
gi|153 YVTDYKVDQVDILVDCISGDLYPNEKRELQLLVKAKRLSYSRNLLDPTFDSINSSEEN
690      700      710      720      730      740

710      720      730      740      750      760
Cry1Ac GWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDS
gi|153 GWYGSNGVIGNGDFVQKGNLYLIFSGTNDTQYPTYLYQKIDESKLFKEYSRYKLGFISS
750      760      770      780      790      800

770      780      790      800      810      820
Cry1Ac QDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-
gi|153 QDLEAYVRRYDAKHRTL DV--SDNLLP--DILPENTCGEPSRCAAQYLDENPSSECSM
810      820      830      840      850      860

830      840      850      860      870      880
Cry1Ac RDGEKCAHSHHFLSDIDVGCSDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEA
gi|153 QDG--ILSDSHSFLNIDTSGGNHNENLGIWVLFKISTLEGYAKFGNLEVI EDGPGVIGEA
870      880      890      900      910

890      900      910      920      930      940
Cry1Ac LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKR
gi|153 LARVKRQTWKRNKLAQMTTETQAIYTRAKQALLNLFANAQDQSHLKDIDVTF AEIAAARKI
920      930      940      950      960      970

950      960      970      980      990      1000
Cry1Ac VHSIREAYLPELSVPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGH
gi|153 VQSIREVYMSWLSVPGVNHPI MTELSGRVQRAFQLYDVRNVVRNGRFLNGLSDWIVTSD
980      990      1000      1010      1020      1030

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1010      1020      1030      1040      1050      1060
Cry1Ac VDVEEQNNQRSLVLPVEWAEVSVQEVVRCVCPGRGYILLRVYTAYKEGEGCVTTHIEIENNTD
gi|153 VNVQEEENGM-VLVLNNWDAQVLRNVKLYQDRGYVLRVTARKIGIEEGYITITDEEGHTD
1040      1050      1060      1070      1080      1090

1070      1080      1090      1100      1110      1120
Cry1Ac ELKFSNCVVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSY
gi|153 QLRFTAC--EEIDASN-----YFIS-----
1100      1110

1130      1140      1150      1160      1170      1180
Cry1Ac TDGRRENPCFNRGRDYTPLPVGYVTKELEYFPETDKVMIEIGETEGTFIVDSVELLLM
gi|153 -----GYITKELEFFPDTEKVHIEIGETEGEFLVESIELFLM
1120      1130      1140      1150

Cry1Ac EE
gi|153 EELC

>>gi|61661422|gb|AA51301.1| Cry7 delta-endotoxin [Bacil (488 aa)
initn: 1613 init1: 621 opt: 1472 Z-score: 1730.8 bits: 331.0 E(): 1.7e-87
Smith-Waterman score: 1528; 50.000% identity (69.355% similar) in 558 aa overlap
(628-1182:1-486)

600      610      620      630      640      650
Cry1Ac GTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNLV
gi|616 AVNALFTA-GRHALQTDVTDYKVDQVSIIV
10 20

660      670      680      690      700      710
Cry1Ac TYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD
gi|616 DCVSGELYPNEKRELLSLVKYAKRLSYSRNLLDPTFDSINSDDKNGWYGSNGIAISSGN
30 40 50 60 70 80

720      730      740      750      760      770
Cry1Ac DVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKH
gi|616 FVFKGNLYLIFSGTNDQYPTYLYQKIDESKLFKEYTRYKLRGFIENSQDLEAYVIRYDAKH
90 100 110 120 130 140

780      790      800      810      820      830
Cry1Ac ETVNVPGTGLWPLSAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSHHFS
gi|616 ETFDV--SNLLP--DISPVNACGEPNRCVALQYLDENPRLECSSVQDG--ILSDSHSFS
150 160 170 180 190 200

840      850      860      870      880      890
Cry1Ac LDIDVGCSDLNEDLGVVWVFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
gi|616 LNINTGSIDFNESVGIWVLFKISTPEGYAKFGNLEVIENGPVIGALARVKRQETKWRNQ
210 220 230 240 250 260

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          900      910      920      930      940      950
Cry1Ac REKLEWETNIVVKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSV
gi|616 LTQLRTEYTAQIYTRAKQALDNLNFANAQDShLKIGTTFAAIVAARKIVQSIREAYMSWLSV
          270      280      290      300      310      320

          960      970      980      990      1000     1010
Cry1Ac IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCNVKGVHDVVEEQNNQRSVLV
gi|616 VPGVNYPIFTELTERVQQAFQLYDVRNVVRNGQFLSGLSDWIVTPDVKVQEDNGN-NVLV
          330      340      350      360      370      380

          1020     1030     1040     1050     1060     1070
Cry1Ac VPWEAEVVSQEVVRCVPCGRGYLLRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEYIP
gi|616 LSNRDAQVLQCLKLYQDRGYLLRVYARKEGLGEGYVTTITDEEGNTDQLTFGAC--EEIDA
          390      400      410      420      430      440

          1080     1090     1100     1110     1120     1130
Cry1Ac NNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDDRRENPCFENRG
gi|616 SN-----AFIS-----

          1140     1150     1160     1170     1180
Cry1Ac YRDYTPLVPGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEEE
gi|616 -----TGYITKELEFFPDTEKVRIEIGETEGTFQVESVELFLMEELC
          450      460      470      480

>>gi|54112021|gb|AAV28716.1| Cry9Bb delta-endotoxin [Bac (1163 aa)
  initn: 1819 initl: 442 opt: 1467 Z-score: 1719.3 bits: 330.1 E(): 7.6e-87
Smith-Waterman score: 2113; 34.146% identity (61.463% similar) in 1230 aa overlap
(2-1182:25-1163)

          10      20      30
Cry1Ac          CMQ-AMDNNPNINECIPYNCLNSPEVEVLGGERIETG
gi|541 MNRNNQNEYEVIDTSTCGCPSGDVMQYPLANDPNAAL---QNMNYKEYLQMYGGDYADAF
          10      20      30      40      50

          40      50      60      70      80
Cry1Ac YTPIDISLSLTQ----FLLSEFVPGA--GFVLGLVDIIWIGIFGSPQ----WDAFLVQIE
gi|541 INPGNVRTGLQGTGIDIVALLVGTGLGAVGGILTLGLSLTFGLFVWSPNDQAVWEAFIEQME
          60      70      80      90      100     110

          90      100     110     120     130     140
Cry1Ac QLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSA
gi|541 ELIEQRISDQVVRTALDNLGTGIQNYNQYLLAFEWEAPNS--VRSNLVLQRFENLHAL
          120     130     140     150     160     170

          150     160     170     180     190     200
Cry1Ac LTTAIPLFAV---QNYQVPLLSVYVQAANLHLSVLRDVSFVQRWGFDAATINSRYNDL
gi|541 FVSSMPSFGSPGSGRFEAQLLLVYAQAANLHLLLRDAEYIYGARWGLRESQIQLYFDEL
          180     190     200     210     220     230

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          210      220      230      240      250      260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTYIP
gi|541 QNNTRDYTNHCVNAYNNGLEQVRGTNAASWLKYHQFRRETTLTAMDVLVALFPYYNLRQYP
          240     250     260     270     280     290

          270      280      290      300
Cry1Ac IRTVSQLTREIYTNPVLENFDGSRFGSA-----QGIEGS-IRSPHLMIDLN
gi|541 IAVNPQLTREYVTDPLGVPFEESSNPSEIRCSRWDQTSAMTFSNLENALVRPPLHFDITR
          300     310     320     330     340     350

          310      320      330      340      350      360
Cry1Ac SITIYDADR--GEY--WSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAVQLGQ
gi|541 NLRITYGTFRVNNMNFIEGWIGHSVTNNRLGIS-TEFTR----NYGITPIINSYFANG
          360     370     380     390     400     410

          370      380      390      400      410
Cry1Ac GVYR--TSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSVDLSDEIP
gi|541 DVYQINTRSNTSL----IAFENAPLFGITRAQFQPGGTYSVTQRLLCEQNYNSTDEL
          420     430     440     450     460

          420     430     440     450     460     470
Cry1Ac PQNNVPPRQGFSHRLSHV-SMFRSGFSNSSVSIIRA--PMFSWIHRSAEFNNIIASDSI
gi|541 SLDPDEPISRSYSHRLSHITSYLHRVFTIDGNNIYSGNLPTVYVWTHRVDLNTITADRI
          470     480     490     500     510     520

          480     490     500     510     520     530
Cry1Ac TQIPAVKGNFLPFGSVISGPGFTGGDLVRLNSSGNNIQNGYIEVPIHPSTSTRYRVRV
gi|541 THLPLIKSNVQRSGLPVKGPGFTGGDLVLRSSSDADVS---IIGVSAGAPLTQ-QYRIRV
          530     540     550     560     570     580

          540     550     560     570     580     590
Cry1Ac RYASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYPESANAFT----SSLGNI
gi|541 RYASNVDVTIRFVRHNTSHLLG-IGTLRMTNSGSESRYESYRTVDVITNFRLNSSESEQI
          590     600     610     620     630     640

          600     610     620     630     640
Cry1Ac -VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|541 RIVTEGLRANGQLYLDSEFIPINPTREAEEDLEAAKAVASLFTTRTD-GLQANVTDYQ
          650     660     670     680     690

          650     660     670     680     690     700
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|541 VDRAANLVCLSDQYAHDKMLLEAVRAAKRLSRERNLLQDPDFNEINSTEDSGWKTSN
          700     710     720     730     740     750

          710     720     730     740     750     760
Cry1Ac GITIQQGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIY
gi|541 GIISBGGPFFKGRALQLASA-RENYPTYIYQKVDSSMLKPYTRYKLDGFVQSSQDLEIE

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gi|293  ETKQQLKARKAVNHLFTDGSKKALKEGTTDYEIDQAAANVVDCISDE-CGHEKMILLDEV
      680      690      700      710      720      730
Cry1Ac  KHAKRLSDERNLLQDSNFKDINRQPER--GWGGSTGITIQQGDDVFKENYVTLSTGTFD--
      680      690      700      710      720      730
gi|293  KYAKQLSQARNLLNGNFDLDPALERENPWKTSPhVTIRQDNPIFKGHYLSMAGANDIE
      740      750      760      770      780      790
Cry1Ac  ---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAKHETV-NVPGTGSLS
      740      750      760      770      780
gi|293  ATNDTFPTYVYQKIDEAKLKPTRYKVRGFGVSSKALELLVTRYNEEVDAILDVPDN---
      800      810      820      830      840
Cry1Ac  WPLSAQSPIGKCGEPNRCAPHL-----EWNPD-----DCSC-----RDGEKCA
      790      800      810      820
gi|293  IP-HAPTPV--CGEFDRCCKPYSYPLLPECNPEFINQMPPSCHHNQMVYNNRKHRC-
      850      860      870      880      890      900
Cry1Ac  HSHHFSLDIDVGGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
      830      840      850      860      870      880
gi|293  HQAHQFEFHIDTGTIDLVDLGIWVIFKICATDGYASLDDLEVIIEGALGVEALELVKRR
      910      920      930      940      950      960
Cry1Ac  EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREA
      890      900      910      920      930      940
gi|293  EKKWRHQEKQCHSQTKHKYDAAKHAVMALFTNTRYEKLFKFTTISNILYADHLVQSIPIVY
      970      980      990      1000     1010     1020
Cry1Ac  YLPELSVIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVVEEQN
      950      960      970      980      990      1000
gi|293  YNKYVPEVPGMNYELYTELNTLVQNAFYLYDQRNLIKNGRFSNGLMYQATPHARVE-QE
      1030     1040     1050     1060     1070     1080
Cry1Ac  NQRSVLVPEWEAEVSEVVRVCPGRGYILRVTAAYKEGYEGCVTIIHEIENNTDELKFSNC
      1010     1020     1030     1040     1050     1060
gi|293  YEKSVLVLPNWDANVSQDLCEIHNRYVLRVTARKEDPGAGNVTFSDCANHVDKLSFTSC
      1090     1100     1110     1120     1130     1140
Cry1Ac  -VEEEIYP----NNTVTCNDY----TVNQEEYG--GAYTSRNRGY-----NEAPSVP-
      1070     1080     1090     1100
gi|293  DIATNAVPGAQANDPAAGVAYGQQCQIDRVFYQGSYRTDGTNGMPYQSGNRRADGVPY
      1150     1160     1170     1180     1190     1200
Cry1Ac  --ADYAS-----VYEEKSY-TDG-----RRENPC-----EFN
      1110     1120     1130
gi|293  RQSGYGTGVAHDQPGYRADGVAYEQSGYRADGVTYDQSANQTRKYHGCHTVGLPHPEHG
      1210     1220     1230     1240     1250     1260
Cry1Ac  RGYRDYTP--LPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1140     1150     1160     1170     1180

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      1270     1280     1290     1300     1310
gi|293  CCYPDRVSDGQQLAYVTKSIDLFPDTPDKVRIDIGETEGNFRVESVELICMEK
>>gi|111927189|gb|ABH71841.1| Sequence 4 from patent US (1316 aa)
      initn: 2039 initl: 675 opt: 1466 Z-score: 1717.3 bits: 329.9 E(): 9.8e-87
      Smith-Waterman score: 2226; 35.725% identity (62.402% similar) in 1282 aa overlap
      (11-1182:74-1316)
      10      20      30      40
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPI
gi|111  SSNALLYSPNKYPYATDPNVIAEGGSYKNWLDMCTGTGDRSPETAASKGAVSAAIT--
      50      60      70      80      90      100
Cry1Ac  DISLSLTQFLLSEFVPGAG-FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEEFARNQ
      50      60      70      80      90
gi|111  -ISTGLLGLLVFPASQIGAFYTFLLNTLWPA-SNTQWEQFIAHVEELINAKLTDHVRNS
      110     120     130     140     150
Cry1Ac  AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
      100     110     120     130     140     150
gi|111  ALTKLNGLRNNIEIYNEALIVWKQDPNNSKDKDDVRSKFFVGLNSQFEEYIPQFKEGFEV
      160     170     180     190     200     210
Cry1Ac  PLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
      160     170     180     190     200     210
gi|111  QLLTIYAQSANLHLLLRDSSLYGASWGFQAATIDNNYNRQIRKTAEYANHCTTWTYQTGL
      220     230     240     250     260     270
Cry1Ac  ERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVPLEN
      220     230     240     250     260     270
gi|111  QRLQGTASSWLSYHRFRREMTLTVLDICALFSNYDARSYPLEVRGELTREIYTDVPVAPG
      280     290     300     310     320     330
Cry1Ac  FDGSFRG-SAQGIEG-SIRSPHLM-DILNSITYTDAHRG---EYYWSGHQIMASPVGF
      280     290     300     310     320     330
gi|111  TNWIDRAPSFABEINLVIRAPRTVTVWISGDLIVYTGRLYGYTGNDYWAHRL--DFLET
      340     350     360     370     380     390
Cry1Ac  SGPEFTFPYLGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNOQLSVLDGTGF
      340     350     360     370     380     390
gi|111  NGRYFEGPTYGSTINISRTSDSIPMN-SIDVYSTTVTVGSAWPTGGFV--LGVASARFF
      400     410     420     430     440     450
Cry1Ac  AYGTSNL-----PSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSN
      400     410     420     430     440
gi|111  SKSPSTGLLGERVYQNPVYFSSSTLTF--NLPQVDQDTPAADYSHKLSGITAFRTGL-N
      460     470     480     490     500     510
Cry1Ac  SSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLN
      450     460     470     480     490     500

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gi|111 GTV-----PVFGRYSATVSRDNRIEPDKITQIPAVKSNSLDNCVVRGTGFGGDWLKTS
          520      530      540      550      560
Cry1Ac SSGNNIQNRGYIEVP IHFPSTSTR----YRVRVRYASVTPIHNLVNWGNSSIFSNTVPAT
          510      520      530      540      550      560
gi|111 -----YLSVVFV-LTITSSRAGQSYRIRVRYAAAVDLIMSI-YSNDFPISKGISLT
          570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLGNIVGVRNFGSFTAGVVIDRFEFIPVTATL---
          570      580      590      600      610
gi|111 KSMPLPLETVPYEAFFKADFGVFTTATANKRYTFQFHGTGGAAIIDRIEFVPIEGSLFEY
          620      630      640      650      660      670
Cry1Ac EAENLNERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
          620      630      640      650      660      670
gi|111 ETKQOLEKARKAVNHLFTDGSKKALKEGTTDYEIDQAANVVDICISDE-CGHEKMILLDEV
          680      690      700      710      720      730
Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPER--GWGGSTGITIQQGDDVFKENYVTLSGTFD--
          680      690      700      710      720      730
gi|111 KYAKQLSQARNLLNGNFDDLYPALERENPWKTSPhVTIRQDNPIFKGHYLSMAGANDIE
          740      750      760      770      780      790
Cry1Ac ---ECYPTYLYQKIDESKLKAFTRYQLRGYIEDSDLEIYSIRYNAKHETV-NVPGTGSLS
          740      750      760      770      780
gi|111 ATNDTFPTYVYQKIDEAKLKPTRYKVRGVFGSSKALELLVTRYNEEVDAILDVPDN---
          800      810      820      830      840
Cry1Ac WPLSAQSPIGKCGEPNRCAPHL-----EWNPD-----DCSC-----RDGEKCA
          790      800      810      820
gi|111 IP-HAPTpv--CGEFDRCKPYSYPLLPECNPEFINQMPPSSCHHNQMVYDNNRKHRC-
          850      860      870      880      890      900
Cry1Ac HSHHFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRA
          830      840      850      860      870      880
gi|111 HQAHQFEFHIDTGTIDLVEDLGIWVIFKICATDGYASLDLDEVIEEGALGVEALELVKRR
          910      920      930      940      950      960
Cry1Ac EKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREA
          890      900      910      920      930      940
gi|111 EKKWRHQEQHCSQTKHKYDAKHAVMALFTNTRYEKLFETTISNILYADHLVQSIPYV
          970      980      990      1000      1010      1020
Cry1Ac YLPELSVIPGVNAAIFEELEGRIFTFASLYDARNVIKNGDFNNGLSVCNVKGVHDVVEEQN
          950      960      970      980      990      1000
gi|111 YNKYVPEVPGMNYELYTELNTLVQNAFYLYDQRNLKNGRFNGLMYWQATPHARVE-QE
          1030      1040      1050      1060      1070      1080
Cry1Ac
          1010      1020      1030      1040      1050      1060

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Cry1Ac NQRSVLVPEWEAEVSEQEVRVCPGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNC
          1090      1100      1110      1120      1130      1140
gi|111 YEKSVLVLPNWDANVSDQLCIEHNRGYVLRVTARKEDPGAGNVTFSDCANHVDKLSFTSC
          1070      1080      1090      1100
Cry1Ac -VEEIIYP----NNTVTCNDY----TVNQEEYG--GAYTSRRNGY-----NEAPSVP-
          1150      1160      1170      1180      1190      1200
gi|111 DIATNAVPGAQANDPAAGVAYGQQGCQIDRVYPYQSGYRTDGTNGMPYQSGNRRADGVPY
          1110      1120      1130
Cry1Ac --ADYAS-----VYEEKSY-TDG-----RRENPC-----EFN
          1210      1220      1230      1240      1250      1260
gi|111 RQSGYGTGVAHDQPGYRADGVAYEQSGYRADGVTYDQSANQTRKYHGCHTVGLPHPEHG
          1140      1150      1160      1170      1180
Cry1Ac RGYRDYTP--LPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
          1270      1280      1290      1300      1310
gi|111 CCYPDRVSDGQQLAYVTKSIDLFPDTRKVIDIGETEGNFRVSVELICMEK

>>gi|46409863|gb|AAS93799.1| cry1 type crystal protein [ (782 aa)
initn: 2775 initl: 1142 opt: 1453 Z-score: 1705.3 bits: 326.9 E(): 4.6e-86
Smith-Waterman score: 2838; 56.629% identity (75.589% similar) in 807 aa overlap
(13-805:2-782)

          10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          10      20      30      40
gi|464 MQCVPYNCLSNPEEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
          70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIQFQSDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFRE
          50      60      70      80      90      100
gi|464 ISGLLDKIWALRPSDWELFLEQIEQLIDRIERTVRAKAIAELEGLGRSYQLYGEAFKE
          130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSVLRDVS
          110      120      130      140      150      160
gi|464 WEKTPDNTAARSVTERFRIIDAQIEANIPSRVSGFVPLLVYTAANLHLLLRDVS
          190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFREL
          170      180      190      200      210      220
gi|464 VFGERWGLTTTNDIYNRQVNRIGEYSKHCVDTYKTELERLGFRIAQWRIYNQFREL
          250      260      270      280      290
Cry1Ac TLTVLDIVSLFPNYSRTPYIRTVSQTREIYTNVLENFDGSRGFRS---AQGIEGSIRS
          230      240      250      260      270      280
gi|464 TLTVLDIVAVFPNYSRTPYIRTVSQTREIYTNVLENFDGSRGFRS---AQGIEGSIRS
          300      310      320      330      340      350

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Cry1Ac PHLMDILNSITTYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ
gi|464 PHLMDFFNSMIMYTSNRRREHYWSGLEMTATNT--EGHQRSFPLAGTIGNSAPPVTVRNN
290 300 310 320 330 340

360 370 380 390 400 410
Cry1Ac LGQGVYRTLSSTLYRRPFNIGINNQQLSVLD--GTEFAYG--TSSNLPASVYRKSQTVDS
gi|464 -GEGYRILSDTFYSAPF-LG----TSVLGSRGEEFASFASNTTSLPSTIYRNRGTVDS
350 360 370 380 390 400

420 430 440 450 460 470
Cry1Ac LDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNVSIVIRAPMFSWIHRSAEFNIIASD
gi|464 LVSIPPQDYSPVPHRGSYHLLSHVTM----RNSS-----PIFHWTHRSATPRNTIDPD
410 420 430 440

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYV
gi|464 SITQIPAVKGAIFNSPVITGPGHTGGDIIRFNP--NTQNN--IRIPFH-SNAVQRYRI
450 460 470 480 490 500

540 550 560 570 580
Cry1Ac RVRYAS---VTPIHLNVNWGNSSIFSNT-VPATATSLDNLQSSDFGFYFESANAFTSSL-
gi|464 RMRVAAEADCILESGVNIITGAGVTFRPIPIKATMTPGSPLTYYSFYADLNINLTAPIR
510 520 530 540 550 560

590 600 610 620 630 640
Cry1Ac -GNIVGVNRFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVT
gi|464 PNNFVSIRRSNQPGLNLYIDRIEFIPIDPIREAEHDLERAQKAVNALFTSSNQLGLKTDVVT
570 580 590 600 610 620

650 660 670 680 690 700
Cry1Ac DYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG
gi|464 DYHIDQVSNLVACLSDKFLDEKRELSEKVKHAKRLSDERNLLQDQNFTEGINRQVDRGWR
630 640 650 660 670 680

710 720 730 740 750 760
Cry1Ac GSTGTIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDL
gi|464 GSTDITIQGGNDVFKENYVTLPGTFDECYPTYLYQKIDESKLFKAFTRYELRGIYIEDSQDL
690 700 710 720 730 740

770 780 790 800 810 820
Cry1Ac EIYSIRYNAKHETLVNVPGTGSLWPLSAQSPIKGCPEPNRCAPHLEWNPDLDCSCRDGEKC
gi|464 EVYLIRYNAKHETLVNVPGTGSLWPLAAESSIGRCPEPNR
750 760 770 780

830 840 850 860 870 880
Cry1Ac AHSHHFLSLDIDVGCTDLNEDLGWVWVIFIKITQDGHARLGNLEFLEEKPLVGEALARVKR

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>>gi|4574730|gb|AAD24189.1|AF132928_1 Cry28Aa1 delta-end (1109 aa)
initn: 1418 initl: 541 opt: 1450 Z-score: 1699.5 bits: 326.4 E(): 9.6e-86

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Smith-Waterman score: 1875; 34.136% identity (59.635% similar) in 1204 aa overlap
(22-1182:23-1109)

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10 20 30 40 50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFV-PGA
gi|457 MAQTYKIGIVQSTEVNSESIFFNPEVDSSDTVAVVSAGIVV-VGTLTAF--ASFVNPV
10 20 30 40 50

60 70 80 90 100 110
Cry1Ac GFV-LG-LVDIIWGI--FGPSQ-WDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQI
gi|457 VLISFGTLAPLVLPDPEEDPKKIWSQFMKHGEDLLNQTISTAVKEIALAHLNGFKVDLTY
60 70 80 90 100 110

120 130 140 150 160 170
Cry1Ac YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHL
gi|457 YERAFNDWKRNP SANTARL-VSQRFENAHFNFSNMPQLQPLTYDITLLSCYTEANLHL
120 130 140 150 160 170

180 190 200 210 220
Cry1Ac SVLRDVSFVQQRWGFDA-----TINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|457 NLLHQGVQFADQWNAQPHSPMLKSSGTYDELLVYIEKYINXCTKYHKLNLHKESEK
180 190 200 210 220 230

230 240 250 260 270 280
Cry1Ac RDWIRYNQFRELTLTVLDIVSLFPNYSRTYPIRTVSQTLTREIYTNVLENFDDGSGFRGS
gi|457 ITWDAYNTYRREMTLIVLDLVATFPFYDIRRFPGRVLELTVREYVTS-----
240 250 260 270 280

290 300 310 320 330
Cry1Ac AQGIEGSIRSPHLMDILNSITTYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGN
gi|457 ---LDHLTRPPGLFTWLSDIELYTESVAEGDYLSG--IRESKY-YTGNQF-PTMKNIYGN
290 300 310 320 330

350 360 370 380 390 400
Cry1Ac AAPQQRIVAQLGQGVYRTLSSTLYRRPFN-IGINNQQLSVLDGTEFAYGTSSNLPASVYR
gi|457 TNRLSKQLITLLPGFEMTHLSI--NRPFQTIAGINKLYSLIQKIVFTTFKNDNE---YQ
340 350 360 370 380 390

410 420 430 440 450
Cry1Ac KSGTVDSLDEIPPQNNVPPRQ-----FSHRLSHVSMF--RSGFSNVSIVIRAPMFS
gi|457 KNFNVNQNNE-PQETTNYPNDYGGNSQKFKHNLSHFPLI IHKLEFAEYFHSIF---ALG
400 410 420 430 440

460 470 480 490 500 510
Cry1Ac WIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYI
gi|457 WTHNSVNSQLISESVSTQIPLVKAYEVTNNSVIRGPGFTGGDLIELRDK-CSIKCKA--
450 460 470 480 490 500

520 530 540 550 560 570
Cry1Ac EVPIHFPSTSTRYRVRVYASVTPPIHLNVNWGNSSIFSNTVPATAT-----SLDNLQSS

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gi|457 -----SSLKKYAIISLFYAANNAIAVSIIDVGDSDGAVLLQPTFSRKGNNNFTIQDLNFK
          510      520      530      540      550
Cry1Ac  580      590      600      610      620
DFGYFESANAFTSSLGNIVGV--RNFSGTAGVI--IDRFEPFIPVTATLEAEYNLERAQK
gi|457  DFQYHTLLVDIELPESEEIHIHLKREDDYEEGVILLIDKLEFKPIDENYTNEMNLEKAKK
          560      570      580      590      600      610
Cry1Ac  630      640      650      660      670      680
AVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERN
gi|457  AVNVLFINATN-ALKMDVTDYHIDQVANLVEICISDDLYAKEKIKFTPCIKFAKQLSQARN
          620      630      640      650      660      670
Cry1Ac  690      700      710      720      730      740
LLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESK
gi|457  LLSDFNFNNLN--AENSWTANTGVTIIEGDPLYKGRAIQLSAARDENFPPTYLYQKIDESL
          680      690      700      710      720      730
Cry1Ac  750      760      770      780      790      800
LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKC-----
gi|457  LKPYTRYQLRGFVEGSDLELDLVRYGATDIVMNVPG--DLEILSYSAPINPCEEIETRL
          740      750      760      770      780      790
Cry1Ac  810      820      830      840      850
---GEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVGTDLNEDLGWVWIFKI
gi|457  DTTCCGALDRCKQSNVNSAADVR---PDQVNGDPHAFSFDITGTDDNRRNLGIWIFKI
          800      810      820      830      840
Cry1Ac  860      870      880      890      900      910
KTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDAL
gi|457  ATPDGYATFGNLELIELGPLSGEALAQVQRKEQKWGNNTQKREEAAKLYAAAKQTINQL
          850      860      870      880      890      900
Cry1Ac  920      930      940      950      960      970
FVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSL
gi|457  FADSGTKLRFDTFESNILSADKLVYKIRDVYSEVLVPIGLNYDLFMELENRIQNAIDL
          910      920      930      940      950      960
Cry1Ac  980      990      1000     1010     1020     1030
YDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQRSVLVPEWAEVSEQEVRVCPGRGYIL
gi|457  YDARNTVTNGEPRNGLANWMASSNTEVR-QIQAHPCWYSLGWNAQVAQSLNVKPDHGYVL
          970      980      990      1000     1010     1020
Cry1Ac  1040     1050     1060     1070     1080     1090
RVTAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNNVTVCNDYTVNQEEYGGAYTS
gi|457  RVTAKKEGIGNGYVTILDCANHIDTLTFSSC-----D-----SGFTTS
          1030     1040     1050     1060
Cry1Ac  1100     1110     1120     1130     1140     1150

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Cry1Ac  RNRGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYRDTPLPVGYVTKELEYFPET
          :          :          :          :          :          :          :
gi|457  SN-----ELAA-----YVTKTLEIFPDT
          1070          1080
Cry1Ac  1160     1170     1180
DKVWIEIGETEGTFIVDSVELLMEE
gi|457  DQIRIEIGETRSTFYVESVDLIRMED
          1090     1100
>>gi|161784134|gb|ABX79555.1| crystal Cry7-like protein (490 aa)
  initn: 1377 init1: 612 opt: 1420 Z-score: 1669.4 bits: 319.6 E(): 4.6e-84
Smith-Waterman score: 1434; 47.585% identity (67.263% similar) in 559 aa overlap
(628-1182:1-486)
Cry1Ac  600     610     620     630     640     650
GTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLV
gi|161  AVNALFTE-GRNALQKHVTDYKVDQVSIIV
          10      20
Cry1Ac  660     670     680     690     700     710
TYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD
gi|161  DCISGLDLYPNEKRELQNLVKYAKRLSYSRNLDDPTFDCINSSENGWYGSNGVIGNGD
          30      40      50      60      70      80
Cry1Ac  720     730     740     750     760     770
DVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKH
gi|161  FVFKGNLYLIFSQNTDQYPTYLYQKIDESKLFKEYTRYKLGKFISSQDLEAYVIRYDAKH
          90      100     110     120     130     140
Cry1Ac  780     790     800     810     820     830
ETVNVPGTGLWPLSAQSPIGKCGEPNRCAP--HLEWNPDLDCSC-RDGEKCAHSHHFS
gi|161  RTLDV--SDNLLP--DILPENTCGEPNRCAAQYLDENPSSECSMQDG--ILSDSHSSS
          150     160     170     180     190     200
Cry1Ac  840     850     860     870     880     890
LDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDK
gi|161  LNIDTGSINHNNENLGIWVWFKIPTLEGYAKFGNLEVEDGDPVIGEALARVKRQETKWRNK
          210     220     230     240     250     260
Cry1Ac  900     910     920     930     940     950
REKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSV
gi|161  LAQMTTETQAIYTRAKQALEYLFANAQDLSHLKRNVTFAEIAAARKIVQSIREAYMSWLSV
          270     280     290     300     310     320
Cry1Ac  960     970     980     990     1000     1010
IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQRSVLV
gi|161  VPGVNHPIFTELSGRVQRAFQLYDVRNVVNRGRFLNGLSDWIVTSDVKVQVEENG--NLVL
          330     340     350     360     370     380
Cry1Ac  1020     1030     1040     1050     1060     1070

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Cry1Ac VPEWEAEVSVQEVRCVPCGRGYILRVVTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYP
gi|161 LNNWDAQVLQNVKLYQDRGYILHVTARKIGIGEGYITITDEBEGHTDQLRFTAC--EEDIDA
390 400 410 420 430 440

Cry1Ac 1080 1090 1100 1110 1120 1130
NNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFENRG
gi|161 SN-----AFIS-----

Cry1Ac 1140 1150 1160 1170 1180
YRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTIFVDSV-ELLMEE
gi|161 -----GYITKELEFFPDTEKWHIEIGGTEGIFLVEGILEVFLRLLESYVI
450 460 470 480 490

>>gi|71793184|emb|CAJ21051.1| unnamed protein product [B (1206 aa)
initn: 1955 initl: 799 opt: 1411 Z-score: 1653.0 bits: 317.9 E(): 3.8e-83
Smith-Waterman score: 2602; 40.536% identity (67.672% similar) in 1194 aa overlap
(22-1179:59-1203)

Cry1Ac 10 20 30 40 50
CMQAMDNNPNINECIPYNCLSNFEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160 170
YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
gi|717 YQLYLTALEEWENPNRSRALRDVRNRFEILDLSLFTQYMPSPFRVTNFVEVFLTVYAMAAN
150 160 170 180 190 200

Cry1Ac 180 190 200 210 220 230
LHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
gi|717 LHLLLLK DASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS AKW
210 220 230 240 250 260

Cry1Ac 240 250 260 270 280
IRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGS
gi|717 VDNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVTYDPLGAVNVSSIGS WYDK
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
AQG---IEGS-IRSPHLM DILNSITITYTDAH-----RGEYYWSGHQIMASPVGFSGPEFT
gi|717 APSFGVIESSVIRPPHFVDYITGLTVYTSRSISSARIYRHWAGHQISYHRVS-RGSNLQ
330 340 350 360 370 380

340 350 360 370 380

Cry1Ac FPLYGTMGNAAPQQRIVAQQLGGVYRTLSSSTL-----YRRPFNIGINNQQLSVLDG
gi|717 -QMYGTRNQNLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEFFMVNQ
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
TEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSV
gi|717 LNNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--TGNIT
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
SIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNS
gi|717 GLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHTGGDLLQYNR
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
SGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHLMNVWNGSSIFSNTPATATSLD
gi|717 STGSGVGLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPGE
560 570 580 590 600 610

Cry1Ac 570 580 590 600 610 620
NLQSSDFGYFESAN----AFTSSLG--NIVGVRNFSGTAGVI-IDRFEPVPTATLEAEY
gi|717 DLTSTKTFKVADAITTLNLATDSSLALKHNLGEPNSTLSGIVYVDRIEFIPVDETYEAEQ
620 630 640 650 660 670

Cry1Ac 630 640 650 660 670 680
NLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVHAK
gi|717 DLEAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECLSDDLYPNKRLFLDAVREAK
680 690 700 710 720

Cry1Ac 690 700 710 720 730
RLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFD---ECYPT
gi|717 RLSEARNLLQDDPDFQEIIN--GENGWASTGIEVIEGDALFKGRYLRLPGAREIDTETYPT
730 740 750 760 770 780

Cry1Ac 740 750 760 770 780 790
YLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWPLSAQSPI
gi|717 YLYQKVEEGVLPKPYTRYRLRGFVGSQGLEIFITIRHQTNRIVKNVPD---DLLP--DVSPV
790 800 810 820 830 840

Cry1Ac 800 810 820 830 840 850
GKCGEPNRCAPHEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLGVVWIFKIK
gi|717 NSDGSINRCSEQKYVNSRLEVENRSGE-----AHEFSIPIDTGEIDYENENAGIWWGFKIT
850 860 870 880 890

Cry1Ac 860 870 880 890 900 910
TQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALF
gi|717 DPEGYATLGNLELVEEGPLSGDALERLQREEQQWKIQMTRRREEDDRRYMASKQAVDRLY
900 910 920 930 940 950

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920      930      940      950      960      970
Cry1Ac VNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLY
gi|717 ADYQDQQLNPDVEITDLTAAQDLIQSIPVYVYEMFPEIPGMNYTKFTELTDRLQQAWSLY
960      970      980      990      1000     1010

980      990      1000     1010     1020     1030
Cry1Ac DARNVIKNGDFNGLSCWNVKGHVDVEEQNNQORSVLVPEWAEVSEQEVRVCPGRGYILR
gi|717 DQRNAIPNGDFRNGLSNWNATPGVEVQ-QINHTSVLVIPNWDEQVSQQFTVQPQNRQYVLR
1020     1030     1040     1050     1060     1070

1040     1050     1060     1070     1080     1090
Cry1Ac VTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEE--IYPNNTVTCDNYTVNQEEYGGAYT
gi|717 VTARKEGVNGYVSIIRDGGNQETELTFSASDYDTNGMYNTQVSNITNGYNTNNA-YNTQAS
1080     1090     1100     1110     1120     1130

1100     1110     1120     1130     1140     1150
Cry1Ac SRNRGYNEAPSPADYASVYEKSYTDGRRNPCEFNRGYRDTPLPVGYVTKLELYFPE
gi|717 STN-GYN-ANNM---YNT---QASNTNGYNTNSV-----YNDQT---GYITKTVTFIPY
1140     1150     1160     1170

1160     1170     1180
Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE
gi|717 TDQMWIEMSETEGTFYIESVELIVDVE
1180     1190     1200

>>gi|115828938|gb|ABJ38777.1| Sequence 2 from patent US (1206 aa)
  initn: 1955 initl: 799 opt: 1411 Z-score: 1653.0 bits: 317.9 E(): 3.8e-83
Smith-Waterman score: 2602; 40.536% identity (67.672% similar) in 1194 aa overlap
(22-1179:59-1203)

10      20      30      40      50
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLL
gi|115 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPPEVLVSGDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
gi|115 VPFVGPVLSYLTQLIDILWPSGEKSQWEIFMQVEELINQKIAEYARNKALSELEGLGNN
90      100     110     120     130     140

120     130     140     150     160     170
Cry1Ac YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
gi|115 YQLYLTALEEWEENPGSRALRDVRRNRFIELDSLFTQYMPSFRVNTFVPPFLTVMYAMAAN
150     160     170     180     190     200

180     190     200     210     220     230
Cry1Ac LHLVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
gi|115 LHLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCWKWYETGLAKLKGTSKQW
210     220     230     240     250     260

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240      250      260      270      280
Cry1Ac IRYNQFRRELTTLTVLIDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFD--GSFRGS
gi|115 VDYNQFRREMTLAVLDVVALFPNYSRTYPIRTVSQLTREIYTNPVLNFD--GSFRGS
270     280     290     300     310     320

290     300     310     320     330
Cry1Ac AQG---IEGS-IRSPHLMIDLNSITITYTDAH-----RGEYIYWSGHQIMASPVGFSGPEFT
gi|115 APSFGVIESSVIRPPHVFYDITGLTVYVYQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ
330     340     350     360     370     380

340     350     360     370     380
Cry1Ac FPLYGTMGNAAPQQRIVAVLQGGVYRTLSSTL-----YRRPFNIGINNQQLSVLDG
gi|115 -QMYGTNQNHLSTSTF-DFTNYDIYKTLKSDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQ
390     400     410     420     430     440

390     400     410     420     430     440
Cry1Ac TEFAYGTSSNLPSAVYRKSGETVDSLDEIIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSV
gi|115 LNNTRKTLKYNPVSKDIIASTRSELELPPETSQDPNYESYSHRLCHITSIPA--TGNTT
450     460     470     480     490

450     460     470     480     490     500
Cry1Ac SIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNS
gi|115 GLV--PVFVSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPFV-PVVKGPHTGGDLLQYNR
500     510     520     530     540     550

510     520     530     540     550     560
Cry1Ac SGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTPATATSLD
gi|115 STGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVNV--DAQI---QMPKTMNPGGE
560     570     580     590     600     610

570     580     590     600     610     620
Cry1Ac NLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAEY
gi|115 DLTSKTFKVADAITTLNLATDSSLALKHNLGDPNSTLSGIVYVDRIEFIPVDETYEAEQ
620     630     640     650     660     670

630     640     650     660     670     680
Cry1Ac NLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVKHAK
gi|115 DLEAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECLSDDLYPNEKRLFLDAVREAK
680     690     700     710     720

690     700     710     720     730
Cry1Ac RLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFD--ECYPT
gi|115 RLSEARNLLQDPPDFQEI--GENGWASTGIEVIEGDALFKGRYLRLPGAREIDTETYPT
730     740     750     760     770     780

740     750     760     770     780     790
Cry1Ac YLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAKHETVNVVPGTGSWFLSAQSPI
gi|115 YLYQKVEEGVLPYTRYRLRGLFVGVSSQGLIEFTIRHQTNRIVKNVPP--DLLP--DVSPV
790     800     810     820     830     840

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680      690      700      710      720
Cry1Ac  RLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---ECYPT
gi|252  RLSEARNLLQDPDFQEQIN--GENGWTAAGTSTGIEVIEGDALFKGRYLRLPGAREIDTETYPT
730      740      750      760      770      780
Cry1Ac  YLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGSWLPLSAQSPI
gi|252  YLYQKVEEGVLEKPYTRYRLRGRFVGSQGLEIFITIRHQTNRIKVNVPD--DLLP--DVSPV
790      800      810      820      830      840
Cry1Ac  GKCCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCDDLNEGLGVVWVFKIK
gi|252  NSDGSINRCSEQKYVNSRLEVENRSGE----AHEFSIPIDTGEIDYNENAGIWWGFKIT
850      860      870      880      890
Cry1Ac  TQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALF
gi|252  DPEGYATLGNLELVEEGPLSGDALERLQREEQWQKIQTMRREEDRRYMASKQAVDRLY
900      910      920      930      940      950
Cry1Ac  VNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLY
gi|252  ADYDQQLNPDVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFELTDLRQQAWSLY
960      970      980      990      1000     1010
Cry1Ac  DARNVIKNGDFNGLSCWNVKGHVDFVEEQNNQRSVLVPEWEAEVSVQEVVRCPRGYILR
gi|252  DQRNAIPNGDFRNGLSNWNATPGVEVQ-QINHTSVLVIPNWDEQVSVQVQFTVQPNQRYVLR
1020     1030     1040     1050     1060     1070
Cry1Ac  VTAYKEGYGEGCVTIHEIENNTDELKFSNCVVEE--IYPNNTVTCNDYTVNQEEYGGAYT
gi|252  VTARKEGVNGYVSIIRDGGNQTTETLTFASDYDTNGMYNTQVSNNTNGYNTNNA-YNTQAS
1080     1090     1100     1110     1120     1130
Cry1Ac  SRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGYRDYTPPLVGYVTKLELYFPE
gi|252  STN-GYN-ANM---YNT---QASNTNGYNTNSV-----YNDQT---GYITKTVTFFPY
1140     1150     1160     1170
Cry1Ac  TDKVWIEIGETEGTFIVDSVELLMEE
gi|252  TDQMWIEMSETEGTFYIESVELIVDVE
1180     1190     1200

```

```

>>gi|46409859|gb|AAS93797.1| cry1B type crystal protein (849 aa)
initn: 1568 initl: 655 opt: 1377 Z-score: 1615.1 bits: 310.4 E(): 4.8e-81

```

```

Smith-Waterman score: 2119; 47.000% identity (70.875% similar) in 800 aa overlap
(55-805:72-849)

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```

30      40      50      60      70      80
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVGLVLDIWIWIFGP---SQWDAFL
gi|464  AEGNNIDPFVFASTVQVTGGINIAGRILGVLGVPFAGQIASFYSFLVGLWPRGRDPWEIFL
50      60      70      80      90      100
Cry1Ac  VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNMD
gi|464  EHVEQLIRQVVTENTRTDALARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIAL
110     120     130     140     150     160
Cry1Ac  NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYNDLT
gi|464  ELDFLNAMPPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQV
170     180     190     200     210     220
Cry1Ac  RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|464  EKTREYSDYCARWYNTGLNLRGTNAESWLRYNQFRDLTLGLVLDLVALFPPSYDTRVYPM
230     240     250     260     270     280
Cry1Ac  RTVSQLTREIYTNVLEN-----FDGS--FRGSA---QGIEGS-IRSPHMLDILNSITII
gi|464  NTSAQLTREIYTDPIGRNTNAPSGFASTNWFNNNAPSFSIAEAAVIRPPHLLDFPEQLTIF
290     300     310     320     330     340
Cry1Ac  TDAHR---GEY---YWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQ-QRIVAQL-GQGVY
gi|464  SVLSRWSNTQYMNWVWGHRLSRTI--RGSLSLST---STHGNTNTSINPVTLQFTSRDVIY
350     360     370     380     390
Cry1Ac  RTLS---STLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSQT--VDSLDEI
gi|464  RTESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTIIGYTGVTQLFDSSETEL
400     410     420     430     440     450
Cry1Ac  PPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|464  PPETTERPNYESYSHRLSNIRLI-SG-----NTLRAPVYSWTHRSADRNTIISSDSITQ
460     470     480     490     500
Cry1Ac  IPAVKGNFLFNG-SVLSGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTST-RYRVRV
gi|464  IPLVKSNFLNSGTSVVSQPGFTGGDIIRTNVNGS-VLSMG-----LNFNNTSLQRYRVRV
510     520     530     540     550
Cry1Ac  RYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR-

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770      780      790      800      810      820
Cry1Ac -NVPGTGSLWPLSAQSPIGKCGEPNRCAPHL-----EWNPDL-----DCSC-----
gi|624 LDVDPDN---IP---HAPIPVCGEFDRCKPYSYPPLLPECNPEFINQMOPSSCHHTQMVDY
      830      840      850      860      870
Cry1Ac -----RDGEKCAHSHHSHHSLDIDVIGCTDLNEDLGVWVI
gi|624 NNMNMSTSTTMNPTLTPEIASSQSGFGRKHKRC-HQAHQFEFHIDTGTIDLVEDLGLWVI
      880      890      900      910      920      930
Cry1Ac -----RDGEKCAHSHHSHHSLDIDVIGCTDLNEDLGVWVI
gi|624 NNMNMSTSTTMNPTLTPEIASSQSGFGRKHKRC-HQAHQFEFHIDTGTIDLVEDLGLWVI
      860      870      880      890      900      910
Cry1Ac FKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESV
gi|624 FKICATDGYASLDDLEVIIEGALGVEALELVKKREKKWRHQKEQHCQSQTKKHYDAAKHAV
      920      930      940      950      960      970
Cry1Ac DALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTA
gi|624 MALFTNTRYEKLFETTISNLLYADHLVQSIPIYVYNKYVPEVPGMNYELYSELNTLVQNA
      980      990      1000      1010      1020      1030
Cry1Ac FSLYDARNVIKNGDFNNGLSWVVKGHVDVEEQNNQQRVSLVPEWAEVSEVVRVCPGRG
gi|624 FYLYDQRNLIKNGRFSNGLMYWQAAPHARVE-QEFEKSVLVPNWDANVSDLCIEHNRG
      1040      1050      1060      1070      1080
Cry1Ac YLLRVTAYKEGYGEGCVTIHEIENNTDELKFSNC-VEEIYIP----NNTVTCNDY----
gi|624 YVLRVTARKEDPGAGNVTFSDCENHVDKLSFTSCDIATNAVPGAQANDPAAGVAYGQQGC
      1090      1100      1110
Cry1Ac TVNQEEYGG-----AYTS-----RNRGY-----NEAPSVPADYAS-
gi|624 QIDRVYPYQSGYRADGVAYEQSGHRTDGVVYRQSGYGTGVTYEQSGHRADGMPYQSGY
      1120      1130      1140
Cry1Ac -----VYEEKSY-----TDG-RRENPCFNRGRY----DYTPLP-----
gi|624 RADGVAYEQSGHRADGVYQSGYGTGVTYDQSANQTRKYHGCHTDGLPHEHGCCYPD
      1150      1160      1170      1180
Cry1Ac -----VGIVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|624 RVSDGQQALVYTKSIDLFPDTPDKVRIDIGETEGNFRVESVELICMEK
      1300      1310      1320      1330      1340

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>>gi|46359600|dbj|BAD15301.1| parasporal crystal protein (1344 aa)
initn: 1795 initl: 638 opt: 1314 Z-score: 1537.9 bits: 296.7 E(): 9.7e-77

```

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Smith-Waterman score: 2068; 33.789% identity (60.137% similar) in 1317 aa overlap
(29-1182:65-1344)

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10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVP--
gi|463 NKYPYATDPNVIAEGRSYKNWLDMCVGEVGDGTRSLEAIAVAVGVRSHTIFRLLG-VPYS
      60      70      80      90
Cry1Ac --GAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLGLSNLYQIY
gi|463 AQGEQLFSFLDITLW-LEGNTQWEELMRHAEELINEQVDPYVTRKALAEITDLGNLNLNY
      100      110      120      130      140      150
Cry1Ac AESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
gi|463 IAAFEDWKRNPSSQEVTRTRVIDRFNILDGLFEAYLPSFAVPGYEVPLLSVYANVNIHLL
      160      170      180      190      200      210
Cry1Ac VLRDVSFVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWIYRN
gi|463 VLRDSSIYGLDWGLSSTSVDNRYNRQQRNSATYANHCTTWYQTLQRLQSDASSVWVNYN
      220      230      240      250      260      270
Cry1Ac QFRRETLTVLDIVLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQG----
gi|463 RFRREITLVLDICALFSNYDVSYPQLRGLTRGIYTDPAVYSGTGSYSWLSQAPSPA
      280      290      300      310      320      330
Cry1Ac -IEG-SIRSPHLMIDILNSITIYTDHRGEY-----YWSGHQIMASPVGFSGPEFTFPPLY
gi|463 EIENIAIREPSNFTWASARVTTGTL--EYLSKKNDFWKSHYMNMYTETN-SGILIQGPY
      340      350      360      370      380
Cry1Ac G-TMGNAAPQQRIVAQLGQGVY-RTLSSSTLYRRPFNIGINNQQLSVLDGTE-FAYGTSSN
gi|463 GMTTGTNIRIESVSMQEIYSVRLEAVAHAGAGGPF-LGISTSEFFWLSLGVRRYQNSRSPQ
      390      400      410      420      430      440
Cry1Ac LPSAVYRKSGETVDSLDEIPQNNVPPRQGFVSHRSHVSMFRSGFSNNSVSIIRAPMFSW
gi|463 FASQIITR-----QLPGVNSAVPSALDHSHELSTYIT---AFPVRSVGTIIL--VHEW
      450      460      470      480      490
Cry1Ac IHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNNSGNNIQNRGYIE
gi|463 TSTTVSRNRNRIEPAKITQIPAVKSHTLNCSQVVSQVSGTGTGGNWRPDSNDS-----FRL
      500      510      520      530      540
Cry1Ac VPIHFPSTSTRYRVRVRYASVTFIHLNVNWNSSIFSNITVPATATS-LDNLQSSDFGYFE

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60      70      80      90      100     110
Cry1Ac --GAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 AQGEQLFSLDLTLW-LEGNTQWEELMRHAELINEQVPDYVRTKALAEPLDGLNNLNLY
100     110     120     130     140     150

120     130     140     150     160     170
Cry1Ac AESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 IAAFEDWKRNPSSQEVTRTRVIDRFNILDGLFEAYLPSFAVPGYEVPLLSVYANVNIHLL
160     170     180     190     200     210

180     190     200     210     220     230
Cry1Ac VLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 VLRDSSIYGLDWGLSSTSVDNINRQQRNSATYANHCTTWYQTGLQRLQGSASSWVNYN
220     230     240     250     260     270

240     250     260     270     280     290
Cry1Ac QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPLENFDGSRGSAQG----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 RFRREITLIVLDICALFSNYDVRSYPIQLRGELTRGIYTDPAVYSGTGSYSWLSQAPSA
280     290     300     310     320     330

300     310     320     330     340
Cry1Ac -IEG-SIRSPHMDILNSITTYTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 EIENIAIREPSNFTWASARVTTGTL--EYLSKKNDFWKSHYMNVTETN-SGILIQGPTY
340     350     360     370     380

350     360     370     380     390
Cry1Ac G-TMGNAAPQQRIVAQLGQGVY-RTLSSTLYRRPFNIGINNQQLSVLDGTE-FAYGTSSN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 GMTTGTNIRIESVSMQEIYSVRLAVALHAGAGGPF-LGISTSEFFWSLGVRRYQNSRSPQ
390     400     410     420     430     440

400     410     420     430     440     450
Cry1Ac LPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGLSNSSVSIIRAPMFSW
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 FASQIITR-----QLPGVNSAVPSALDHSHELSEYIT---AFPVRSVGTIL--VHEW
450     460     470     480     490

460     470     480     490     500     510
Cry1Ac IHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNLSGNNIQRGYIE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 TSTTVSRNRIEPDKITQIPAVKSHLNSCQVVSQVSGTGGNWLRLPSDNLS-----FRL
500     510     520     530     540

520     530     540     550     560     570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATS-LDNLQSSDFGYFE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 TITSFSSQS--YRIRIHYASATFFYLDIRTGDTSNFAVTPPTLSSGSGTVPYESFGFPI
550     560     570     580     590     600

580     590     600     610     620     630
Cry1Ac SANAFSTSSLGNIVGVRNFS---GTAGVIIDRFEFIPVTATL---EAEYNLERAQKAVNA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 IPYFTTAPTESRYTFDFMFYSIGSANVLIDRIEIVPIGVPLFEYETKQQLKARKAVNH
610     620     630     640     650     660

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640     650     660     670     680     690
Cry1Ac LFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 LFTDGSKKALKEDTDDYEIDQAANVVDICISDE-CGHDKMILLDEVKYARQLSQARNLLLN
670     680     690     700     710     720

700     710     720     730     740
Cry1Ac SNFKDINR--QPERGWGGSTGITIQGGDDVFKENYVTLVSGTFD----ECYPTYLYQKID
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 GNFDDLYSALEKENPWKTSFNVITIRQDNPIFKGHYLSMAGANDIEATNDTFPTYVYQKID
730     740     750     760     770     780

750     760     770     780     790     800
Cry1Ac ESKLKAFTRYQLRGLYIEDSQDLEIYSIRYNAKHETV-NVPGTGSWPLSAQSPIGKCGEP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 EAKLKPTRYKVRGFGVSSKALELLVTRYNEEVDAILDVPDN---IP-HAPTVP--CGEF
790     800     810     820     830

810     820
Cry1Ac NRCAPHL-----EWNPD-----DCSC-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 DRCKPYSYPLLPECNPEFINQMPPSSCHHNQMVVDYNNMNTSTSTTMNPSMNPPLTPEIA
840     850     860     870     880     890

830     840     850     860     870
Cry1Ac -----RDGEKCAHSHHSLDIDVCGCTDLNEDLGVWVIFKIKTQDGHARLGNLFLLEE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 SSQSGFGRKHKRC-HQAQHFPHIDTGTIDLVEDLGIWVIFKICATDGYASLDDLEVIEE
900     910     920     930     940     950

880     890     900     910     920     930
Cry1Ac KPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAM
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 GALGVEALELVKREKKWRHQKEQHCSTKHKYDAAKHAVMALFTNKRYEKLKFETTISD
960     970     980     990     1000    1010

940     950     960     970     980     990
Cry1Ac IHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 ILYADHLVQSIPIVYNYKYPVPGMNYELSELNLTLVQNAFYLYDRNLIKNGRFSNGLM
1020    1030    1040    1050    1060    1070

1000    1010    1020    1030    1040    1050
Cry1Ac CWNVKGHVDVEEQNNQSRVLPVEWAEVSVQEVVRCVGRGRIYILRVYAYKEGYEGCVTIH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 HWQATPHARVE-QEYKSVLVLPNWDANVSQDLCIEHNRGYVLRVTARKEDPGAGNVTFP
1080    1090    1100    1110    1120    1130

1060    1070    1080    1090
Cry1Ac EIENNTDELKFSNC-VEEEIYP---NNTVTCNDY----TVNQEEYGG-----AYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 DCENHVDKLSFTSCDIATNAVPGAQANDPAAGVAYGQGCQIDRVYPGQSGYRADGVAYE
1140    1150    1160    1170    1180    1190

1100    1110    1120
Cry1Ac S-----RNRGY-----NEAPSVPADYAS-----VYEEKSY-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 QSGHRTDGVPIYRQSGYGTGVTYEQSGHRADGVPIYQSGYRADGVAYEQSGHRADGVPIY

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Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERN
gi|293 AVNHLFTDGSKKALKEGTTDYEIDQAANVVDICISDE--CGHEKMILLDEVKYAKQLSQARN
      700      710      720      730      740      750

      690      700      710      720      730      740
Cry1Ac LLQDSNFKDINRQPER--GWGGSTGITIQGGDDVFKENYVTLSGTFD----ECYPTYLY
gi|293 LLLNGNFDDLYPALERENPWKTSFNVVTRQDNPIFKGHYLSMAGANDIEATNDTFPTYAY
      760      770      780      790      800      810

      750      760      770      780      790
Cry1Ac QKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV--NVPGTGSLWPLSAQSPIGK
gi|293 QKIDEAKLKPYPTRYKVRGFGVSSKALELLVTRYNEEVDAILDVPDN--IP--HAPIPV
      820      830      840      850      860

      800      810      820
Cry1Ac CGEPNRCAPHL-----EWNPDL----DCSC-----
gi|293 CGEFDRCPKPYSYPLLPEPCNPEFINQMOPSSCHHTQMVDYNNMNMSTSTTMMPTLTPEIA
      870      880      890      900      910      920

      830      840      850      860      870
Cry1Ac -----RDGEKCAHSHHFLSLDIDVGCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEE
gi|293 SSQSGFGRKRKRC--HQAHQFEFHIDTGTIDLVEDLGIWVIFKICATDGYASLDDLEVIEE
      930      940      950      960      970      980

      880      890      900      910      920      930
Cry1Ac KPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAM
gi|293 GALGVEALELVKREKWRHQEQHCSQTKHKYDAAKHAVMALFNTTRYEKLFKFTTISD
      990      1000      1010      1020      1030      1040

      940      950      960      970      980      990
Cry1Ac IHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS
gi|293 ILYADHLVQSIPIYVYNKYVPEVPGMNYELYSLNLTLVQNAFYLYDQRNLIKNGRFSNGLM
      1050      1060      1070      1080      1090      1100

      1000      1010      1020      1030      1040      1050
Cry1Ac CWNVKGHVDEVEQNNQRSVLVPEWEAEVSEVVRVCPGRGYILLRVTAAYKEGYGEGCVTIH
gi|293 HWQATPHARVE--QEHEKSVLVLPNWDANVSQDLCIEHNRGVVLRVTARKEDPAGNVTFFS
      1110      1120      1130      1140      1150      1160

      1060      1070      1080      1090      1100
Cry1Ac ELENTDELKFSNC--VEEIIYP----NNTVTCDNY----TVNQEEYG--GAYTSRNRGY
gi|293 DCANHVNKLSTFSCDIAATNAVPGAQANDPAAGVAYGQQGCQIDRVYPYQSGYRTDGTNGM
      1170      1180      1190      1200      1210      1220

      1110      1120
Cry1Ac -----NEAPSVP-----ADYAS-----VYEEKSYT----
gi|293 PYGQSGNRADGVPYRQSGYGTGVAHDQPGYRADGAAAYEQSGHRADGVAYEQSGYRAGGV
      1230      1240      1250      1260      1270      1280

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      1130      1140
Cry1Ac ----DGRRENPCFNR--GY-----RDY-----TPLP-----
gi|293 AYEQSGHRADGVPYQSGYGTGVTYDQSVKQTRKYHGCHTDGLPHPEHGCCYPDRVSDG
      1290      1300      1310      1320      1330      1340

      1150      1160      1170      1180
Cry1Ac --VGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|293 QQLAYVTKSIDLFPDITDKVIRIDIGETEGNFRVESVELICMEK
      1350      1360      1370      1380

>>gi|111927190|gb|ABH71842.1| Sequence 6 from patent US (1386 aa)
      initn: 2039 init1: 655 opt: 1285 Z-score: 1503.5 bits: 290.4 E(): 8e-75
Smith-Waterman score: 2146; 34.459% identity (59.835% similar) in 1332 aa overlap
(35-1182:92-1386)

      10      20      30      40      50      60
Cry1Ac MDNNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLG
gi|111 NVIAEGRSYKNWLDMCVGVGDDTRSPEARVTAQSSISTSLGITSTIIGALGIPVVGAEIG
      70      80      90      100      110      120

      70      80      90      100      110
Cry1Ac ----LVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLBGLSNLYQIYAESFR
gi|111 IFGALLDWLWPA--GADPWVIFMNHVEELINSKITETVKNEAITRLDGLGNVLAQKAFK
      130      140      150      160      170      180

      120      130      140      150      160      170
Cry1Ac EWEADTPNAPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|111 EWQHPPTLESARLRVTDVDFSNVNFEEAFMPSFRVPGYEVPLLSVYVQAANLHLLLRDS
      190      200      210      220      230      240

      180      190      200      210      220      230
Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
gi|111 SIFGLDWLGSQTHVNDNYNLQIRRSADYANHCTTWYRTGLQRLQGTNASSWVNYNFRRE
      250      260      270      280      290      300

      240      250      260      270      280      290
Cry1Ac LTLTVDLIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQGLEGSI--RSP
gi|111 MTLTVDLVCALFSSYDYSYPMELRGELTREIYTDVPGASFWVNRAPNFASIENTVVRQP
      310      320      330      340      350      360

      300      310      320      330      340      350
Cry1Ac HLMDILNSITITDAHRG-----EYWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQOR
gi|111 HPFTWLVTITVNTGQVRSQVSGDGNSSNYWKSQTVSETGGSGP--IQSPTCGSTGIYRTDN
      370      380      390      400      410

      360      370      380      390      400      410
Cry1Ac IV--AQLGQGVYRTLSSLYRRPFNI--GINNQQLSVLDGTEFAYGTSNNLPSAVYRKSQV
gi|111 LLFNPFLLDGIYTIINTGVSYLANLFGIYSARFTTTRSIELLYENQRVFPAYNHQ-----
      420      430      440      450      460      470

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420      430      440      450      460      470
Cry1Ac DSLDEIPQNNVPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSA-EFNNII
gi|111 --IRELPGVNSDRPTAADYSHRSLSYISGFATDVGGTVL-----VYGWTSSTATRENNIT
480      490      500      510      520

480      490      500      510      520      530
Cry1Ac ASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNLSGNNIQNRGYIEVP IHFPSTSTR
gi|111 LDDRIVQLPAVKGTSLNNCQVVRGTGFTGGDWLKP-----NNGTFSLALGFRSTYT-
530      540      550      560      570

480      490      500      510      520      530
Cry1Ac YRVRVRYASVTPIHNLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESA--NAFT-SSL
gi|111 YRLRIRYAAAAG----GSGFSLVISDQYGEFPTTIVLSSTMYSLPQNVPEAFKIVDL
580      590      600      610      620      630

590      600      610      620
Cry1Ac GNIVGVRNFSGT-----AGVIIDRFEFIPVTATL--EAEYNLERAQK
gi|111 PSTVTIRNTSPASTTFRDLDFRIVPLGILANILIDRIEFVPIEGSLFEYETKQQLKARK
640      650      660      670      680      690

630      640      650      660      670      680
Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
gi|111 AVNHLFTDGSKKALKEGTTDYEIDQAAANVVDICISDE-CGHEKMILLDEVKYAKQLSQARN
700      710      720      730      740      750

690      700      710      720      730      740
Cry1Ac LLQDSNFKDINRQPER--GWGGSTGITIQGGDDVFKENYVTLSGTFD----ECYPTYLY
gi|111 LLLNGNFDDLYPALERENPWKTSNVVTRQDNPIFKGHYLSMAGANDIEATNDTFFPTYAY
760      770      780      790      800      810

750      760      770      780      790
Cry1Ac QKIDESKLFATRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGTGLSLWPLSAQSPIGK
gi|111 QKIDEAKLKPYYTRYKVRGFGVSSKALELLVTRYNEEVDAILDVPDN--IP---HAPIPV
820      830      840      850      860

800      810      820
Cry1Ac CGEPNRCAPHL-----EWNPD-----DCSC-----
gi|111 CGEFDRCKPYSYPLLPPECNPEFINQMOPSSCHHTQMVDYNNMNMSTTTMNPILTPEIA
870      880      890      900      910      920

830      840      850      860      870
Cry1Ac -----RDGEKCAHSHHFLSLDIDVGCCTDLNEDLGVVWVIFKIKIQDGHARLGNLEFLEE
gi|111 SSQSGFGGRKHKR--HQAHQFHFHIDTGTIDLVEDLGIWVIFKICATDGYASLDDLEVIEE
930      940      950      960      970      980

880      890      900      910      920      930
Cry1Ac KPLVGBEARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAM
gi|111 GALGVEALELVKREKKWRHQEQHCSQTKHKYDAAKHAVMALFNTRYEKLFKFTTISD
990      1000      1010      1020      1030      1040

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940      950      960      970      980      990
Cry1Ac IHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLS
gi|111 ILYADHLVQSIPIVYVNYVPEVPGMNYELYSELNLTLVQNAFYLDQRNLKIKGRFSNGLM
1050      1060      1070      1080      1090      1100

1000      1010      1020      1030      1040      1050
Cry1Ac CWNVKGHVDEEQQNQRSLVLPVEWAEVVSQEVVRVCPGRGYLLRVYAYKEGYEGCVTIH
gi|111 HWQATPHARVE--QEHEKSVLVLPNWDANVSQDLCEIHNRYVLRVTARKEDEPGAGNVTF
1110      1120      1130      1140      1150      1160

1060      1070      1080      1090      1100
Cry1Ac EIENNTDELKFSNC-VEEIIYP---NNTVTCNDY----TVNQEEYG--GAYTSRNRGY
gi|111 DCANHVNKLSTSCDIATNAVPGAQANDPAAGVAYGQQGCQIDRVYPYQSGYRTDGTNGM
1170      1180      1190      1200      1210      1220

1110      1120
Cry1Ac -----NEAPSVP-----ADYAS-----VYEEKSYT----
gi|111 PYQSGSNRAGDVPYRQSGYGTGVAHQDQPGYRADGAAYEQSGHRADGVAYEQSGYRAGGV
1230      1240      1250      1260      1270      1280

1130      1140
Cry1Ac ---DGRRENPCFENR-GY-----RDY-----TPLP-----
gi|111 AYEQSGHRADGVYPYQSGYGTGVTYDQSVKQTRKYHGCHTDGLPHPEHGCCYPDRVSDG
1290      1300      1310      1320      1330      1340

1150      1160      1170      1180
Cry1Ac --VGYVTKLELYFPETDKVWIEIGETEGTFIVDSVLELLMEE
gi|111 QQLAYVTKSIDLFPDIDKVRIDIGETEGNFRVSVELICMEK
1350      1360      1370      1380

>>gi|112088057|gb|ABI06963.1| Sequence 42 from patent US (710 aa)
initn: 1382 init1: 693 opt: 1280 Z-score: 1501.9 bits: 289.2 E(): 9.8e-75
Smith-Waterman score: 1498; 38.472% identity (68.194% similar) in 720 aa overlap
(3-688:10-710)

10      20      30      40
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEV--LGGERIE--TGYTPIDISLSLTQF
gi|112 MKSKNQMNHQSLSNATVDKNFTGSLNNTNTELQNFNHEGIEPFVSVSTIQGTGIGIAGK
10      20      30      40      50      60

50      60      70      80      90      100
Cry1Ac LLSEF-VPGAGFVLGLVDI IWGIFGP---SQWDAFLVQIEQLINQRIE EFARNQAI SRLE
gi|112 ILGNLGVFPAGQVASYLSF ILGELWPKGKSQWEIFMEHVEELINQKISTYARNKALADLK
70      80      90      100      110      120

110      120      130      140      150      160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|112 GLGDALAVYHESLESWIENRNNTTRTSVVKSQYITLLELMFVQSLPFAVSGEEVPLLPYI
130      140      150      160      170      180

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170      180      190      200      210      220
Cry1Ac VQAANLHLVSLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
.: : : : : . : : : : . : : : : . : : : : . : : : : . : : : : . : : : :
gi | 112 AQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKEYSDHCVKWYNTGLNRLMGN
190      200      210      220      230      240

230      240      250      260      270      280
Cry1Ac DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV----LENF
.: : : : : . : : : : . : : : : . : : : : . : : : : . : : : :
gi | 112 NAESWVRYNQFRDMLMVLDLVALFPSYDTQMYPKTTAQLTREVYTDIAGTVHPHPSF
250      260      270      280      290      300

290      300      310      320      330
Cry1Ac DGS--FRGSAQG---IEGSI-RSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSG
.: : . : . : . : : . : : : : . : : : . : : : . : : : . : : : . : : :
gi | 112 TSTTWYNNNAPSFSSTIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMMN---WGG
310      320      330      340      350

340      350      360      370      380      390
Cry1Ac PEFTFPLYGTMGNAAPQQRIVVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVDLGT
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 HKLEFRTIGTTLNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVD
360      370      380      390      400      410

400      410      420      430      440
Cry1Ac FAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHRSHVSMFRSG
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 FHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSHIGLI---
420      430      440      450      460      470

450      460      470      480      490      500
Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDL
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 ----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI
480      490      500      510      520

510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNWGNSSIFSNTVPAT
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 LRRKNTGT---FGDIRVNIN-PPFAQRVVRIRYASTDLQFHSTINGKAINQGNFSAT
530      540      550      560      570      580

570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAE
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 MNRGEDLDYKFTRTVGFTHPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVETYEAE
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELSEKVKHA
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 YDFEKAQEVEVTLFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKPYLDEKRELFEIVKYA
650      660      670      680      690      700

680      690      700      710      720      730
Cry1Ac KRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYL
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 112 KQLHIERNM

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710
>>gi|33765731|gb|AAQ52382.1| Sequence 42 from patent US (710 aa)
initn: 1382 initl: 693 opt: 1280 Z-score: 1501.9 bits: 289.2 E(): 9.8e-75
Smith-Waterman score: 1498; 38.472% identity (68.194% similar) in 720 aa overlap
(3-688:10-710)

10      20      30      40
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEV--LGGERIE--TGYPIDISLSLTQF
.: : : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 MKSKNQNMHQSLSNATVDKNFTGSELENNNTTELQNFNHEGIEPPVSVSTIQTGIGIAGK
10      20      30      40      50      60

50      60      70      80      90      100
Cry1Ac LLSEF-VPGAGFVLGLVDI IWGIFGP---SQWDAFLVQIEQLINQRIEEFARNQAISRLE
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 ILGNLGVPPAGQVASLYSFLGELWPKGKSQWEIFMEHVEELINQKISTYARNKALADLK
70      80      90      100      110      120

110      120      130      140      150      160
Cry1Ac GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 GLGDALAVYHESLESWIENRNNTTRRSVVKSQYITLELMFVQSLPSFAVSGEEVPLLIY
130      140      150      160      170      180

170      180      190      200      210      220
Cry1Ac VQAANLHLVSLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
.: : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 337 AQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKEYSDHCVKWYNTGLNRLMGN
190      200      210      220      230      240

230      240      250      260      270      280
Cry1Ac DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV----LENF
.: : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 337 NAESWVRYNQFRDMLMVLDLVALFPSYDTQMYPKTTAQLTREVYTDIAGTVHPHPSF
250      260      270      280      290      300

290      300      310      320      330
Cry1Ac DGS--FRGSAQG---IEGSI-RSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSG
.: : . : . : . : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 337 TSTTWYNNNAPSFSSTIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNTQYMMN---WGG
310      320      330      340      350

340      350      360      370      380      390
Cry1Ac PEFTFPLYGTMGNAAPQQRIVVAQLGQGVYRTLSSTLYRRPFNIGIN---NQQLSVDLGT
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 HKLEFRTIGTTLNTSTQGSTNTSINPVTLPFTSRDVRVYTESLAGLNLFLTQPVNGVPRVD
360      370      380      390      400      410

400      410      420      430      440
Cry1Ac FAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHRSHVSMFRSG
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 FHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSHIGLI---
420      430      440      450      460      470

450      460      470      480      490      500
Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDL
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 ----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI
480      490      500      510      520

510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNWGNSSIFSNTVPAT
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 LRRKNTGT---FGDIRVNIN-PPFAQRVVRIRYASTDLQFHSTINGKAINQGNFSAT
530      540      550      560      570      580

570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAE
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 MNRGEDLDYKFTRTVGFTHPFSDVQSTFTTIGAWNFSSGNEVYIDRIEFVPEVETYEAE
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELSEKVKHA
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 YDFEKAQEVEVTLFTSTNPRGLKTDVKDYHIDQVSNLVESLSDKPYLDEKRELFEIVKYA
650      660      670      680      690      700

680      690      700      710      720      730
Cry1Ac KRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYL
.: : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi | 337 ----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAVVRGPGFTGGDI

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      10      20      30      40      50      60
Cry1Ac  TPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFPGP---SQWDAFLVQIEQLINQRIEE
gi|126  --IGIA---GKILGTLGVFPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKIST
      70      80      90     100     110
Cry1Ac  FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
gi|126  YARNKALTDLKGGLDALAVYHDSLESWVGNRNNTRRARSVVKSQYIALELMFVQKLPFAV
      120     130     140     150     160     170
Cry1Ac  QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
gi|126  SGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYS DHCVKW
      180     190     200     210     220     230
Cry1Ac  YNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|126  YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPPSYDTQMPYIKTTAQLTREYVTD
      240     250     260     270     280     290
Cry1Ac  PV-----LENFDGS--FRGSA---QGIIEGSI-RSPHLMIDLNSITIIYTDahrgeyywsgH
gi|126  AIGTVHPPHSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSR----WSNT
      300     310     320     330     340     350
Cry1Ac  QIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---
gi|126  QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLFPFTRDVRTESLAGLNLFL
      360     370     380     390     400     410
Cry1Ac  NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|126  TQPVNGVPRVDFHWKVFVTHPIASDNFYYPGVYVIGTQLQDSENELPPEATGQPNYESYSH
      420     430     440     450     460     470
Cry1Ac  RLSHVMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
gi|126  RLSHIGLI-----SASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAV
      480     490     500     510     520
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN
gi|126  VRGPGFTGGDLRRNTGT---FGDIRVNIN-PPFAQRVRYRIRYASTTDLQFHTSING
      530     540     550     560     570
Cry1Ac  SSIFNTVPATATSLDNLQSSDFGY--FESANAFSSSLGNI-VGVRNFSGTAGVIIDRFE
gi|126  ..: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|126  KAINQGNFSATMNRGEDLDYKTFRTVGFTHPPFSLDVQSTFTTIGAWNFSSGNEVYIDRIE
      580     590     600     610     620     630
Cry1Ac  FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDE
gi|126  FVPVEVTYEAEDYFEKAQEKVTLFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLD
      640     650     660     670     680     690
Cry1Ac  KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL
gi|126  KRELFEIVKYAKQLHIERNM
      700     710
>>gi|55583756|gb|AAV53390.1| delta endotoxin [Bacillus t (719 aa)
      initn: 1383 init1: 689 opt: 1266 Z-score: 1485.3 bits: 286.1 E(): 8.2e-74
      Smith-Waterman score: 1486; 38.873% identity (67.465% similar) in 710 aa overlap
      (8-688:36-719)
      10      20      30
Cry1Ac  CMQAMDNPNPINECIPYNCLSNPEVEVLGGERIETGY
gi|555  QDKHQFSFSSNAKVDKISTDSLKNETDIELQNIHEDCLMSEYENVE-PFVSASTIQTG-
      40      50      60      70      80      90
Cry1Ac  TPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFPGP---SQWDAFLVQIEQLINQRIEE
gi|555  --IGIA---GKILGTLGVFPAGQVASLYSFILGELWPKGKNQWEIFMEHVEEIIINQKIST
      70      80      90     100     110
Cry1Ac  FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
gi|555  YARNKALTDLKGGLDALAVYHDSLESWVGNRNNTRRARSVVKSQYIALELMFVQKLPFAV
      120     130     140     150     160     170
Cry1Ac  QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
gi|555  SGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYS DHCVKW
      180     190     200     210     220     230
Cry1Ac  YNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|555  YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPPSYDTQMPYIKTTAQLTREYVTD
      240     250     260     270     280     290
Cry1Ac  PV-----LENFDGS--FRGSA---QGIIEGSI-RSPHLMIDLNSITIIYTDahrgeyywsgH
gi|555  AIGTVHPPHSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTTIYSLLSR----WSNT
      300     310     320     330     340     350
Cry1Ac  QIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---
gi|555  QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLFPFTRDVRTESLAGLNLFL
      360     370     380     390     400     410
Cry1Ac  NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|555  TQPVNGVPRVDFHWKVFVTHPIASDNFYYPGVYVIGTQLQDSENELPPEATGQPNYESYSH
      420     430     440     450     460     470
Cry1Ac  RLSHVMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
gi|555  RLSHIGLI-----SASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAV
      480     490     500     510     520
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN
gi|555  VRGPGFTGGDLRRNTGT---FGDIRVNIN-PPFAQRVRYRIRYASTTDLQFHTSING
      530     540     550     560     570
Cry1Ac  SSIFNTVPATATSLDNLQSSDFGY--FESANAFSSSLGNI-VGVRNFSGTAGVIIDRFE
gi|555  ..: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|555 QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTEFLAGLNLFL
360 370 380 390 400 410

Cry1Ac NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSQV--DSLDEIPPQNNVPPRQGFSA
390 400 410 420 430

gi|555 TQPVNGVPRVDFHWKRVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSH
420 430 440 450 460 470

Cry1Ac RLSHVSMPFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
440 450 460 470 480 490

gi|555 RLSHIGLI-----SASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGAAV
480 490 500 510 520

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
500 510 520 530 540 550

gi|555 VRGPGFTGGDILRRNTTGT---FGDIRVNIN-PPFAQRVVRIRYASTTDLQFHTSING
530 540 550 560 570

Cry1Ac SSIFSNTPATATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFE
560 570 580 590 600

gi|555 KAINQGNFSATMNRGEGDLDYKTFRTVGFSTPFSLDVQSTFTIGAWNFSNGEVYIDRIE
580 590 600 610 620 630

Cry1Ac FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
610 620 630 640 650 660

gi|555 FVPVEVTYAEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLD
640 650 660 670 680 690

Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL
670 680 690 700 710 720

gi|555 KRELFEIVKYAKQLHIERNM
700 710

>>gi|51998350|emb|CAH33947.1| unnamed protein product [B (601 aa)
initn: 816 initl: 476 opt: 1263 Z-score: 1482.9 bits: 285.4 E(): 1.1e-73
Smith-Waterman score: 1305; 38.636% identity (67.857% similar) in 616 aa overlap
(18-612:13-600)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
10 20 30 40 50 60

gi|519 MNSKEHDYLVKVCNDLSDANINM---ERFDKN-DALEIGMSIVSELIG-MIPG-GT
10 20 30 40

Cry1Ac VLGLV-DIIWIFGSPQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFR
70 80 90 100 110

gi|519 ALQFVFNQLWSRLGDSGWNAMMEHVEELIDTKIEGYAKNKALSELAGIQRNLETYIQLRN
50 60 70 80 90 100

Cry1Ac EWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
120 130 140 150 160 170

gi|519 EWENDIENSKAQKGVANYYESLEQAVERSMPQFAVENFEVPLLTVYVQAANLHLLLRDV
110 120 130 140 150 160

Cry1Ac SVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVW--GPDSDRWIRYNQFR
180 190 200 210 220 230

gi|519 SVYGKCVWSEQKIKIYYDKQIKYTHEYTNHCNVNWKGLERLKNKSSYQDWNYNRFR
170 180 190 200 210 220

Cry1Ac RELTLTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLENFDGSRFGSAQ----GIE
240 250 260 270 280 290

gi|519 REMTLTLVLDIVALFPHYDQVQYPIITVAQLTREVYTDPLL-NFNPKLHVSQSPFSFDM
230 240 250 260 270 280

Cry1Ac G-SIRSPHMLDILNSITIYTDADR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNA-
300 310 320 330 340

gi|519 NATIRTPHLMFLRMLTIYTDWYVSVGRNYYWGGHRVTSYHVG--GENIRSPLYGREANQE
290 300 310 320 330 340

Cry1Ac APQQR-----IVAQLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSA
350 360 370 380 390 400

gi|519 VPRDFYFYGVFKTLKSKPTLRPLQPAPAPPFN-----LRSLEGVEFHTPTGFSFM---
350 360 370 380 390

Cry1Ac VYRKSQVDSLDEIPPQNNVPPRQGFSAHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRS
410 420 430 440 450 460

gi|519 -YRERGSVDSFNLPPFNVPGLPHKVYSHRLCHATFVR--KSGTPLYLTGAIKFSWTHRS
400 410 420 430 440 450

Cry1Ac AEFNIIASDSITQIPAVKGNFLFNGSVI-SGPGFTGGDLVRLNSSGNNIQRNGYIEVPI
470 480 490 500 510 520

gi|519 AETNTIESNIIITQIPLVKAYQIGSGTTVRKGGFTGGDILRRTPGPG---TFGDMRINI
460 470 480 490 500

Cry1Ac HFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|519 NAP-LSQRVVRIRYASTTDLQFVTSINGTTINIGNFPKTIINNLTLGSEGYRTVSFSTP
510 520 530 540 550 560

Cry1Ac FTSSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
590 600 610 620 630

gi|519 FFSNAQSIFRLGIQAFSGVQEVYVDKIEFIPVE
570 580 590 600

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
640 650 660 670 680 690

>>gi|51998348|emb|CAH33946.1| unnamed protein product [B (629 aa)
initn: 816 initl: 476 opt: 1263 Z-score: 1482.6 bits: 285.4 E(): 1.2e-73
Smith-Waterman score: 1305; 38.636% identity (67.857% similar) in 616 aa overlap
(18-612:41-628)

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Cry1Ac          10      20      30      40
                CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLT
gi|519 STNRTCCLLKIINIGGRGMNSKEHDYLVKVCNDLSDANINM---ERFDKN-DALEIGMSIV
                20      30      40      50      60

Cry1Ac          50      60      70      80      90      100
                QFLLSEFVPGAGFVGLGLV-DIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEG
gi|519 SELIG-MIPG-GTALQVFVNQLWSRLGDSGWNAMFMEHVEELIDTKIEGYAKNKALSELAG
                70      80      90      100     110     120

Cry1Ac          110     120     130     140     150     160
                LSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|519 IQRNLETYIQLRNEWENDIENSKAQGKVANYYESLEQAVERSMPQFAVENFEVPLLTIVYV
                130     140     150     160     170     180

Cry1Ac          170     180     190     200     210     220
                QAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW--G
gi|519 QAAHLHLLLRDVSVYKCGWSEQKIKIYYDKQIKYTHEYTNHCNVNWKGLERLKNKG
                190     200     210     220     230     240

Cry1Ac          230     240     250     260     270     280
                PDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSF
gi|519 SSYQDWYNNRFRREMTLTVLDIVALFPHYDVQTYPIITVAQLTREVYTDPLL-NFNPKL
                250     260     270     280     290     300

Cry1Ac          290     300     310     320     330
                RGSAQ----GIEG-SIRSPHLMIDLNSITTYTDAHR-GE-YYWGHQIMASPVGFSGPE
gi|519 HSVSQLPFSMDENATIRTPHLMFLRMLTIYTDWYSVGRNYYWGGHVRTSYHVG--GEN
                310     320     330     340     350     360

Cry1Ac          340     350     360     370     380     390
                FTFPLYGTMGNA-APQR-----IVAQLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGT
gi|519 IRSPLYGREANQEVPRDFYFYGPVFKTLKPTLRPLQPAPAPPFN-----LRSLEGV
                370     380     390     400     410

Cry1Ac          400     410     420     430     440     450
                EFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFHSHLSVMSFRSGFSNSSVS
gi|519 EFHTPTGSFM---YRERGSVDSFNELPPFNVPGLPHKVYSHRLCHATFVR---KSGTPY
                420     430     440     450     460

Cry1Ac          460     470     480     490     500
                IIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVI-SGPGFTGGDLVRLNSSG
gi|519 LTTGALFSWTHRSAAETNTIESNIIITQIPLVKAYQIGSGTTVRKGGPGTGGDILRRTPGG
                470     480     490     500     510     520

Cry1Ac          510     520     530     540     550     560
                NNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNL
gi|519 ----TFGDMRININAP-LSQRVYRIRYASTTDLQFVTSINGTTINIGNFPKTIINLNLTL
                530     540     550     560     570     580

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Cry1Ac          570     580     590     600     610     620
                QSSDFGYFESANAFSTSSLGNIV--GVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQ
gi|519 GSEGYRTVSFSTPFSSNAQSIFRLGIQAFSGVQVEVYVVKIEFIPVE
                590     600     610     620

Cry1Ac          630     640     650     660     670     680
                KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
>>gi|32709126|gb|AAP86782.1| Cry1I [Bacillus thuringiens (719 aa)
  initn: 1379 initl: 685 opt: 1262 Z-score: 1480.6 bits: 285.2 E(): 1.5e-73
Smith-Waterman score: 1482; 38.732% identity (67.465% similar) in 710 aa overlap
(8-688:36-719)

Cry1Ac          10      20      30
                CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
gi|327 QDKHQSFSNAKVDKISTDSLKNETDIELQININHEDEKLMSEYENVE-PFVASTIQTG-
                10      20      30      40      50      60

Cry1Ac          40      50      60      70      80      90
                TPIDISLSLTQFLLSEFVPGAGFVGLVDIIWGFIPG---SQWDAFLVQIEQLINQRIEE
gi|327 --IGIA---GKILGTLGVPPFAGQVASLYSFI LGELWPKGNQWEIFMEHVEEINQKIST
                70      80      90      100     110

Cry1Ac          100     110     120     130     140     150
                FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
gi|327 YARNKALTDLGLGDALAVYHDSLESWVGNRNNTRRARSVVKSQYIALELMFVQKLPFAV
                120     130     140     150     160     170

Cry1Ac          160     170     180     190     200     210
                QNYQVPLLSVYVQAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
gi|327 SGEEVPLLPYIAQAAHLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSHCVKW
                180     190     200     210     220     230

Cry1Ac          220     230     240     250     260     270
                YNTGLERWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|327 YSTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFSPSYDTQMPYIKTTAQLTREVYTD
                240     250     260     270     280     290

Cry1Ac          280     290     300     310     320
                PV----LENFDGS--FRGSA---QIEGSI-RSPHLMIDLNSITTYTDAHRGEYYWSGH
gi|327 AIGTVHPHPSFTSTTWYNNNAPSFSIAEAAVVRNPHLLDFLEQVTIYSLLSR---WSNT
                300     310     320     330     340     350

Cry1Ac          330     340     350     360     370     380
                QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGIN---
gi|327 QYMM---WGGHKLFEFTIGGTLNISTQGSTNTSINPVTLPPTSRDVRVYTESLAGLNLFL
                360     370     380     390     400     410

Cry1Ac          390     400     410     420     430
                NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSQVTV--DSLDEIPPQNNVPPRQGFHSH

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initn: 1379 initl: 685 opt: 1262 Z-score: 1480.6 bits: 285.2 E(): 1.5e-73
Smith-Waterman score: 1482; 38.732% identity (67.465% similar) in 710 aa overlap
(8-688:36-719)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
gi|333 PDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVE-PFVSASTIQTG-
Cry1Ac TPIDISLSLTQFLLSEFVPGAGFVLGLVDI IWGIFGP---SQWDAFLVQIEQLINQRIEE
gi|333 --IGIA---GKILGTLGVPFAGQVASLYSFLGELWPKGKNQWEIFMEHVVEEIIINQKIST
Cry1Ac FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
gi|333 YARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPFAV
Cry1Ac QNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
gi|333 SGEEVPLLP IYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYS DHCVKW
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|333 YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTD
Cry1Ac PV-----LENFDGS--FRGSA---QGIEGSI-RSPHLM DILNSITTYTDAHRGEYYWSGH
gi|333 AIGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVTIYSLLSR---WSNT
Cry1Ac QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRITLSSTLYRRPFNIGIN---
gi|333 QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFL
Cry1Ac NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNMVPFRQGFVSH
gi|333 TQPVNGVPRVDPFHWKVTHTPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSH
Cry1Ac RLSHVS MFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLNFGS-V
gi|333 RLSHIGLI-----SASHVKALVYSWTHRSADRINTTIEPN SITQIPLVKAFNLSSGAAV

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNWNWGN
gi|333 VRGPGFTGGDILRRNTGT----FGDIRVNIN-PPFAQRYRVRIRYASITDQLQFHTSING
Cry1Ac SSIFSNTPATATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFGS TAGVIIDRFE
gi|333 KAINQGNFSATMNRGEDLDYKTRFTVGF TTPFSFLDVQSTFTIGAWNFSSGNEVYIDRIE
Cry1Ac FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDE
gi|333 FVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDE
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL S
gi|333 KRELFEIVKYAKQLHIERNMP

>>gi|33325407|gb|AAQ08233.1| Cry1Ia [Bacillus thuringien (746 aa)
initn: 1379 initl: 685 opt: 1262 Z-score: 1480.3 bits: 285.2 E(): 1.6e-73
Smith-Waterman score: 1482; 38.732% identity (67.465% similar) in 710 aa overlap
(8-688:36-719)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
gi|333 QDKHQSFSSNAKVDKISTDSLKNETDIELQININHEDCLKMSEYENVE-PFVSASTIQTG-
Cry1Ac TPIDISLSLTQFLLSEFVPGAGFVLGLVDI IWGIFGP---SQWDAFLVQIEQLINQRIEE
gi|333 --IGIA---GKILGTLGVPFAGQVASLYSFLGELWPKGKNQWEIFMEHVVEEIIINQKIST
Cry1Ac FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
gi|333 YARNKALTDLKGGLDALAVYHDSLESWVGNNRNNTRARSVVKSQYIALELMFVQKLPSPFAV
Cry1Ac QNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
gi|333 SGEEVPLLP IYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYS DHCVKW
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|333 YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTD
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
gi|333 YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYVTD



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        660      670      680      690      700      710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|467 DQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM
        690      700      710
Cry1Ac ITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYS
>>gi|3329593|gb|AAC26910.1| insecticidal protein [Bacill (719 aa)
  initn: 1379 initl: 685 opt: 1261 Z-score: 1479.4 bits: 285.0 E(): 1.8e-73
Smith-Waterman score: 1481; 38.732% identity (67.465% similar) in 710 aa overlap
(8-688:36-719)

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                10      20      30
Cry1Ac          CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 QDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVE-PFVSASTIQTG-
        10      20      30      40      50      60
Cry1Ac TPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFIPG---SQWDAFLVQIEQLINQRIEE
: : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 --IGIA---GKILGTLGVPPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKIST
        70      80      90      100     110

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        100     110     120     130     140     150
Cry1Ac FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 YARNKALTDLKGDLAVYHDSLESWVGNRNNRARSVVKSQYIALELMFVQKLPSPFAV
        120     130     140     150     160     170
Cry1Ac QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
. . : : : : : : : : : : : : : : : : : : : : : : : : : : . . : : : : : : : : : : :
gi|332 SGEEVPLLPYQAANLHLLLRDASIFPKWGLSSSEISTFYNRQVERAGDYSDDHCVKW
        180     190     200     210     220     230

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        220     230     240     250     260     270
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
: : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 YSTGLNNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSTYDTQMYPIKTTAQLTREVYTD
        240     250     260     270     280     290
Cry1Ac PV----LENFDGS--FRGSA--QGIEGSI-RSPHLMIDILNSITTYDAHRGEYVWSGH
: : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 AIGTVHPHPSFTSTTWYNNNAPSFAIEAAVVRNPHLLDFLEQVITYLSLLSR----WSNT
        300     310     320     330     340     350

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        330     340     350     360     370     380
Cry1Ac QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLTSLYRRPFNIGIN---
: : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFL
        360     370     380     390     400     410
Cry1Ac NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
. : . . . . . : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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gi|332 TQPVNGVPRVDFHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSH
        420     430     440     450     460     470
Cry1Ac RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|332 RLSHIGLI-----SASHVKALVYSWTHRSADRINTIEPNSITQIPLVKAFNLSSGAAV
        480     490     500     510     520
Cry1Ac ISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNWNWGN
. : : : : : : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|332 VRGPGFTGGDILRRINTGT---FGDIRVNIK--PPFAQRYRVRIRYASTTDLQFHTSING
        530     540     550     560     570
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI--VGVNRNFSGTAGVIIDRFE
. : : : : : : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|332 KAINQGNFSATMNRGEDLDYKTRFRTVGFSTPPSFLDVQSTFTTIGAWNFSSGNEVYIDRIE
        580     590     600     610     620     630
Cry1Ac FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDE
. : : . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : :
gi|332 FVPVEVTYEAEYDFEKAQEKVTLFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDE
        640     650     660     670     680     690
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL
: : : : : : : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|332 KRELFEIVKYAKQLHIERNM
        700     710

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>>gi|1621216|emb|CAA70124.1| Bt toxin [Bacillus thuringi (719 aa)
  initn: 1376 initl: 689 opt: 1259 Z-score: 1477.0 bits: 284.6 E(): 2.4e-73
Smith-Waterman score: 1479; 38.732% identity (67.465% similar) in 710 aa overlap
(8-688:36-719)

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                10      20      30
Cry1Ac          CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGY
: : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|162 QDKHQSFSSNAKVDKISTDSLKNETDIELQINIHEDCLKMSEYENVE-PFVSASTIQTG-
        10      20      30      40      50      60
Cry1Ac TPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFIPG---SQWDAFLVQIEQLINQRIEE
: : . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 --IGIA---GKILGTLGVPPFAGQVASLYSIFILGELWPKGKNQWEIFMEHVEEIIINQKIST
        70      80      90      100     110

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```

        100     110     120     130     140     150
Cry1Ac FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
: : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|162 YARNKALTDLKGDLAVYHDSLESWVGNRNNRARSVVRVRSQYIALELMFVQKLPSPFAV
        120     130     140     150     160     170
Cry1Ac QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
. . : : : : : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :

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gi|162 SGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSDDHCVKW
180      190      200      210      220      230

          220      230      240      250      260      270
Cry1Ac YNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTN
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 YSTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPSYDTQMYPKTKTAQLTREYVTD
240      250      260      270      280      290

          280      290      300      310      320
Cry1Ac PV-----LENFDGS--FRGSA---QGIEGSI-RSPHMLDILNSITITYDAHRGEYYWSGH
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 AIGTVHPPHSFTSTTWNNNAPSFSIAEAAVVRNPHLLDFLEQVTIYSLLSR---WSNT
300      310      320      330      340      350

          330      340      350      360      370      380
Cry1Ac QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 QYMMN---WGGHKLEFRTIGGTLNISTQGSTNTSINPVTLPFTSRDVYRTELAGLNLFL
360      370      380      390      400      410

          390      400      410      420      430
Cry1Ac NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 TQPVNGVPRVDFHWKVFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSH
420      430      440      450      460      470

          440      450      460      470      480      490
Cry1Ac RLSHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 RLSHIGLI-----SASHVKALVYSWTHRSADRNTTIEPNSITQIPLVKAFNLSSGA
480      490      500      510      520

          500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 VRGPGFTGGDILRRTNTGT----FGDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSING
530      540      550      560      570

          560      570      580      590      600
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 KAINQGNFSATMNRGEDLDYKTFRTVGFSTPFSFLDVQSTFTIGAWNFSNGEVYIDRIE
580      590      600      610      620      630

          610      620      630      640      650      660
Cry1Ac FIPVTATLAEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 FVPVEVTYAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLD
640      650      660      670      680      690

          670      680      690      700      710      720
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 KRELFEIVKYANELHIERNM
700      710

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>>gi|46359602|dbj|BAD15303.1| parasporal crystal protein (1332 aa)
initn: 2023 initl: 672 opt: 1262 Z-score: 1476.6 bits: 285.4 E(): 2.5e-73

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Smith-Waterman score: 2205; 35.757% identity (59.718% similar) in 1348 aa overlap
(8-1182:23-1332)

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          10      20      30      40
Cry1Ac CMQAMDNNPN-INECIPYNCLSNPEVEVLGGERIETGYTPIDISL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 MQIIQPSSNALLYSPNKYPYATDPNVIAEGRSYNNWLDTCVGVGDGTRSPEAYIAEEAV
10      20      30      40      50      60

          50      60      70      80      90      100
Cry1Ac SLTQFLLSEFVPGAGFVLG--LVDIIWGFPG--SQWDAFLVQIEQLINQRIEFPARNOA
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 GLSIDILAEIIYYLGFPIASPLTRALSIAIAGQLFSSGDTLMQHEQLINQKIAEYARNSA
70      80      90      100      110      120

          110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 LAEFQGLGRQYGLYLEALEDEWQNRLSQPHKERVQTFRILDNSFTSSIPSAVRNYEVP
130      140      150      160      170      180

          170      180      190      200      210      220
Cry1Ac LLSVYVQANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 LLSVYADAANLHLLILRDSYIYGAFWGFDEDEYRNYARQIRLSAEYANHCTTWYQTGLR
190      200      210      220      230      240

          230      240      250      260      270
Cry1Ac RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLEN-
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 RLQGTTRATDWINYRFRREMTLTVLDICALFSSYDIPSPMGTKIQLTREIYTDVPHVSD
250      260      270      280      290      300

          280      290      300      310      320
Cry1Ac -FDGSRFG--SAQGIEG-SIRSPHMLDILNSITITYDAHR---GEY---YWSGHQIMA
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 WLQSTSPGLISFSSLENLVVRAPHLFTWLSRVITDITGILSTVIGGQYSNNNFWRTHYQTL
310      320      330      340      350      360

          330      340      350      360      370      380
Cry1Ac SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQLSVL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 RTTG--GTSFQSPYTG--TAFPIQRTNLTLPFSGDVYTISSVVTRSSLYGANSVAFTGT
370      380      390      400      410

          390      400      410      420      430      440
Cry1Ac DGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNS
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 TGRSL-YENPTVYPPA--QKL-----IHELPGVDSGRPNATINSHRSLYSIGFSLGYS
420      430      440      450      460

          450      460      470      480      490      500
Cry1Ac SVSIIIRAPMFSWIHRSA-EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLN
.: : : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 GTGLV---YGWTS'TTATRENNITLDDRIVQLPAVKGASLNNCQVVKGTFGGDWLKP
470      480      490      500      510      520

          510      520      530      540      550      560
Cry1Ac SSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSL

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      : : . . . . . : : : : : . . . . . : : : : : : :
gi|463 -----NNGTFSMYFAFRSAYT-YHFRIRYASSASFSFVISEEYGRFPPTTVPLLSMTS
      530      540      550      560      570

      570      580      590      600      610
Cry1Ac DNLSQSDFGYFFSANA-----FTSSLGNIVGVRNFS---GTAGVIIDRFEPVPTAT
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 PLPQNTPFPAFKTVDLDPSTVTIRYTSAASTTFQL-NFRFTVPGSANVLIDRIEFVPIEGS
      580      590      600      610      620      630

      620      630      640      650      660      670
Cry1Ac L---EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 LFEYETKQOLEKARKAVNHLFTDGSKKALKEDTTDYEIDQAANVVDICISDE-CGHEKMIL
      640      650      660      670      680      690

      680      690      700      710      720      730
Cry1Ac SEKVKHAKRLSDERNLLQDSNFKDINRQPER--GWGGSTGITIQGGDDVFKENYVTLSGT
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 LDEVKYAKQLSQARNLLNNGNFDLLYPALERENPWKTSFNVVIRQDNPIFKGHYLSMAGA
      700      710      720      730      740      750

      740      750      760      770      780
Cry1Ac FD----ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLLEIYSIRYNAKHETV-NVPG
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 NDIEATNDFTPYVYQKIDEAKLKPTRYKVRGFFVSSKDLLELVTRYNEEVDAILDVPD
      760      770      780      790      800      810

      790      800      810      820
Cry1Ac TGSLWPLSAQSPIGKCGEPNRCAPHL-----EWNPD-----DCSC-----
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 N---IP-HAPTVP--CGEFDRCKPYSYPLLEPCNPEFINQMOPSSCHHNQMVDDYNNMNT
      820      830      840      850      860

      830      840      850
Cry1Ac -----RDGEKCAHSHHFLSDIDVCGTDLNEDLVGVVIF
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 STSTTMNPSMNPPLTPEIASSQSGFGRKHKC-HQAHQFEFHIDTGTIDLVEDLGIWVIF
      870      880      890      900      910      920

      860      870      880      890      900      910
Cry1Ac KIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVD
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 KICATDGYASLDDLEVEEGALGVEALELVKKREKKWRHQEQHCSQTKHKYDAAKHAVM
      930      940      950      960      970      980

      920      930      940      950      960      970
Cry1Ac ALFVNSQYDQLQADNTIAMIHAADKRVHSI---REAYLPELSVIPGVNAAIFEELEGRIF
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 ALFTNTRYEKLFETTISDILYADHLVQSIPIVYNKYVPEVS---GMNYELYTELNTLVQ
      990      1000      1010      1020      1030      1040

      980      990      1000      1010      1020      1030
Cry1Ac TAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVPEWEAEVQSEVRCVCPG
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 NAFYLYDQRNLKNGRFSNGLMYQATPHARVE-QEYDRSVLVLPNDANVVSQQLCIEHN
      1050      1060      1070      1080      1090      1100

      1040      1050      1060      1070      1080

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Cry1Ac RGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNC-VEEEIYP----NNTVTCNDY---
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|463 RGYVLRVTARKEDEPGAGNVTFSDCANHVDKLSFTSCDIATNAVPGAQANDPAGVAYGQQ
      1110      1120      1130      1140      1150      1160

      1090      1100      1110
Cry1Ac --TVNQEEYGG-----AYTS-----RNRGY-----NEAPSVPADYASVYEE
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 GCQIDRVYPGSGYRADGVAYEQSGHRTDGVYPYRQSGYRADGVVAHDQPGYRAD-GVAYEQ
      1170      1180      1190      1200      1210      1220

      1120      1130      1140
Cry1Ac KSYT-----DGRRENPCFNRR-GY-----RDY-----TPLP-----
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 SGYRADGVAYEQSGHRRADGVYPYQSGYGTGDTGVTYDQSAKQTRKYHGCHTDGLPHEHGCC
      1230      1240      1250      1260      1270      1280

      1150      1160      1170      1180
Cry1Ac -----VGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|463 YPDRVSDGQQLAYVTKSIDLFPDPTDKVRIDIGETEGNFRVSVELICMEK
      1290      1300      1310      1320      1330

>>gi|111927193|gb|ABH71845.1| Sequence 18 from patent US (1332 aa)
      initn: 2023 initl: 672 opt: 1262 Z-score: 1476.6 bits: 285.4 E(): 2.5e-73
      Smith-Waterman score: 2205; 35.757% identity (59.718% similar) in 1348 aa overlap
      (8-1182:23-1332)

      10      20      30      40
Cry1Ac          CMQAMDNNPN-INECIPYNCLSNPEVEVLGGERIETGYTPIDISL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 MQIIQPSSNALLYSPNKYPYATDPNVAIEGRSYNNWLDTCVGVGDGTRSPEAYAAIEEAV
      10      20      30      40      50      60

      50      60      70      80      90      100
Cry1Ac SLTQPLLSEFVPGAGFVLG--LVDIIWGIFGP--SQWDAFLVQIEQLINQRIEFPARNQA
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|111 GLSIDILAEIIYYLGFPIASPLTRALSIAIAGQLFSSGDTLMQHIEQLINQKIAEYARNKA
      70      80      90      100      110      120

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMSALTTAIPLFAVQNYQVP
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|111 LAEFQGLGRQYGLYLEALEDWEQNRLSQPHKERVQRIFRILDNSFTSSIPSAVRYNEVP
      130      140      150      160      170      180

      170      180      190      200      210      220
Cry1Ac LLSVYVQAAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAWRVYNTGLE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 LLSVYADAANLHLLILRDSYIYGAFWGFDEDEYRNYARQIRLSAEYANHCCTTWYQTGLR
      190      200      210      220      230      240

      230      240      250      260      270
Cry1Ac RVWGPDSDRWIRYNQFRELTLTVLDIVSLFPNYSRTPYIRTVSOLTREIYTNPVLEN-
      : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|111 RLQGTDRATDWINYRFRREMTLTVLDICALFSSYDIPSPMGTKIQLTREIYTDVPHVSD
      250      260      270      280      290      300

      280      290      300      310      320

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Cry1Ac -FDGSFRG--SAQGIIEG-SIRSPHLMIDLNSITIIYTDADR----GEY----YWSGHQIMA
gi|111 WLQSTSPGLISFSSLENLVRAPHLFTWLSRVITDITGILSTVIGGOYSNNFNWRTHYQTL
      310      320      330      340      350      360
Cry1Ac 330 340 350 360 370 380
Cry1Ac SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRFPNIGINNQQLSVL
gi|111 RTTG--GTSFQSPITYGS--TAFPIQRTNLTFTSGDVYTIESSVVRTSSLYGANSVAFTGT
      370      380      390      400      410
Cry1Ac 390 400 410 420 430 440
Cry1Ac DGTEFAYGTSSNLPSAVYRKSGTVDLSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNS
gi|111 TGRSL-YENPTVYPPFA--QKL-----IHLELPGVDSGRPNATNYSHRLSYISGFSGLGYSFS
      420      430      440      450      460
Cry1Ac 450 460 470 480 490 500
Cry1Ac SVSIIIRAPMFSWIHRSA-EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLN
gi|111 GTGLV----YGMTSTTATRENNITLDDRIVQLPAVKASLNNCQVVKGTGFTGGDLWLPKN
      470      480      490      500      510      520
Cry1Ac 510 520 530 540 550 560
Cry1Ac SSGNNIQNRGYIEVP IHFPSTSTRYRVVRYASVTP IHLNVNWGSSIFSNTVPATATSL
gi|111 -----NNGTFSMYAFRSAYT-YHFRIRYASSASFSFVISEEYGRPPTTTVPLLSTMS
      530      540      550      560      570
Cry1Ac 570 580 590 600 610
Cry1Ac DNLSQSDFGYFESANA-----FTSSLGNIVGVRNFS---GTAGVIIDREFIPVTAT
gi|111 PLPQNTPEAFKTVDLSPSTVTIRYTSAASTTFQL-NFRFTVPGSANVLIDRIEFVPIEGS
      580      590      600      610      620      630
Cry1Ac 620 630 640 650 660 670
Cry1Ac L---EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
gi|111 LFEYETKQLEKARKAVNHLFTDGSKKALKEDTTDYEIDQAANVDCISDE-CGHEKMIL
      640      650      660      670      680      690
Cry1Ac 680 690 700 710 720 730
Cry1Ac SEKVKHAKRLSDERNLLQDSNFKDINRQPER--GWGGSTGITIQGGDDVFKENYVTLSGT
gi|111 LDEVKAYAKLSQARNLLNNGFNDDLYPALERENPKWTSFVNTIRQDNPIFKGHYLSMAGA
      700      710      720      730      740      750
Cry1Ac 740 750 760 770 780
Cry1Ac FD----ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
gi|111 NDIEATNDTFFPTYVYQKIDEAKLKPTRYKVRGFGVSSKDLLELVTRNEEVDAILDVPD
      760      770      780      790      800      810
Cry1Ac 790 800 810 820
Cry1Ac TGSWLPLSAQSPIGKCGEPNRCAPHL-----EWNPDL-----DCSC-----
gi|111 N---IP-HAPTPV--CGEFDRCKPYSYPPLLPECPNPEFINMQPSSCHHNQMVDDYNNMNT
      820      830      840      850      860

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Cry1Ac -----RDGEKCAHSHHFLSLDIDVGTDLNEDLVGVVIF
gi|111 STSTTMNPNMPLTPEIASSQSGFGRKHKRC-HQAHQFEFHIDTGTIDLVEDLGIWVIF
      870      880      890      900      910      920
Cry1Ac 860 870 880 890 900 910
Cry1Ac KIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVD
gi|111 KICATDGYASLDDLEVEIEGALGVEALELVKKREKKWRHQEQHCSQTKHKYDAAKHAVM
      930      940      950      960      970      980
Cry1Ac 920 930 940 950 960 970
Cry1Ac ALFVNSQYDQLQADTNIAMHAADKRVHSI---REAYLPELSVIPGVNAAIPEELEGRIF
gi|111 ALFTNTRYEKLFKPFETTISDILYADHLVQSIPIVYVYKYPVEVS---GMNYELYTELNTLVQ
      990      1000      1010      1020      1030      1040
Cry1Ac 980 990 1000 1010 1020 1030
Cry1Ac TAFSLYDARNVIKNGDFNNGLSQWNVKGVHDVVEEQNNQRSLVLPVEWEAEVSEQEVRVCPG
gi|111 NAFYLYDQRNLKNGRFSNGLMYQATPHARVE-QEYDRSVLVLPLNWDANVSQQLCIEHN
      1050      1060      1070      1080      1090      1100
Cry1Ac 1040 1050 1060 1070 1080
Cry1Ac RGYILRVTAKEGYEGECVTHEIENNTDELKFSNC-VEEEIYP----NNTVTCNDY---
gi|111 RGYVLRVTAKEKDPGAGNVTFSDCANHVDKLSFTSCDIATNAVPGAQANDPAAGVAYGQQ
      1110      1120      1130      1140      1150      1160
Cry1Ac 1090 1100 1110
Cry1Ac --TVNQEYGG-----AYTS-----RNRGY-----NEAPSVPADYASVYEE
gi|111 GCQIDRVYPGPGSYRADGVAYEQSGHRTDGVYPYRQSGYRADGVAHDQPGYRAD-GVAYEQ
      1170      1180      1190      1200      1210      1220
Cry1Ac 1120 1130 1140
Cry1Ac KSYT-----DGRRENPCFN-RGY-----RDY-----TPLP-----
gi|111 SGYRADGVAYEQSGHRRADGVYPYQSGYGTGVTYDQSAKQTRKYHGCHTDGLPHEHGCC
      1230      1240      1250      1260      1270      1280
Cry1Ac 1150 1160 1170 1180
Cry1Ac -----VGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|111 YPDRVSDGQQLAYVTKSIDLFPDTPDKVRIDIGETEGNFRVSVELICMEK
      1290      1300      1310      1320      1330
>>gi|29329431|emb|CAD83755.1| unnamed protein product [P (1332 aa)
initn: 2023 init1: 672 opt: 1262 Z-score: 1476.6 bits: 285.4 E(): 2.5e-73
Smith-Waterman score: 2205; 35.757% identity (59.718% similar) in 1348 aa overlap
(8-1182:23-1332)
Cry1Ac 10 20 30 40
Cry1Ac CMQAMDNNPN-INECIPYNCLSNPEVEVLGGERIETGYTPIDISL
gi|293 MQIIQPPSSNALLYSPNKYPYATDPNVIAEGRSYNNWLDTCVGVGDGTRSPEAYAIIEEAV
      10      20      30      40      50      60

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50      60      70      80      90      100
Cry1Ac  SLTQFLLESEFVPGAGFVLG--LVDIWGF--SQWDAFLVQIEQLINQRIEEFARNQA
gi|293  GLSIDILAEIYYLGFPIASPLTRALSATAGQLFSSGDTLMQHIEQLINQKIAEYARNKA
70      80      90      100      110      120

110     120     130     140     150     160
Cry1Ac  ISRLEGLSNLYQIYAESFREWEADPTNAPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|293  LAEFQGLGRQYGLYLEALEDEWQNRLSQPHKERVQTFRILDNSFTSSIPSFAVRNYEVP
130     140     150     160     170     180

170     180     190     200     210     220
Cry1Ac  LLSVYVQAANLHLSVLRDVSFVQWRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|293  LLSVYADAANLHLLILRDSYIYGAFWGFDEDEYRNYARQIRLSAEYANHCTTWYQTGLR
190     200     210     220     230     240

230     240     250     260     270
Cry1Ac  RVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLN-
gi|293  RLQGTTRATDWINYNRFRREMTLTVLDICALFSSYDIPSPMGTKIQLTREIYTDVPHVSD
250     260     270     280     290     300

280     290     300     310     320
Cry1Ac  -FDGSRFG--SAQGIIEG-SIRSPHLMIDILNSITIYTDADR---GEY---YWSGHQIMA
gi|293  WLQSTSPGLISFSSLENLVVRAPHLFTWLSRVTIDTIGILSTVIGGQYSNNFWRTHYQTL
310     320     330     340     350     360

330     340     350     360     370     380
Cry1Ac  SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVL
gi|293  RTTG--GTSFQSPTYGS--TAFPIQRTNLTFSGDVYTISSVVTSSLYGANSVAFTGT
370     380     390     400     410

390     400     410     420     430     440
Cry1Ac  DGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFNS
gi|293  TGRSL-YENPTVYPFA--QKL-----IHLEPGVDSGRPNATNYSHRLSYISGFSLGYSPS
420     430     440     450     460

450     460     470     480     490     500
Cry1Ac  SVSIIIRAPMFWSIHRSA-EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLN
gi|293  GTGLV----YGWTS'TATRENNITLDDRIVQLPAVKASLNNCQVVKGTGPTGGDWLKP
470     480     490     500     510     520

510     520     530     540     550     560
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNVWGNSSIFSNTVPATATSL
gi|293  -----NNGTFSMYFAFRSAYT-YHFRIRYASSASFSFVISEEYGRFPTTVPVLLSTMS
530     540     550     560     570

570     580     590     600     610
Cry1Ac  DNLQSSDFGYFESANA-----FTSSLGNIVGVRNFS---GTAGVIIDRFEFIPVTAT
gi|293  PLPQNTPEFAKFTVDLPSTVTIRYTSAASTFQL-NFRFTVPGSANVLIDRIEFVPIEGS
580     590     600     610     620     630

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620     630     640     650     660     670
Cry1Ac  L---EAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDEFCLDEKREL
gi|293  LFEYETKQQLKARKAVNHLFTDGSKKALKEDTTDYEIDQAANVVDICISDE-CGHEKMIL
640     650     660     670     680     690

680     690     700     710     720     730
Cry1Ac  SEKVKHAKRLSDERNLLQDSNFKDINRQPER--GWGGSTGITIQQGDDVFKENYVTLSTG
gi|293  LDEVKYAKQLSQARNLLLNNGNFDLLPALERENPWKTSPNVTIRQDNPFIKGYLSMAGA
700     710     720     730     740     750

740     750     760     770     780
Cry1Ac  FD----ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
gi|293  NDIEATNDTFPTYVYQKIDEAKLKPTRYKVRGFGVSSKDELLLVTRYNEEVDAILDVPD
760     770     780     790     800     810

790     800     810     820
Cry1Ac  TGSWLPLSAQSPIGKCGEPNRCAPHL-----EWNPD-----DCSC-----
gi|293  N---IP-HAPTPV---CGEFDRCCKPYSYPLLPECNPEFINQMPPSSCHHNQMVYNNMNT
820     830     840     850     860

830     840     850
Cry1Ac  -----RDGEKCAHSHHFLDLDVIGCTDLNEDLGIWVIF
gi|293  STSTTMNPSMNPPLTPEIASSQSGFGRKHKRC-HQAHQFHFHIDTGTIDLVEDLGIWVIF
870     880     890     900     910     920

860     870     880     890     900     910
Cry1Ac  KIKTDGCHARLGNLEFLLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKESVD
gi|293  KICATDGYASLDDLEVEEGALGVEALELVKKREKKWRHQEQHCSQTKHKYDAAKHAVM
930     940     950     960     970     980

920     930     940     950     960     970
Cry1Ac  ALFVNSQYDQLQADTNIAMIAHADKRVHSI---REAYLPELSVIPGVNAAIFEELEGRIF
gi|293  ALFTNTRYEKLFETTISDILYADHLVQSIPYVYNYKYPVEVS---GMNYELYTELNTLVQ
990     1000     1010     1020     1030     1040

980     990     1000     1010     1020     1030
Cry1Ac  TAFSLYDARNVIKNGDFNNGLSNVCWVKGHVDEEQQNQRSVLPVPEWEAEVSEVVRVCPG
gi|293  NAFYLYDQRNLKNGRFSNGLMYQATPHARVE-QEYDRSVLVLNWDANVSQQLCIEHN
1050     1060     1070     1080     1090     1100

1040     1050     1060     1070     1080
Cry1Ac  RGYILRVTAKEGEGCVTIHEIENNTDELKFSNC-VEEIIYP---NNTVTCNDY---
gi|293  RGYVLRVTARKEDEPGAGNVTFSDCANHVDKLSFTSCDIATNAVPGAQANDPAAGVAYGQQ
1110     1120     1130     1140     1150     1160

1090     1100     1110
Cry1Ac  --TVNQEEYGG-----AYTS-----RNRGY-----NEAPSVPADYASVYEE
gi|293  GCQIDRVYPYGPSYRADGVAYEQSGHRTDGVYPRQSGYRADGVAHDQPGYRAD-GVAYEQ

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gi|322 RLSHIGLI-----SASHVKALVYSWTHRSADRTNTIEPNSITQIPLVKAFNLSSGAAV
          480      490      500      510      520

          500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|322 VRGPGFTGGDILRRNTTGT---FGDIRVNIN-PPFAQRYRVRIRYASTTDLQFHTSING
          530      540      550      560      570

          560      570      580      590      600
Cry1Ac SSIFSNTPATATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|322 KAINQGNFSATMNRGEDLDYKTRFTVGFSTPPSFQVSTFTIGAWNFSSGNEVYIDRIE
          580      590      600      610      620      630

          610      620      630      640      650      660
Cry1Ac FIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|322 FVPVEVTYEAAYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVESLSDEFYLDE
          640      650      660      670      680      690

          670      680      690      700      710      720
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|322 KRELFEIVKYANELHIERNM
          700      710

```

>>gi|159131958|gb|ABW88019.1| Cry1Ib-type protein [Bacil (719 aa)  
 initn: 1392 initl: 685 opt: 1255 Z-score: 1472.3 bits: 283.7 E(): 4.3e-73  
 Smith-Waterman score: 1477; 40.030% identity (68.601% similar) in 672 aa overlap  
 (55-688:76-719)

```

          30      40      50      60      70      80
Cry1Ac VEVLGGERIEGTGYPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGP---SQWDAFL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 SEHESIDPFVRASTIQTGIGIAGKILGTLGVFPAGQIASLSYFILGELWPKGKSQWEIFM
          50      60      70      80      90      100

          90      100      110      120      130      140
Cry1Ac VQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 EHVEEIIINQKILTYARNKAPSDLRGLGDALAVYHESLESWVENRNNTRRASVVKNYIAL
          110      120      130      140      150      160

          150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQWRGFDAAATINSRYNDLT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 ELMFVQKLPFAVSGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSASEISTFYNRQV
          170      180      190      200      210      220

          210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 ERTRDYSDHCIKWYNTGLNLRGTNAKSWVRYNQFRKDMTLMVLDLVALFSPSYDTLVYPI
          230      240      250      260      270      280

          270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPVL----ENFDGS--FRGSA--QGIEGS-IRSPHLMIDLNSITFY
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi|159 KTTSQLTREVYTDAGTVHPNQAFASSTTWYNNNAPSFSIAEAAVIRSPHLLDFLEKVTIY
          290      300      310      320      330      340

          320      330      340      350      360
Cry1Ac TDAHR---GEYY--WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 SLLSRWSNTQYMMMWGGHRLSRPIG-----GAL-NTSTQGSTNTSINPVTLQF
          350      360      370      380      390

          370      380      390      400      410
Cry1Ac LSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNLPASAVYRKSGTV--DSL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 TSRDVYRTESWAGLNLFLTQPVNGVPRVDFHWKFPFLPIASDNFYLYGAGVGTQLQDSE
          400      410      420      430      440      450

          420      430      440      450      460      470
Cry1Ac DEIPPNQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDS
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 NELPPETTQPNYESYSHRLSHIGLI-----SASHVKALVYSWTHRSADRTNTIEPNS
          460      470      480      490      500

          480      490      500      510      520      530
Cry1Ac ITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 ITQIPLVKAFNLSSGAAVVRGPGFTGGDILRRNTTGT---FGDIRVNIN-PPFAQRYR
          510      520      530      540      550      560

          540      550      560      570      580      590
Cry1Ac VRVRYASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLG--NI-
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 RIRYASTTDLQFHTSINGKAINQKFSATMNRGEDL---DYKTRFTVGF-FTTFFGFSDVQ
          570      580      590      600      610

          600      610      620      630      640
Cry1Ac ---VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 STFTIGAWNFSSGNEVYIDRIEFVVPVEVTYEAAYDFEKAQEKVTALFTSTNPRGLKTDVK
          620      630      640      650      660      670

          650      660      670      680      690      700
Cry1Ac DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGW
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|159 DYHIDQVSNLVESLSDEFYLDEKRELFEIVKYAKQIHIERNM
          680      690      700      710

          710      720      730      740      750      760
Cry1Ac GSTGITIQQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDL

```

>>gi|40290|emb|CAA44633.1| delta-endotoxin [Bacillus thu (719 aa)  
 initn: 1368 initl: 674 opt: 1251 Z-score: 1467.6 bits: 282.8 E(): 8e-73  
 Smith-Waterman score: 1471; 38.592% identity (67.324% similar) in 710 aa overlap  
 (8-688:36-719)

```

          10      20      30
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 QDKHQFSSSNAKVDKISTDSLKNETDIELQNINHEDCLMSEYENVE-PFVSASTIQTG-
          10      20      30      40      50      60

```

```

      40      50      60      70      80      90
Cry1Ac TPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGIFGP---SQWDAFLVQIEQLINQRIEE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 --IGIA---GKILGTGLGVFPAGQVASLYSFLGELWPKGKNQWEIFMEHVEEIIINQKIST
      70      80      90      100     110

```

```

      100     110     120     130     140     150
Cry1Ac FARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 YARNKALTDLKLGDALAVYHDSLESWVGNRRNTRARSVVKSQYIALELMFVQKLPSPFAV
      120     130     140     150     160     170

```

```

      160     170     180     190     200     210
Cry1Ac QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 SGEEVPLLPPIYAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGDYSYHCVKW
      180     190     200     210     220     230

```

```

      220     230     240     250     260     270
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 YSTGLNLRGTNAESWVRYNQFRDMTLMVLDLVALFPDYTQMPIKTTAQLTREYVTD
      240     250     260     270     280     290

```

```

      280     290     300     310     320
Cry1Ac PV-----LENFDGS--FRGSA---QGIEGSI-RSPHLMIDILNSITTYTDAHRGEYYWSGH
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 AIGTVHPPSFTSTTWNYNNAFSAIEAAVVRNPHLLDFLEQVTIYSLLSR----WSNT
      300     310     320     330     340     350

```

```

      330     340     350     360     370     380
Cry1Ac QIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN---
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 QYMMN---WGGHKLFBRTIGGTNLNISTQGSTNTSINPVTLPFTSRDVRTESLAGLNLFL
      360     370     380     390     400     410

```

```

      390     400     410     420     430
Cry1Ac NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSSH
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 TQPVNGVPRVDFHWKVFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATQPNYESYSH
      420     430     440     450     460     470

```

```

      440     450     460     470     480     490
Cry1Ac RLSHVSMSFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-V
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 RLSHIGLI-----SASHVKALVYSWTHRSADRNTTIEPNISITQIPLVKAFNLSSGAAV
      480     490     500     510     520

```

```

      500     510     520     530     540     550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLMNVNWN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 VRGPGFTGGDLRLRNTGT---FGDIRVNIIN-PPFAQRVYRIRYASTTDLQFHTSING
      530     540     550     560     570

```

```

      560     570     580     590     600
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI-VGVRNFSGTAGVIIDRFE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 KAINQGNFSATMNRGEDLDYKTFRTVGFPTTFFSFLDVQSTFTIGAWNFSSGNEVYIDRIE
      580     590     600     610     620     630

```

```

      610     620     630     640     650     660
Cry1Ac FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTVLSDEFCLDE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 FVPVEVTYEAEYDFEKAQEKVTALFTSTNPRGLKTDVKDYHIDQVSNLVTVLSDEFYLD
      640     650     660     670     680     690

```

```

      670     680     690     700     710     720
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVPKENYVTVLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 KRELFEIVKYAKQLHIERNM
      700     710

```

>>gi|39653331|gb|AAR29332.1| Cry1A [Bacillus thuringiensis (193 aa)  
 initn: 1242 init1: 1242 opt: 1242 Z-score: 1465.5 bits: 280.5 E(): 1e-72  
 Smith-Waterman score: 1242; 96.373% identity (97.409% similar) in 193 aa overlap  
 (245-437:1-193)

```

      220     230     240     250     260     270
Cry1Ac YNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|396                                LDIVALFPNYDSRRYPVRTVSQLTREIYTN
                                      10          20          30

```

```

      280     290     300     310     320     330
Cry1Ac PVLENFDGSFRGSAQGIIEGSI-RSPHLMIDILNSITTYTDAHRGEYYWSGHQIMASPVGFGS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|396 PVLENFDGSFRGSAQGIERSIRSPHLMIDILNSITTYTDAHRGYYWSGHQIMASPVGFGS
      40      50      60      70      80      90

```

```

      340     350     360     370     380     390
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINQQLSVLDGTEFAY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|396 PEFTFPLYGSMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINQQLSVLDGTEFAY
      100     110     120     130     140     150

```

```

      400     410     420     430     440     450
Cry1Ac GTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMSFRSGFSNSSVSIIRA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|396 GTSSNLPSAVYSISGTVDSLDEIPPQNNVPPRQGFSHRLSHV
      160     170     180     190

```

```

      460     470     480     490     500     510
Cry1Ac PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNIIQN

```

>>gi|5531642|gb|AAD44366.1|AF047579\_1 insecticidal cryst (719 aa)  
 initn: 1354 init1: 678 opt: 1246 Z-score: 1461.7 bits: 281.7 E(): 1.7e-72  
 Smith-Waterman score: 1462; 38.802% identity (67.760% similar) in 701 aa overlap  
 (18-688:41-719)

```

      10      20      30      40
Cry1Ac          CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|553 SFSSNATVDKSFDTPLHEHTNMELQNSNHEDCLKMSEYESV---EPFVSVSTIQTGIGIA
      20      30      40      50      60

```

```

      50      60      70      80      90     100
Cry1Ac QFLLSEF-VPGAGFVLGLVDIIWGIFGP---SQWDAFLVQIEQLINQRIEEFARNQAIISR
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```





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Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGY  
gi|436 YEIIDATPSTSVSSDSNRYPFANEPTDALQNMNYKDYLKMSGGENPEL--FGNPETFISS  
10 20 30 40 50 60

Cry1Ac TPIDISLSLTQFLLSEF-VPGAGFVLGLVDIIWGFPGSQ---WDAFLVQIEQLINQRI  
gi|436 STIQTGIGIVGRILGALGVPPASQIASFYSFIVGQLWPSKSVDIWGEIMERVEELVDQKI  
70 80 90 100 110 120

Cry1Ac EEFARNQALSRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTITAIPLF  
gi|436 EKYVKDKALAEKGLGNALDVYQQLSLEDWLENRNDARTRSVSNQFIALDLNLFVSSIPSF  
130 140 150 160 170 180

Cry1Ac AVQNYQVPLLVSYYQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGNYTDHAV  
gi|436 AVSGHEVLLLVAVYAQAVNLHLLLLLDASIFGEEWGFPTPEISRFYNRQVQLTAEYSYCV  
190 200 210 220 230 240

Cry1Ac RWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPVRTVSQLTREIY  
gi|436 KWYKIGLDKLGKTTSSKSWLNHYQFRREMTLLVLDLVALFPNYDTHMYPIETTAQLTRDVIY  
250 260 270 280 290 300

Cry1Ac TNPVLENFDGFSFR----GSAQGI-----EGSIRSPLHMDILNSITITYTDAHRG----  
gi|436 TDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVIRPPHFLFDLSSVEINTS--RGGITLN  
310 320 330 340 350 360

Cry1Ac --EY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLSTLYR  
gi|436 NDAYINYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLSTLYR  
370 380 390 400 410

Cry1Ac RPFNIGINNQQLSVLDGTEFAY---GTSSNLPASAVYRKSQTV-----DSLDEIPPPQN  
gi|436 ---NLANYQKAYGVPGSWFHMVKRGTSSST--AYLYSKTHTALQCGTQVYESSDEIP-LD  
420 430 440 450 460 470

Cry1Ac NNVPPRQGFSHRLSHVSMFRSGFS--NSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
gi|436 RTVPVAESYSHRLSHIT--SHSFSKNGSAYYGSFPVFWTHTSADLNNTIYSDKITQIPA  
480 490 500 510 520 530

Cry1Ac VKGNFLF-NGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS  
gi|436 VKGDMLYLGGSVVQPGFTGGDILK---RTNPSILGTFAVTVN--GSLQRVYRVRIRYAS

Cry1Ac VTP IHLNVNWGNS---SIFSNTVPATAT-SLDNLQS---SDFGYFESANAFSTSSLGNIV  
gi|436 TDFEFTLYLGDITIEKNRFRNKMDNGASLTYETFKFASFITDFQFRETQDKILLSMGD--  
540 550 560 570 580 590

Cry1Ac GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHID  
gi|436 ---FSSGQEVYIDRIEFIPVDETYEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVN  
600 610 620 630 640 650

Cry1Ac QVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGI  
gi|436 QAANLVECLSDLLYPNEKRLLDVAVREAKRLSGARNLLQDPDFQEI--GENGWAASTGI  
660 670 680 690 700 710

Cry1Ac TIQGGDDVPKENVYVTLSGTFD--ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI  
gi|436 EIVEGDAVFKGRYLRLPGAREIDTETYPTYLYQKVEEGVLKPYTRYRLRGFVSSQGLEI  
720 730 740 750 760 770

Cry1Ac YSIRYNAKHETVNVVPGTGLSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAH  
gi|436 YTIIRHQTNIRIVKNVP--DDLPL--DVSPVNSDGSINRCSEQKYVNSRLEGENRSGD---  
780 790 800 810 820 830

Cry1Ac HSHHFLSLDIDVCGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAE  
gi|436 -AHEFSLPIDIGELDYNENAGIWWGFKITDPEGYATLGNLELVEEGPLSGDALERLQREE  
840 850 860 870 880 890

Cry1Ac KKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNLAMIHAADKRVHSIREAY  
gi|436 QQWKIQMTRRREETDRRYMASKQAVDRLYADYQDQQLNPDVEITDLTAAQDLIQSIPYVY  
900 910 920 930 940 950

Cry1Ac LPELSVIPGVNAIIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHVDVEEQNN  
gi|436 NEMFPEIPGMNYTKFTELTDRLQQAOWNLYDQRNAIPNGDFRNGLSNWNATPGVEVQ-QIN  
960 970 980 990 1000 1010

Cry1Ac QRSVLVVPWEAEVSVQEVRCVGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFSNCV  
gi|436 HTSVLVIPNWDQVSVQQTVPQNRVYVLRVTRARKEGVGNGYVSIIRGGNQSETLTFSA--  
1020 1030 1040 1050 1060 1070

Cry1Ac EEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRREN  
1080 1090 1100 1110 1120



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gi|161 NEMFPEIPGMNYTKFTELTDRLQQAWNLYDQRNAIPNGDFRNLGNWATPGEVQ-QIN
990 1000 1010 1020 1030 1040

Cry1Ac QRSVLVPEWEAEVSEQEVRVCPGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCV

gi|161 HTSVLVIPNWDEQVSQQFTVQPNQRYVLRVTARKEGVNGVYSIRDGNGQSETLTFSA--
1050 1060 1070 1080 1090 1100

Cry1Ac EEEIYPNNVTVCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRREN

gi|161 -----SDYDTN-----GVIYNDQT-----
1110

Cry1Ac CEFNRGYRDYTPPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|161 -----GYITKTVTFIPYTDQMWIEISETEGTFYIESVELIVDVE
1120 1130 1140 1150

>>gi|61891427|emb|CAI72241.1| unnamed protein product [B (712 aa)
initn: 1318 initl: 661 opt: 1214 Z-score: 1424.0 bits: 274.8 E(): 2.1e-70
Smith-Waterman score: 1430; 38.914% identity (68.175% similar) in 663 aa overlap
(55-688:69-712)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPG---SQWDAFL
30 40 50 60 70 80

gi|618 SEHESIDPFVNVSTIQTGIGIAGKILGTLGVPPFAGQIASLSYFILGELWPKGKSQWEIFM
40 50 60 70 80 90

Cry1Ac VQIEQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
90 100 110 120 130 140

gi|618 EHVEELIDQKISTYARNIALADLKLGLDALAVYHESLESWIKNRNARATS VVKSQYIAL
100 110 120 130 140 150

Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLT
150 160 170 180 190 200

gi|618 ELLFVQKLPSPFAVSGEEVPLLPPIYAQAANLHLLLRDASVFGKEWGLSNSQISTFYNRQV
160 170 180 190 200 210

Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDDIVSLFPNYSRTYPI
210 220 230 240 250 260

gi|618 ERTSDYSDHCVKWYSTGLNLRGTNAESWVRYNQFRKDMTMLVLDLIALFPYSYDLVYPI
220 230 240 250 260 270

Cry1Ac RTVSQLTREIYTNPV-LENFDGSRGSA-----QIEGSI-RSPHLMIDILNSITII
270 280 290 300 310

gi|618 KTTSQLTREYVYDAIGTVHPNASFASTTWNNAAPSFAIESAVVRNPHLLDFLEQVYTIY
280 290 300 310 320 330

Cry1Ac TDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRILSSTL
320 330 340 350 360 370

gi|618 SLLSR----WSNTQYMM--WGGHRLFEFRTIGGVLNTSTQGSTNTSINPVTLPFTSRDV
340 350 360 370 380 390

Cry1Ac YRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNLPASAVYRKSQTV--DSLDEIPP
380 390 400 410

gi|618 YRTESLAGLNFLTPQVNVGPRVDFHWKFATLP IASDNFYYPGYAGIGTQLQDSENELPP
400 410 420 430 440 450

Cry1Ac QNNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNII IASDSITQIP
420 430 440 450 460 470

gi|618 ETTGQPNYESYSHRLSHIGLI-----SASHVKALVYSWTHRSADRTNTEIPNSITQIP
460 470 480 490 500

Cry1Ac AVKGNFLFNNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYA
480 490 500 510 520 530

gi|618 LVKAFNLSSGAAVVRGPGFTGGDILRRNTGT----FGDIRVNIIN-PPFAQRYRVRIRYA
510 520 530 540 550

Cry1Ac SVTPIHLNVWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFSSLGNI-VGVRN
540 550 560 570 580 590

gi|618 STTDLQFHTSINGRAINQGNFSA TMNRGEDLEYRTFRTVGFPTTFFSDFVQSTFTIGAWN
560 570 580 590 600 610

Cry1Ac FSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
600 610 620 630 640 650

gi|618 FSSGNDVYIDRIEFVPEVPEYEEYDFEKVQEEVTALFTSTNPRELKTVDYHIDQVSN
620 630 640 650 660 670

Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQG
660 670 680 690 700 710

gi|618 LVESLSEDFYLDEKRELFEIVKYVKQLNIERDM
680 690 700 710

Cry1Ac GDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNA
720 730 740 750 760 770

>>gi|61891425|emb|CAI72240.1| unnamed protein product [B (719 aa)
initn: 1318 initl: 661 opt: 1214 Z-score: 1424.0 bits: 274.8 E(): 2.1e-70
Smith-Waterman score: 1430; 38.914% identity (68.175% similar) in 663 aa overlap
(55-688:76-719)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPG---SQWDAFL
30 40 50 60 70 80

gi|618 SEHESIDPFVNVSTIQTGIGIAGKILGTLGVPPFAGQIASLSYFILGELWPKGKSQWEIFM
50 60 70 80 90 100

Cry1Ac VQIEQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
90 100 110 120 130 140

gi|618 EHVEELIDQKISTYARNIALADLKLGLDALAVYHESLESWIKNRNARATS VVKSQYIAL
110 120 130 140 150 160

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150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQWRGFDAAATINSRYNDLT
gi|618 ELLFVQKLPSPFAVSGEEVPLLPPIYAQAANLHLLLRDASVFKWGLSNSQISTFYNRQV
170      180      190      200      210      220

210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|618 ERTSDYSDHCVKDYSTGLNNLRGTNAESVWRVYNQFRKDMTMLVLDLIALFPPSYDTLVYPI
230      240      250      260      270      280

270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPV-LENFDGSRGSA-----QGIEGSI-RSPHLMIDLNSITIIY
gi|618 KTTSQLTREVYTDAGTVHPNASFASTTWYNNNAPSFAIESAVVRNPHLLDFLEQVTIY
290      300      310      320      330      340

320      330      340      350      360      370
Cry1Ac TDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL
gi|618 SLLSR----WSNTQYMMN---WGGHRLFEFRTIGGVLNLTSTQGSTNTSINPVTLPFSTRDV
350      360      370      380      390

380      390      400      410
Cry1Ac YRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSQTV--DSLDEIPP
gi|618 YRTESLAGLNLFLTQPVNGVPRVDFHWKATLPIASDNFYYPGYAGIGTQLQDSENELPP
400      410      420      430      440      450

420      430      440      450      460      470
Cry1Ac QNNNVPRQGFQSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIP
gi|618 ETTGQPNYESYSHRLSHIGLI-----SASHVKALVYSWTHRSADRTNTIEPNSITQIP
460      470      480      490      500      510

480      490      500      510      520      530
Cry1Ac AVKGNFLPFGS-VISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYA
gi|618 LVKAFNLSSGAAVVRGPGFTGGDILRRTNTGT---FGDIRVNIIN-PPFAQRYRVRIRYA
520      530      540      550      560

540      550      560      570      580      590
Cry1Ac SVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSSLGNI-VGVRN
gi|618 STTDLQFHSTINGRAINQGNFSATMNRGEDLEYRTFRTVGFSTPPFSFSDVQSTFTIGAWN
570      580      590      600      610      620

600      610      620      630      640      650
Cry1Ac FSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSN
gi|618 FSSGNDVYIDRIEFVFPVEVPEEYDFEKVQEEVTLFTSTNPRELKTVDYHIDQVSN
630      640      650      660      670      680

660      670      680      690      700      710
Cry1Ac LVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQG
gi|618 LVESLSDEFYLDEKRELFIVKYVKQLNIERDM

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690      700      710
Cry1Ac GDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNA

>>gi|13173244|gb|AAK14339.1| insecticidal crystal protei (1155 aa)
initn: 4071 initl: 1181 opt: 1211 Z-score: 1417.3 bits: 274.2 E(): 5e-70
Smith-Waterman score: 3977; 59.932% identity (73.487% similar) in 1173 aa overlap
(5-1153:1-1120)

10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|131 MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
10      20      30      40      50

70      80      90      100      110
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI---SRLEGLSNLYQIYAES
gi|131 VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIENSLGTPFLDWKAKQSLSNLRI----
60      70      80      90      100      110

120      130      140      150      160      170
Cry1Ac FREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLR
gi|131 FREWEADPTNPALREEMRIQFNARTSALTTAIPLFAVQNYQVPLLSVYVQAANLRFST-R
120      130      140      150      160      170

180      190      200      210      220      230
Cry1Ac DVSVFQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFR
gi|131 RVQPFSSRVAVTPG-YQSRYN-FKRCYWGAREFL---EDVGAIR---DKSNFKKEDSKQ
180      190      200      210      220

240      250      260      270      280      290
Cry1Ac RELTTLVLDIVSLF----PNYDSRTYPIRT--VSQLTREIYTNPVLENFDGSRGSAQGI
gi|131 LCCYLGIFRLSSYFFKIYEKFRTRVYPISESKFSPINKRNLYKPSIKKFSMVVFEARLRA
230      240      250      260      270      280

300      310      320      330      340      350
Cry1Ac EGSIRSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ
gi|131 RRKYWSPHLWIYLNQDNHLLTDVHRGFNYWSGHQIIASPVGFQDPEFAFPLFGNAGNAAPP
290      300      310      320      330      340

360      370      380      390      400      410
Cry1Ac QRIVAQLGQGVYRTLSSTLYRRPF-NIGINNQQLSVDGTEFAYGTSSNLPSAVYRKSQT
gi|131 VRIVYQLGQGVYRTLSSTLYEDLFIRDKVINITYL-FLAGSNLLMEPPHICHGPRYRKSQT
350      360      370      380      390      400

420      430      440      450      460      470
Cry1Ac VDSLDEIPPQNNNVPRQGFQSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNII
gi|131 VDSLDEIPHQNNNVPRQGFQSHRLSHVSMFRSGFSNSVSIIRAPMFSWILRSAEFNII
410      420      430      440      450      460

480      490      500      510      520

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Cry1Ac  ASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST
gi|131  PSSQITQIPLTKSTNLGSGTSVVKGPGFTGGDILRRTSPGQI1STLRVNITAPL-----SQ
      470      480      490      500      510

530      540      550      560      570      580
Cry1Ac  RYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGN
gi|131  RYRVRIRYASTTNLQFHTSIDGRPINQGNFSAATMSSGSLNLSQASFRTVGFTTTPFNFSNGS
      520      530      540      550      560      570

590      600      610      620      630      640
Cry1Ac  IV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVT
gi|131  SVFTLSAHVFNNGNEVYIDRIEFVPAEVIFFAEYDLERAQKAVNELFTSSNQIGLKTDTV
      580      590      600      610      620      630

650      660      670      680      690      700
Cry1Ac  DYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWG
gi|131  DYHIDQVSNLVECLSEDFCLDEKQELSEKVKHAKRLSDERNLLQDPNFRGINRQLDRGWR
      640      650      660      670      680      690

710      720      730      740      750      760
Cry1Ac  GSTGTITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDL
gi|131  GSTDITIQGGDDVFKENYVTLGTFDECYPTYLYQKIDESKLFKAYTRYQLRGYIEDSQDL
      700      710      720      730      740      750

770      780      790      800      810      820
Cry1Ac  EIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC
gi|131  ESIYIRESVESVSD-----APRME--SDLRLFRGDRGQKM
      760      770      780

830      840      850      860      870      880
Cry1Ac  AHHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKR
gi|131  CPSFSPFLLRHYVCGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKR
      790      800      810      820      830      840

890      900      910      920      930      940
Cry1Ac  AEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIRE
gi|131  AEKKWRDKREKLEWETNIVYKEAKESVHALFVNSQYDQLQADTNIAMIAHADKRVHSIRK
      850      860      870      880      890      900

950      960      970      980      990      1000
Cry1Ac  AYLPELSVIPGVNAALFEELGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQ
gi|131  AYLPELAVIPGVNAGIFEELGRIFTAFSLYDARNVIKNGAFY-----MAYPAGTERA
      910      920      930      940      950      960

1010     1020     1030     1040     1050     1060
Cry1Ac  NNQRSVLVPEWEAEVSEVRV----C-PGRGYILRVTAYPEGEGCVTIHEIENNTD
gi|131  CRCRRTKQPPFGCCSGMGRSVTRSSCLSGSWLYPSCHSQGGIGEGCVTIHEIENNTD
      970      980      990      1000     1010     1020

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      1070     1080     1090     1100     1110
Cry1Ac  ELKFNSNCVEEIEYPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEE---
gi|131  ELKFNSNCVEEIEYVNNVTVCIKIILRLKKNRRVPTYTSRNRGYDGAYESNSSVQLIMHQPMK
      1030     1040     1050     1060     1070     1080

1120     1130     1140     1150     1160     1170
Cry1Ac  KSYTDGRRENPF-CEFNRGYRDYTPPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVE
gi|131  KKHQMDEETILVNLTFEDMGITHHYQRGYVTKLEYFQKPIRYGLRSEKREKHESSWTAWN
      1090     1100     1110     1120     1130     1140

1180
Cry1Ac  LLLMEE
gi|131  YFLWRNNICFIM
      1150

>>gi|71792204|emb|CAJ21129.1| unnamed protein product [B (765 aa)
      initn: 1202 init1: 398 opt: 1200 Z-score: 1407.0 bits: 271.7 E(): 1.9e-69
      Smith-Waterman score: 1310; 37.263% identity (64.228% similar) in 738 aa overlap
      (20-721:57-762)

      10      20      30      40
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|717  YPLASEQNGVLQNMNYKEYLQTYDGDYTGSLINPNSINTRDVLQGTITVGRVLG---F
      30      40      50      60      70      80

50      60      70      80      90      100
Cry1Ac  LLSEFVPGAG---FVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLE
gi|717  LG---VPFAGQLVTFYTFLLNQLWPTNNAVWEAFMAQVEELIDQRISDQVVRNALDDLT
      90      100     110     120     130     140

110     120     130     140     150     160
Cry1Ac  GLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALTTAIPLFAV---QNYQVP
gi|717  GLHDYYNEYLAALEEWLDRP-NGA-RANLAFQRFENLHTAFVTRMPSFGTGPQSQRDAVA
      150     160     170     180     190

170     180     190     200     210
Cry1Ac  LLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYN--DLTRLIGNYTDHAVRWYNT
gi|717  LLTVYAQAANLHLLKDAEIIYGARWGLQSQINLYFNAQQDRTRI---YTNHCVATYNR
      200     210     220     230     240     250

220     230     240     250     260     270
Cry1Ac  GLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL
gi|717  GLEDLKGNTESWYNYHQFRREMTLMAMDVLFPPYNNVRQYPNGANPQLTREIYTPDVPV
      260     270     280     290     300     310

280     290     300     310     320
Cry1Ac  ENF---DGSFR--GSA----QGIEGS-IRSPHLMIDLNSITTYTDAHRGEY-----YW
gi|717  FNPPANQGLCRRRWGNNPYMTFSGLENAFIRPPHLDRLNLSLTI--NSHRFPISSNFMDYW
      320     330     340     350     360     370

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150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLT
gi|151 ELMFVQKLPSPFAVSGEEVPLLPPIYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQV
170      180      190      200      210      220

210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|151 ERTRDYSYHCVKWNNNTGLNLRATNGQSWVRYNQFRKDIELMVLVDLVRVFPVSYDTLVYPI
230      240      250      260      270      280

270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPV-LENFDGSGFRGSA-----QGIEGS-IRSPHLMIDLNSITIIY
gi|151 KTTSQLTREVYTDAGTVDPNQALRSTTWYNNNAPSFSIAEAAVIRSPHLLDFLEKVTIY
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac TDAHR---GEYY--WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
gi|151 SLLSRWSNTQYMMWGGHRLSRPIG-----GAL-NTSTQGSTNTSINPVTLQF
350      360      370      380      390

370      380      390      400      410
Cry1Ac LSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSL
gi|151 TSRDFYRTESWAGLNLFLTQPVIGVPRVDFHWKFPPTLP IASDNFYLYGAVGTQLQDSE
400      410      420      430      440      450

420      430      440      450      460      470
Cry1Ac DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDS
gi|151 NELPPETTGQPNYESYSHRLSHIGLI-----SASHVKALVYSWTHRSADRTNTIEPNS
460      470      480      490      500

480      490      500      510      520      530
Cry1Ac ITQIPAVKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRV
gi|151 ITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTKSGT---FGHIRVNIIN-PPFAQRYRV
510      520      530      540      550      560

540      550      560      570      580      590
Cry1Ac RVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI-
gi|151 RMSYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFPTTFFSFDVQSTFT
570      580      590      600      610      620

600      610      620      630      640      650
Cry1Ac VGVRFNSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|151 IGAWNFSSGNEVYIGRIEFVPEVYEAAYDFEKAQEKVTALFTSTNPRGLKTDVKDYHI
630      640      650      660      670      680

660      670      680      690      700      710
Cry1Ac DQVSNLVTYLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|151 DQVSNLVESELSDLYLDEKRELFEIVKYAKQIHERNM

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690      700      710
Cry1Ac ITIQGGDDVFKENYVLSGTFDECYPTYLYQKIDESKLFATRYQLRGYIEDSQDLEIYS
720      730      740      750      760      770
>>gi|10061243|gb|AAE37099.1| Sequence 2 from patent US 5 (719 aa)
initn: 1245 initl: 608 opt: 1142 Z-score: 1339.0 bits: 259.0 E(): 1.2e-65
Smith-Waterman score: 1365; 38.174% identity (67.515% similar) in 668 aa overlap
(55-688:76-719)

30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVGLVDI IWGIFGP---SQWDAFL
gi|100 SEHESIDPFVSASTIQTGTGIGIAGKILGTLGVFPFGQIASLYSFI LGELWPKGKSQWEIFM
50      60      70      80      90      100

90      100      110      120      130      140
Cry1Ac VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|100 EHVEALINRKISTYARNKALTDLKGGLDALAVYHESLESWVGNRNNTARSVVKNQYIAL
110      120      130      140      150      160

150      160      170      180      190      200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLT
gi|100 ELMFVQKLPSPFAVSGEEVPLLPPIYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQV
170      180      190      200      210      220

210      220      230      240      250      260
Cry1Ac RLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|100 ERTRDYSYHCVKWNNNTGLNLRATNGQSWVRYNQFRKDIELMVLVDLVRVFPVSYDTLVYPI
230      240      250      260      270      280

270      280      290      300      310
Cry1Ac RTVSQLTREIYTNPV-LENFDGSGFRGSA-----QGIEGS-IRSPHLMIDLNSITIIY
gi|100 KTTSQLTREVYTDAGTVDPNQALRSTTWYNNNAPSFSIAEAAVIRSPHLLDFLEKVTIY
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac TDAHR---GEYY--WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
gi|100 SLLSRWSNTQYMMWGGHRLSRPIG-----GAL-NTSTQGSTNTSINPVTLQF
350      360      370      380      390

370      380      390      400      410
Cry1Ac LSSTLYRRPFNIGIN---NQQLSVLDGTEFAYG-----TSSNLPSAVYRKSGTV--DSL
gi|100 TSRDFYRTESWAGLNLFLTQPVIGVPRVDFHWKFPPTLP IASDNFYLYGAVGTQLQDSE
400      410      420      430      440      450

420      430      440      450      460      470
Cry1Ac DEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDS
gi|100 NELPPETTGQPNYESYSHRLSHIGLI-----SASHVKALVYSWTHRSADRTNTIEPNS
460      470      480      490      500

480      490      500      510      520      530
Cry1Ac ITQIPAVKGNFLFNFS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRV
gi|100 ITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTKSGT---FGHIRVNIIN-PPFAQRYRV
510      520      530      540      550      560

540      550      560      570      580      590
Cry1Ac RVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI-
gi|100 RMSYASTTDLQFHTSINGKAINQGNFSATMNRGEDLDYKTFRTVGFPTTFFSFDVQSTFT
570      580      590      600      610      620

600      610      620      630      640      650
Cry1Ac VGVRFNSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|100 IGAWNFSSGNEVYIGRIEFVPEVYEAAYDFEKAQEKVTALFTSTNPRGLKTDVKDYHI
630      640      650      660      670      680

660      670      680      690      700      710
Cry1Ac DQVSNLVTYLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|100 DQVSNLVESELSDLYLDEKRELFEIVKYAKQIHERNM
480      490      500      510      520      530

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Cry1Ac ITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRV
gi|100 ITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTKSGT---FGHIRVNIN-PPFAQRYRV
510 520 530 540 550 560

540 550 560 570 580 590
Cry1Ac RVRVYASVTP IHLNVNWNSSIFSNTPATATSLDNLQSSDFGY--FESANAFTSSLGNI-
gi|100 RMSYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYKTFRTVGFSTPFSFSDVQSTFT
570 580 590 600 610 620

600 610 620 630 640 650
Cry1Ac VGVRFNSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|100 IGAWNFSSGNEVYIGRIEFVPEVYEAEDFEKAQEKVTLFTSTNPRGLKTDVKDYHI
630 640 650 660 670 680

660 670 680 690 700 710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|100 DQVSNLVESLSDELTYLDEKRELFEIVKYAKQIHIERNM
690 700 710

720 730 740 750 760 770
Cry1Ac ITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYS

```

>>gi|3702807|gb|AAC62933.1| crystal protein toxin [Bacil (719 aa)  
 initn: 1245 initl: 608 opt: 1142 Z-score: 1339.0 bits: 259.0 E(): 1.2e-65  
 Smith-Waterman score: 1365; 38.174% identity (67.515% similar) in 668 aa overlap  
 (55-688:76-719)

```

30 40 50 60 70 80
Cry1Ac VEVLGGER IETGYTPIDISLSLTQFLLSEFVPGAGFVGLVDIIWGFIPG---SQWDAFL
gi|370 SEHESIDPFVSASTIQTGIGIAGKILGTLGVPFPQGIASLYSIFLIGELWPKGKSQWEIFM
50 60 70 80 90 100

90 100 110 120 130 140
Cry1Ac VQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|370 EHVEAI INRKISTYARNKALTDLKGGLDALAVYHESLESWVGNRNNTRARSVVKNQYIAL
110 120 130 140 150 160

150 160 170 180 190 200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLT
gi|370 ELMFVQKLP SFAVSGEEVPLLP IYAQAANLHLLLRDASIFEKNGGLSASEISTFYNRQV
170 180 190 200 210 220

210 220 230 240 250 260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPI
gi|370 ERTRDYSYHCVKWNNTGLNLRATNGQSWVRYNQFRKDIELMVLDLVRVFPSPSYDYLTVYPI
230 240 250 260 270 280

270 280 290 300 310
Cry1Ac RTVSQLTREIYTPNV-LENFDGSRFGSA-----QGIEGS-IRSPHLM DILNSITYY
gi|370 KTTSQLTREVYTDAGTVDPNQALRSTTWYNNNAPSFAIEAAVIRSPHLLDFLEKVTIY

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290 300 310 320 330 340
Cry1Ac TDAHR---GEYY--WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRT
gi|370 SLLSRWSNTQYMMWGGHRLSRPIG-----GAL-NTSTQGSTNTSINPVTLQF
350 360 370 380 390

370 380 390 400 410
Cry1Ac LSSTLYRRFPNIGIN---NQQLSVLDGTEFAYG-----TSSNLP SAVA YRKS GTV---DSL
gi|370 TSRDFYRTESWAGLNLFLTQPVNGVPRVDFHWKFPPLPIASDNFYLYGAGVGTQLQDSE
400 410 420 430 440 450

420 430 440 450 460 470
Cry1Ac DEIPPQNNVPPRQGF SHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDS
gi|370 NELPPETTGQPNYVESHRLSHIGLI-SG-----SHVKALVYSWTHRSADRNTTIEPNS
460 470 480 490 500

480 490 500 510 520 530
Cry1Ac ITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRV
gi|370 ITQIPLVKAFNLSSGAAVVRGPGFTGGHILRRTKSGT---FGHIRVNIN-PPFAQRYRV
510 520 530 540 550 560

540 550 560 570 580 590
Cry1Ac RVRVYASVTP IHLNVNWNSSIFSNTPATATSLDNLQSSDFGY--FESANAFTSSLGNI-
gi|370 RMSYASTTDLQPHSTINGKAINQGNFSATMNRGEDLDYKTFRTVGFSTPFSFSDVQSTFT
570 580 590 600 610 620

600 610 620 630 640 650
Cry1Ac VGVRFNSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|370 IGAWNFSSGNEVYIGRIEFVPEVYEAEDFEKAQEKVTLFTSTNPRGLKTDVKDYHI
630 640 650 660 670 680

660 670 680 690 700 710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
gi|370 DQVSNLVESLSDELTYLDEKRELFEIVKYAKQIHIERNM
690 700 710

720 730 740 750 760 770
Cry1Ac ITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYS

>>gi|21311715|gb|AAM46818.1|AF490398_1 truncated CryIA(b (210 aa)
  initn: 1257 initl: 1097 opt: 1111 Z-score: 1310.4 bits: 252.0 E(): 4.5e-64
  Smith-Waterman score: 1190; 79.915% identity (84.188% similar) in 234 aa overlap
  (615-848:2-209)

590 600 610 620 630 640
Cry1Ac SSLGNIVGVRFNSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|213 VTFEAEYDLERAQKAVNELFTSSNQIGLKTD
10 20 30

650 660 670 680 690 700

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Cry1Ac VTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERG
gi|213 VTDYHIDQVSNLVECLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINRQLDRG

Cry1Ac WGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ
gi|213 WRGSTDITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQ

Cry1Ac DLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEG
gi|213 DLEIYLIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEG

Cry1Ac KCAHSHHFLSDIDVGCCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLKPLVGEALARV
gi|213 --AHSHHFLSDIDVGCCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLKPLVGEALARV

>>gi|216288|dbj|BAA00178.1| 130 kDa insecticidal protein (1135 aa)
initn: 1699 initl: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64
Smith-Waterman score: 1930; 33.918% identity (62.072% similar) in 1197 aa overlap
(38-1182:43-1135)

Cry1Ac NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL----G
gi|216 GSMKNTNYKDWLWAMCENNQYGVNPAAINSSVSTALKVAGAILKFNPPAGTVLTVLSA

Cry1Ac LVDIWGFQPSQ---WDAFLVQIEQLINQRIEIEFARNQAIISRLLEGLSNLYQIYAESPFE
gi|216 VLPILWPTNTPPERVWVNDFTMTNTGNLIDQVTAVVRTDANAKMTVVKDYLDQYTTKFNFT

Cry1Ac WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|216 WKREPNNQSYRTAVITQFNLTSAKLRRETAVYFVSNLVGYELLLPIYAQVANFNLLLRDGL

Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRRE
gi|216 LINAQEWLACAG-DQLYNTMVQYTKYIAHSITWYKGLDVLNRKSNQWITFNDYKRE

Cry1Ac LTLTVDLIVSLFPNYSRTYPIRTV-----SQLTREIYTPNVLNFDGSAQGGIE
gi|216 MTIQVLDLILALFASYPRLPADKIDNTKLSKTEFTREIYDALV---ESPSSKIAALE

Cry1Ac LTLTVDLIVSLFPNYSRTYPIRTV-----SQLTREIYTPNVLNFDGSAQGGIE

Cry1Ac GSI-RSPHLMILNSITIIYTDA-HRGEYYWSGHQIMASPVGFSGPEFTFPFLYGTMGNAAP
gi|216 AALTRDVLHFTWLKRVYFWNTIYQDLRFLSANKIGFSYTNSSAMQES-GIYSSSGFGSN

Cry1Ac QQRIVAQQLGGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQT
gi|216 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYNSTNITPTPEGLRTTFF

Cry1Ac VDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNII
gi|216 GFSTNENTP---NQPTVNDYTHLSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI

Cry1Ac ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST
gi|216 YTDAITQVPAVKSNNFLNATAKVIKPGHTGGDLVALTSNGT-LSGRMEIQCKTISIFNDPT

Cry1Ac R-YRVRVRYASVTPPIHLNVNWNSSIFSNTPATATSL---DNLQSSDFGY--FESANAF
gi|216 RSYGLRIRYAANSPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPDLDKYEYFKDPDF

Cry1Ac TS-----SLGNIVGVR---NFSGTAGVIIDRFEPVPTATL--EAE-YNLERAQKAVN
gi|216 DAIVPMLSSNQLITTAIQPLNMTSNNQVIIDRIEIIPIITQSVLDETENQLESREEVVN

Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQ
gi|216 ALFTNDAKDALNIGTTDYDIDQAANLVECISEELYPKKMLLLDEVKNAKQLSQRNVLQ

Cry1Ac DSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFD---ECYPTYLYQKIDESK
gi|216 NGDFESAT---LGTWTSNITIQEDDPIFKGHYLMHSGARDIDGTIFPTYIFQKIDESK

Cry1Ac LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPNR
gi|216 LKPYTRYLVRGVFGSSKDVVLSRYGEEIDAIMNVPADLNLVYLPSTFD----CEGSRN

Cry1Ac C----AP-HLEWNPDLDCSCR--DGEK---CAHSHHFLSDIDVGCCTDLNEDLGVVWVIFK
gi|216 CETSAVPANIGNTSMDLYSCQYDTGKHKHVVC-QDSHQFSFTIDTGALDNTNENIGVWVMPK

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      860      870      880      890      900      910
Cry1Ac  IKTDQGHARLGNLEFLEEKPLVGEALARVKAERKWRDKREKLEWETNIVYKEAKESVDA
      . . . . .
gi | 216  ISSPDGYASLDNLEVEIEEGPIDGEALSrvkhMEKKWNDQMEAKRSETQQAYDVAKQAIDA
      890      900      910      920      930      940

```

```

      920      930      940      950      960      970
Cry1Ac  LFNVSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELSVIPGVNAAIFFEELGRIFTAFS
      . . . . .
gi | 216  LFTNVQDEALQFDTTLAQIQYAEYLVQSIPVYVNDWLSVPMGMNYDIYVELDARVAQARY
      950      960      970      980      990     1000

```

```

      980      990     1000     1010     1020     1030
Cry1Ac  LYDARNVIKNGDFNNGLSVCWNVKGHVDVEEQNNQRSVLVPEWEAEVVSQEVRCVPGRGYI
      . . . . .
gi | 216  LYDTRNIKNGDFTQGVMGWHVTGNADVQ-QIDGVSVLVLSNWSAGVSQNVHLQHNHGYY
      1010     1020     1030     1040     1050     1060

```

```

      1040     1050     1060     1070     1080     1090
Cry1Ac  LRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVVEEIIYPNNTVTCDYTVNQEEYGGAYT
      . . . . .
gi | 216  LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----
      1070     1080     1090

```

```

      1100     1110     1120     1130     1140     1150
Cry1Ac  SRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGYRDYTPLPVGYVTKLELYFPE
      . . . . .
gi | 216  -----GYITKTVDFPFD
      1100

```

```

      1160     1170     1180
Cry1Ac  TDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi | 216  TDRVRIEIGETEGSFYIESIELICMNE
      1110     1120     1130

```

```

>>gi|60459410|gb|AAx20050.1| 130 kDa crystal protein [Ba (1136 aa)
  initn: 1791 initl: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64
Smith-Waterman score: 1945; 33.918% identity (62.239% similar) in 1197 aa overlap
(38-1182:43-1136)

```

```

      10      20      30      40      50      60
Cry1Ac  NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL----G
      . . . . .
gi | 604  GSMKNTNYKDWLAMCENNQQYGVNPAAINSSSVSTALKVAGAILKFNPPAGTVLTVLSA
      20      30      40      50      60      70

```

```

      70      80      90     100     110     120
Cry1Ac  LVDIILWIFGPSQ--WDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFRE
      . . . . .
gi | 604  VLPILWPTNTPTPERVWVDFMTNTGNLIDQVTAYVRTANAKMTVVVDYLDQYTTKFN
      80      90     100     110     120     130

```

```

      130     140     150     160     170
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
      . . . . .
gi | 604  WKREPNNQSYRTAVITQFNLTSAKLRRETAVYFSLNVLGYELLLLPIYAQVANFNLLLRD
      140     150     160     170     180     190

```

```

      180     190     200     210     220     230
Cry1Ac  SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
      . . . . .
gi | 604  LINAQEWLSARSAGDQLYNTMVQYTKYIAHSITWYKGLDVLRNKSNQWITFNDYKRE
      200     210     220     230     240     250

```

```

      240     250     260     270     280     290
Cry1Ac  LTLTVLDIVSLFPNYSRTPYIRTV-----SQLTREIYTNVLENFDGSPRGSQAQIE
      . . . . .
gi | 604  MTIQVLDLILALFASYPDRRYPADKIDNTKLSKTEFTREIYTALV---ESPSSKSIAALE
      260     270     280     290     300

```

```

      300     310     320     330     340     350
Cry1Ac  GSI-RSPHLMIDLNSITIYTDA-HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAP
      . . . . .
gi | 604  AALTRDVLHFTWLKRVDFWNTIYQDLRFLSANKIGFSYTNSSAMQES-GIYSSSGFGSN
      310     320     330     340     350     360

```

```

      360     370     380     390     400     410
Cry1Ac  QQRIVAQLGQGVYRLLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQT
      . . . . .
gi | 604  LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYSNITPTPEGLRTPPF
      370     380     390     400     410     420

```

```

      420     430     440     450     460     470
Cry1Ac  VDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNII
      . . . . .
gi | 604  GFSTNENTP---NQPTVNDYTHLSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI
      430     440     450     460     470

```

```

      480     490     500     510     520
Cry1Ac  ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNINQNGRYIEVPIHPSTST
      . . . . .
gi | 604  YTDAITQVPAVKSNFLNATAKVIKPGHGTGGDLVALTSNGT-LSGRMEIQCKTSIFNDPT
      480     490     500     510     520     530

```

```

      530     540     550     560     570     580
Cry1Ac  R-YRVRVRYASVTPIHLLNVNWNQSSIFSNTVPATATSL---DNLQSSDFGY--FESANAF
      . . . . .
gi | 604  RSYGLRIRYAANSPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPITDLKYEFRYKDPF
      540     550     560     570     580     590

```

```

      590     600     610     620     630     640
Cry1Ac  TS-----SLGNIVGVR---NFSGTAGVIIDRFEFIPVTATL--EAE-YNLERAQKAVN
      . . . . .
gi | 604  DAIVPMLRSSNLQITAIQPLNMTSNNQVIIDRIEIPITQSVLDETENQNLESEREVNV
      600     610     620     630     640     650

```

```

      640     650     660     670     680     690
Cry1Ac  ALFTSTNQLGLKTNVTDYHDIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ
      . . . . .
gi | 604  ALFTNDAKDALNIGTTIDYDIDQAANLVECISEELYPKERMLLLDVEKNAKQLSQSRNVLQ
      660     670     680     690     700     710

```

```

      700     710     720     730     740
Cry1Ac  DSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---ECYPTLYQKIDESK
      . . . . .
gi | 604  NGDFESAT----LGWTTSDNITIQEDDPIFKGHYLMHSGARDIDGTIFPTYIFQKIDESK
      720     730     740     750     760     770

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750      760      770      780      790      800
Cry1Ac LKAFTRYQLRGYIEDSQLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPNR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 LKPYTRYLVRFVGSKDVLVVSRYGEEIDAIMNVPADLNYLYPSTFD----CEGSNR
      780      790      800      810      820

```

```

      810      820      830      840      850
Cry1Ac C----AP-HLEWNPDLDCSCR--DGEK---CAHSHSHFSLDIDVGCTDLNEDLVGVVIFK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 CETSAVPANIGNTSMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDTNENIGVWVMFK
      830      840      850      860      870      880

```

```

      860      870      880      890      900      910
Cry1Ac IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 ISSPDGYASLDNLEVEEGLDGEALSrvkhMEKKWQDMEAKRSETQQAYDVAKQAIDA
      890      900      910      920      930      940

```

```

      920      930      940      950      960      970
Cry1Ac LfVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIPGVNAAI FEELEGRIFTAFS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 LFTNVQDEALQFDTTLAQIQYAEYLVQSIPIVYVNDWLSVPGMNYDI VELDARVAQARY
      950      960      970      980      990      1000

```

```

      980      990      1000      1010      1020      1030
Cry1Ac LYDARNVIKNGDFNNGLSWCWNVKGHVDVEEQNNQRSVLVPEWEAEVSEQEVRVCPGRGYI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 LYDTRNIIKNGDFTQGVGMWHVTGNADVQ-QIDGVSVLVLSNWSAGVSNVHLQHNGHYV
      1010      1020      1030      1040      1050      1060

```

```

      1040      1050      1060      1070      1080      1090
Cry1Ac LRVTAyKEGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----
      1070      1080      1090

```

```

      1100      1110      1120      1130      1140      1150
Cry1Ac SRNRGYNEAPSPADYASVYEKESYTDGRRENPCFNRGYRDTPLPVGYVTKLELYPPE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 -----GYITKTVDFVFPD
      1100

```

```

      1160      1170      1180
Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|604 TDRVRIEIGETEGSFYIESIELICMNE
      1110      1120      1130

```

```

>>gi|21685442|emb|CAD30095.1| pesticidal crystal protei (1136 aa)
  initn: 1791 initl: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64
Smith-Waterman score: 1945; 33.918% identity (62.239% similar) in 1197 aa overlap
(38-1182:43-1136)

```

```

      10      20      30      40      50      60
Cry1Ac NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL----G
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 GSMKNTNYKDWLACENNQQYGVNPAAINSSVSTALKVAGAILKVFVNPAGTVLTVLSA
      20      30      40      50      60      70

```

```

      70      80      90      100      110      120
Cry1Ac LVDIIWGIFGPSQ---WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 VLPILWPTNTPTPERVWVDFMTNTGNLIDQTVTAVVRTDANAKMTVVKYLDQYTTKFTN
      80      90      100      110      120      130

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      130      140      150      160      170
Cry1Ac WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 WKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLLPIYAQVANFNLLLRDG
      140      150      160      170      180      190

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      180      190      200      210      220      230
Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 LINAQEWLSARSAGDQLYNTMVQYTKKEYIAHSITWYNKGLDVLRNKSNQWITFNDYKRE
      200      210      220      230      240      250

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      240      250      260      270      280      290
Cry1Ac LTLTVDLIVSLFPNYSRTPRTV-----SQLTREIYTNVLENFVDFGSRFGSAQGLIE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 MTIQVLDLILFASVDPFRYPADKIDNTKLSKTEFTREIYDALV----ESPSSKSIAALE
      260      270      280      290      300

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      300      310      320      330      340      350
Cry1Ac GSI-RSPHLMIDLNSITTYTDA-HRGEYYWSGHQIMASPVGFSGFEFTFPPLYGTMGNAAP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 AALTRDVHLFTWLKRVDFWTNTTYQDLRFLSANKIGFSYTNSSAMQES-GIYSSGFGSN
      310      320      330      340      350      360

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      360      370      380      390      400      410      420
Cry1Ac QQRIVAQQLGGVYRTLSSTLYRPPFNIGINNQLSVDLGTETAYGTSNNLPSAVYKRSGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYNISNITPTPEGLRITTF
      370      380      390      400      410      420

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      420      430      440      450      460      470
Cry1Ac VDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNII
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 GFSTNENTP---NQPTVNDYTHLSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI
      430      440      450      460      470

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      480      490      500      510      520
Cry1Ac ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYLEVPIHPSTST
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 YTDAITQVPAVKSFLNATAKVIKPGHTGGDLVALTSNGT-LSGRMEIQCKTSIFNDPDT
      480      490      500      510      520      530

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      530      540      550      560      570      580
Cry1Ac R-YRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSL--DNLQSSDFGY--FESANAF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 RSYGLRIRYAANSPIVLNVSYLVQVSRGTTISTESTFSRPNNIIPITDLKYEEFRYKDFP
      540      550      560      570      580      590

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      590      600      610      620      630
Cry1Ac TS-----SLGNIVGVR---NFSGTAGVVIDRFEFIPVTATL--EAE-YNLERAQKAVN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|216 DAIVPMLRSSNLITIAIQPLNMTSNNQVIIDRIEIIPTQSVLDETENQNLSESEREVVN

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gi|403 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYNSTIPTPEGLRTTF
370 380 390 400 410 420

Cry1Ac 420 430 440 450 460 470
VDSLDEIPPQNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNLI
gi|403 GFSTNENTP---NQPTVNDYTHILSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI
430 440 450 460 470

Cry1Ac 480 490 500 510 520
ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST
gi|403 YTDAITQVPAVKSNFLNATAKVIKPGHGTGGDLVALTSNGT-LSGRMEIQCKTSLFNDPT
480 490 500 510 520 530

Cry1Ac 530 540 550 560 570 580
R-YRVRVRYASVTPIHNLNWNWGNSSIFSNTPATATSL---DNLQSSDFGY--FESANAF
gi|403 RSYGLRIRIYAANSPIVLNWSVVLQGVSRGTTTISTESTFSRPNNIIPITDLKYEFPYKDPF
540 550 560 570 580 590

Cry1Ac 590 600 610 620 630
TS-----SLGNIVGVR----NFSGTAGVIDRFEFIPVTATL--EAE-YNLERAQKAVN
gi|403 DAIVPMRLSSNQLITIAIQPLNMTSNNQVIIDRIEIIPTQSVLDETNQNLESREVVN
600 610 620 630 640 650

Cry1Ac 640 650 660 670 680 690
ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQ
gi|403 ALFTNDAKDALNIGTTDYDIDQANLVCEISEELYPKEKMLLLDEVKNQKLSQSRNVLQ
660 670 680 690 700 710

Cry1Ac 700 710 720 730 740
DSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLGTFD---ECYPTYLYQKIDESK
gi|403 NGDFESAT---LGWTTSDNITIQEDDPIFKGHYHMSGARDIDGTIFPTYIFQKIDESK
720 730 740 750 760 770

Cry1Ac 750 760 770 780 790 800
LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCEPNR
gi|403 LKPYTRYLVRFVGGSSKDVLLVVSRYGEEIDAIMNVPADLNLYLPSTFD----CEGSNR
780 790 800 810 820

Cry1Ac 810 820 830 840 850
C---AP-HLEWNPDLDCSCR--DGEK---CAHSHHFLSLDIDVGCTDLNEDLVGWWVIFK
gi|403 CETSAVPANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDTNENIGVWVMFK
830 840 850 860 870 880

Cry1Ac 860 870 880 890 900 910
IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDA
gi|403 ISSPDGYASLDNLEVIEEGPIDGEALSrvkhmeKKWNDQMEAKRSETQAYDVAKAIDA
890 900 910 920 930 940

Cry1Ac 920 930 940 950 960 970

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Cry1Ac LFNVSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFS
gi|403 LFTNVQDEALQFDTTLAQIQYAEYLVQSIIPYVYNDWLSDPVPGMNYDIYVELDARVAQARY
950 960 970 980 990 1000

Cry1Ac 980 990 1000 1010 1020 1030
LYDARNVIKNGDFNNGLSWCWNVKGHVVDVEEQNNQRSVLPVPEWEAEVSVQEVRCPRGYI
gi|403 LYDTRNIIKNGDFTQGVMGWHVTGNADVQ-QIDGVSVLVLNSWSAGVSNVHLQHNHGIV
1010 1020 1030 1040 1050 1060

Cry1Ac 1040 1050 1060 1070 1080 1090
LRVTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYT
gi|403 LRVIKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----GYITKTVDFVFPD
1070 1080 1090

Cry1Ac 1100 1110 1120 1130 1140 1150
SRNRGYNEAPSPVDIYASVYEEKSYTDGRRENPCFENRGYRDYTPPLVGVYVTKLEYFPPE
gi|403 -----GYITKTVDFVFPD
1100

Cry1Ac 1160 1170 1180
TDKVVIEIGETEGTFIVDSVELLLMEE
gi|403 TDRVRIEIGETEGSFYIESIELICMNE
1110 1120 1130

>>gi|40354|emb|CAA30312.1| unnamed protein product [Baci (1136 aa)
initn: 1791 init1: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64
Smith-Waterman score: 1945; 33.918% identity (62.239% similar) in 1197 aa overlap
(38-1182:43-1136)

Cry1Ac 10 20 30 40 50 60
NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGFVL---G
gi|403 GSMKNTNYKDWLACENNQQYGVNPAAINSSSVSTALKVAGAILKFFVNPAGTVLTVLSA
20 30 40 50 60 70

Cry1Ac 70 80 90 100 110 120
LVDIIWGFGPSQ---WDAFLVQIEQLINQRIEFPARNQAISRLEGLSNLYQIYAESFRE
gi|403 VLPILWPTNPTPERVWDFMTNTGNLIDQVTAYVRTDANAKMTVVKDYLDQYTTKFN
80 90 100 110 120 130

Cry1Ac 130 140 150 160 170
WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|403 WKREPNNQSYRTAVITQFNLSAKLRETAVYFNSLVGYELLLLPIYAQVANFNLLLRDG
140 150 160 170 180 190

Cry1Ac 180 190 200 210 220 230
SVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
gi|403 LINAQEWLSARSAGDQLYNTMVQYTKYIAHSITWYNKGLDVLRNKSNQGWITFNDYKRE
200 210 220 230 240 250

Cry1Ac 240 250 260 270 280 290

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Cry1Ac LTLTVLDIVSLFPNYDSRTYPIRTV-----SQLTREIYTNPVLENFDGSGFRGSAQGIE  
gi|403 MTIQVLDLILALFASYDPPRRYPADKIDNTKLSKTEFTREIYDALV---ESPSSKSIAALE  
260 270 280 290 300

Cry1Ac GSI-RSPHLMILNSITITYTDA-HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAP  
gi|403 AALTRDVLHFLTWLKRVDWFTNTIYQDLRFLSANKIGFSYTNSSAMQES-GIYGSSGFGSN  
310 320 330 340 350 360

Cry1Ac QQRIVAQLGQGVYRTLSSTLYRRFPNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQT  
gi|403 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYSNITPTPEGLRITFF  
370 380 390 400 410 420

Cry1Ac VDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNII  
gi|403 GFSTNENTP---NQPTVNDYTHILSYIKTDVLDYNSNRVS-----FAWTHKIVDPNNQI  
430 440 450 460 470

Cry1Ac ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST  
gi|403 YTDAITQVPAVKSNFLNATAKVIKPGHGTGGDLVALTSNGT-LSGRMEIQCKTISIFNDPT  
480 490 500 510 520 530

Cry1Ac R-YRVRVRYASVTPPIHLNWNWGNSSIFSNTPATATSL---DNLQSSDFGY--FESANAF  
gi|403 RSYGLRIRIYAANSPIVLNVSIVLQGVSRGTTISTESTFSRPNIIPTDLKYEEFXYKDFP  
540 550 560 570 580 590

Cry1Ac TS-----SLGNIVGVR---NFSGTAGVIIDRFEFIPVTATL--EAE-YNLERAQKAVN  
gi|403 DAIVPMRLSSNQLITIAIQPLNMTSNNQVIIDRIEIIPIITQSVLDETENQLESERVVN  
600 610 620 630 640 650

Cry1Ac ALFSTSNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ  
gi|403 ALFTNDARKDALNIGTTDYDIDQAANLVECISEELYPKEMLLLDEVKNAKQLSQSRNVLQ  
660 670 680 690 700 710

Cry1Ac DSNFKDINRQPERGWGGSTGITIQQGDDVFKENYVTLSGTFD---ECYPTYLYQKIDESK  
gi|403 NGDFESAT---LGWTTSDNITIQQEDDPIFKGHYHMSGARDIDGTIFPTTYIFQKIDESK  
720 730 740 750 760 770

Cry1Ac LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPNR  
gi|403 LKPYTRYLVRFVGVGSSKDELVVSRYGEEIDAIMNVPADLNYLPSTFD-----CEGSNR  
780 790 800 810 820

Cry1Ac C----AP-HLEWNPDLDCSCR--DGEK---CAHSHHFSLDDIVGCTDLNEDLGWVVIK  
gi|403 CETSAVPANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGDALDNTNENIGVVMFK  
830 840 850 860 870 880

Cry1Ac IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRELEWETNIVYKEAKESVDA  
gi|403 ISSPDGYASLDNLEVIEEGPIDGEALSRVKHMEKKWNDQMEAKRSETQQAYDVAQQAIDA  
890 900 910 920 930 940

Cry1Ac LFNVSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFS  
gi|403 LFTNVQDEALQFDTTLAQIQYAEYLVQSIPIVYVNDWLSVDPGMNYDIYVELDARVAQARY  
950 960 970 980 990 1000

Cry1Ac LYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQRSVLVVPEWEAEVSEVVRVCPGRGYI  
gi|403 LYDTRNIKNGDFTQGVMGVHTGNADVQ-QIDGVSVLVLSNWSAGVSNVHLQNHGHYV  
1010 1020 1030 1040 1050 1060

Cry1Ac LRVTAKEGYGEGCVTIEIENNTDELKFSNCEVEEIIYPNNTVTTCNDYTVNQEYGGAYT  
gi|403 LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----  
1070 1080 1090

Cry1Ac SRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGRYDPTPLPVGYVTKLEIYFPE  
gi|403 -----GYITKTVDFVFPD  
1100

Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE  
gi|403 TDRVRIEIGETEGSFYIESIELICMNE  
1110 1120 1130

>>gi|592801|gb|AAA54408.1| Sequence 3 from Patent WO 880 (1136 aa)  
initn: 1791 init1: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64  
Smith-Waterman score: 1945; 33.918% identity (62.239% similar) in 1197 aa overlap  
(38-1182:43-1136)

Cry1Ac NPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAFVFL---G  
gi|592 GSMKNTNYKDWLAMCENNQQYGVNPAAINSSSVTALKVAGAILKFNVPAGTVLTVLSA  
20 30 40 50 60 70

Cry1Ac LVDIIWIGIFGSPQ---WDAFLVQIEQLINQRIBEFARNQAIISRLEGLSNLYQIYAESFRE  
gi|592 VLPILWPTNTPTPERVWDFMTNTGNLIDQTVTAIVVRTDANAKMTVVKDYLDQYTTKFNFT  
80 90 100 110 120 130

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130      140      150      160      170
Cry1Ac WEADPTN PALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|592 WKREPNNQSYRTAVITQFNLTSAKLRETAVYFNSLVGYELLPLPIYAQVANFNLLLRDGL
140      150      160      170      180      190

180      190      200      210      220      230
Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
gi|592 LINAQEWLSARSAGDQLYNTMVQYTKKEYIAHSITWYKGLDVLNRKNSNGQWITFNDYKRE
200      210      220      230      240      250

240      250      260      270      280      290
Cry1Ac LTLTVDLIVSLFPNYDSRTYPIRTV-----SQLTREIYTNPVLENFDGSRGSAQGIE
gi|592 MTIQVLDLILALFASYPDRRYPADKIDNTKLSKTEFTREIY TALV----ESPSSKSAIALE
260      270      280      290      300

300      310      320      330      340      350
Cry1Ac GSI-RSPHMLDILNSITTYTDA-HRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAP
gi|592 AALTRDVHLFTWLKRVDWFNTIYQDLRFLSANKIGFYSYNTSSAMQES-GIYSSGSGFGSN
310      320      330      340      350      360

360      370      380      390      400      410
Cry1Ac QQRIVAQLGQGVYRSLSSLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPYSAVYRKSQT
gi|592 LTHQI-QLNSNVYKKT-SITDTSPPSN-RVTKMDFYKIDGTLASYSNITPTPEGLRRTFFF
370      380      390      400      410      420

420      430      440      450      460      470
Cry1Ac VDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI
gi|592 GFSTNENTP---NQPTVNDYTHILSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI
430      440      450      460      470

480      490      500      510      520      530
Cry1Ac ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST
gi|592 YTDAITQVPAVKSNFLNATAKVIKPGHGTGGDLVALTSNGT-LSGRMEIQCKTSTIFNDPT
480      490      500      510      520      530

530      540      550      560      570      580
Cry1Ac R-YRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSL---DNLQSSDFGY--FESANAF
gi|592 RSYGLRIRIYAANSPIVLNVSVYLQGVSRGTTLSTESTFSRPNNIPTDLKYEERFKYKDFP
540      550      560      570      580      590

590      600      610      620      630      640      650
Cry1Ac TS-----SLGNIVGVR---NFSGTAGVIIDRFEPVPTATL--EAE-YNLERAQKAVN
gi|592 DAIVPMRLSSNQLITIAIQPLNMTSNNQVIIDRIEIIPIQSVLDETENQNLESREVVN
600      610      620      630      640      650

640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ
gi|592 ALFTNDAKDALNIGTDDYDIDQAANLVECISEELYPKEKMLLLDEVKNAKQLSQSRNVLQ
660      670      680      690      700      710

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700      710      720      730      740
Cry1Ac DSNFKDINRQPERGWGSGGITIQGGDDVFKENYVTLSTGTFD---ECYPTYLYQKIDESK
gi|592 NGDFESAT----LGWTTSDNITIQEDDPIFKGHYLMHSGARDIDGTIFPTYIFQKIDESK
720      730      740      750      760      770

750      760      770      780      790      800
Cry1Ac LKAFTRYQLRGIYEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEENR
gi|592 LKPYTRYLVRGFVGSKDVVELVVSRYGEEIDAIMNVPADLNLYLPSTFD----CEGSRN
780      790      800      810      820

810      820      830      840      850
Cry1Ac C----AP-HLEWNPDLDCSCR--DGEK---CAHSHHFLSLDIDVGCTDLNEDLGVWVIFK
gi|592 CETSAVPANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDTNENIGVWVMFK
830      840      850      860      870      880

860      870      880      890      900      910
Cry1Ac IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKWRDKRELEWETNIVYKEAKESVDA
gi|592 ISSPDGYASLDNLEVEEGPIDGEALSRVKHMEKKWNDQMEAKRSETQQAYDVAQQAIDA
890      900      910      920      930      940

920      930      940      950      960      970
Cry1Ac LFNVSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFS
gi|592 LFTNVQDEALQFDTTLAQIQAIEYLVQSIPIVYNDWLSVDPGMNYDIYVELDARVAQARY
950      960      970      980      990      1000

980      990      1000      1010      1020      1030
Cry1Ac LYDARNVIKNGDFNNGLSWCNVKGVHDVVEEQNNQRSVLVVPEWEAEVSEVRCVPGRYI
gi|592 LYDTRNIIKNGDFTQGVMGVHWVTGNADVQ-QIDGVSVLVLSNWSAGVSNVHLQHNHGYV
1010      1020      1030      1040      1050      1060

1040      1050      1060      1070      1080      1090
Cry1Ac LRVTAKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEYGGAYT
gi|592 LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----
1070      1080      1090

1100      1110      1120      1130      1140      1150
Cry1Ac SRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENRGRDYTPPLVGVYVTKLEYFPPE
gi|592 -----GYITKTVDFPDP
1100

1160      1170      1180
Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE
gi|592 TDRVRIEIGETEGSFYIESIELICMNE
1110      1120      1130

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>>gi|592802|gb|AAA54409.1| Sequence 4 from Patent WO 880 (1136 aa)  
 initn: 1791 initl: 571 opt: 1118 Z-score: 1307.8 bits: 253.9 E(): 6.4e-64  
 Smith-Waterman score: 1945; 33.918% identity (62.239% similar) in 1197 aa overlap  
 (38-1182:43-1136)

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10 20 30 40 50 60  
Cry1Ac NPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL----G  
gi|592 GSMKNTNYKDWLACENNQQYGVNPAAINSSSVSTALKVAGAILKVFVNPAGTVLTLVLSA  
20 30 40 50 60 70

70 80 90 100 110 120  
Cry1Ac LVDIIWGIWFGPSQ--WDFAFLVQIEQLINQRIEFAFNQAIISRLEGLSNLYQIYAESFRE  
gi|592 VLPILWPTNTPTPERVWVDFMTNTGNLIDQTVTAYVRTDANAKMTVVKDYLDQYTTKFN  
80 90 100 110 120 130

130 140 150 160 170  
Cry1Ac WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD  
gi|592 WKREPNNQSYRTAVITQFNLTSAKLRETAVYFVSNLVGYELLLLPIYAQVANFNLLLRD  
140 150 160 170 180 190

180 190 200 210 220 230  
Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYDHAWRWYNTGLERVWGPDSRDRWIRYNQFRRE  
gi|592 LINAQEWSLARSAGDQLYNTMVQYTKYIAHSITWYKGLDVLNRKSNQGWITFNQYKRE  
200 210 220 230 240 250

240 250 260 270 280 290  
Cry1Ac LTLTVDLIVSLFPNYSRTYPIRTV-----SQLTREIYTNVLENFDGSRGSAQGIE  
gi|592 MTIQVLDLIALFASYPDRRYPADKIDNTKLSKTEFTREIYALV---ESPSSKSIAALE  
260 270 280 290 300

300 310 320 330 340 350  
Cry1Ac GSI-RSPHMLDILNSITTYTDA-HRGEYYSWGHQIMASPVGFSGPEFTPLYGTMGNAAP  
gi|592 AALTRDVLHFTWLKRVDFWNTIYQDLRFLSANKIGFSYTNSSAMQES-GIYGSSGFGSN  
310 320 330 340 350 360

360 370 380 390 400 410  
Cry1Ac QQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSNLPASAVYKSGT  
gi|592 LTHQI-QLNSNVYKT-SITDTSSPSN-RVTKMDFYKIDGTLASYSNITPTPEGLRTRTF  
370 380 390 400 410 420

420 430 440 450 460 470  
Cry1Ac VDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFWSIHRSAEFNNII  
gi|592 GFSTNENTP---NQPTVNDYTHILSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI  
430 440 450 460 470

480 490 500 510 520  
Cry1Ac ASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPFSTST  
gi|592 YTDAITQVPAVKSNFLNATAKVIKPGHGTGGDLVALTSNGT-LSGRMEIQCKTSIFNDPT  
480 490 500 510 520 530

530 540 550 560 570 580  
Cry1Ac R-YRVVRVRYASVTPHILNWNWGNSSIFSNTVPATATSL---DNLQSSDFGY--FESANAF  
gi|592 RSYGLRIRYAANSPIVLNVSYVLQVSRGTTISTESTFSRPNNIIPDLDKYEFRYKDFP

540 550 560 570 580 590  
Cry1Ac TS-----SLGNIVGVR---NFSGTAGVVIDRFEFIPVATL--EAE-YNLERAQKAVN  
gi|592 DAIVMRLSSNQLITIAIQPLNMTSNNQVIIDRIEIPITQSVLDETENQNLSEREVVN  
600 610 620 630 640 650

640 650 660 670 680 690  
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQ  
gi|592 ALFTNDAKDALNIGTTDYDIDQAANLVECISEELYPKMKMLLDEVKNAKQLSQSRNLVQ  
660 670 680 690 700 710

700 710 720 730 740  
Cry1Ac DSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---ECYPTYLYQKIDESK  
gi|592 NGDFESAT---LGTTSNITIQEDDPIFKGHYLMHSGARDIDGTIFPTYIFQKIDESK  
720 730 740 750 760 770

750 760 770 780 790 800  
Cry1Ac LKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPNR  
gi|592 LKPYTRYLVRGFVGSKDVVELVVSRYGEEIDAIMNVPADLNYLYPSTFD---CEGSSNR  
780 790 800 810 820

810 820 830 840 850  
Cry1Ac C----AP-HLEWNPDLDCSCR--DGEK---CAHSHHFFSLDIDVGTDLNEDLGVVWIFK  
gi|592 CETSAVPANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDNTNENIGVWVMFK  
830 840 850 860 870 880

860 870 880 890 900 910  
Cry1Ac IKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKRELEWETNIVYKBAKESVDA  
gi|592 ISSPDGYASLDNLEVEEGPIDGEALSRVKHMEKKWNDQMEAKRSETQQAIVAKAIDA  
890 900 910 920 930 940

920 930 940 950 960 970  
Cry1Ac LFWNSQYDQLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFS  
gi|592 LFTNVQDEALQFDTTLAQIQYAEYLVQSIPIVYVNDWLSVPGMNYDIYVELDARVAQARY  
950 960 970 980 990 1000

980 990 1000 1010 1020 1030  
Cry1Ac LYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSVLVVPEWAEVSVQEVVCPGRGYI  
gi|592 LYDTRNIKNGDFDQVMGWHVTGNADVQ-QIDGVSVLVLSNWSAGVSNVHLQHNHGVV  
1010 1020 1030 1040 1050 1060

1040 1050 1060 1070 1080 1090  
Cry1Ac LRVTAKEGYGEGCVTIEIENNTDELKFSNCVVEEIIYPNNTVTCNDYTVNQBEYGGAYT  
gi|592 LRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----  
1070 1080 1090

1100 1110 1120 1130 1140 1150  
Cry1Ac SRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYTPLPVGYVTKLEYFPFE  
::: . . . .

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gi|592 -----GYITKTVDFVFPD
                               1100

      1160      1170      1180
Cry1Ac TDKVWIEIGETEGTFIVDSVELLLMEE
      ::: : : : : : : : : : : : : : : : : :
gi|592 TDRVRIEIGETEGSFYIESIELICMNE
      1110      1120      1130

>>gi|216290|dbj|BAA00179.1| 130 kDa insecticidal protein (1180 aa)
  inith: 1592 inith: 571 opt: 1112 Z-score: 1300.4 bits: 252.6 E(): 1.6e-63
Smith-Waterman score: 1714; 33.306% identity (59.393% similar) in 1219 aa overlap
(44-1182:70-1180)

      20      30      40      50      60      70
Cry1Ac CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFV--LGLVDIIWG-
      ::      : : : : : : : : : : : : : : : :
gi|216 QSTNYKDWLNMCCQNNQYGGDFETFIDSGELSAITIVVGTVLTGFGFTTPLGLALIGFGT
      40      50      60      70      80      90

      80      90      100      110      120
Cry1Ac ---IFGPSQ----WDAFLVQIEQLINQRIEIEFARNQAIISRLEGLSNLYQIYAESFREWE
      .. : : : : : : : : : : : : : : : : : :
gi|216 LIPVLFPAQDQSNWSDFITQTKNIKKKEIASTYISNANKILNRSFNVIISTYHNHKTWE
      100      110      120      130      140      150

      130      140      150      160      170
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLL SVVQAAANLHL
      : : : : : : : : : : : : : : : : : :
gi|216 NNP-NPQNTQDVRTQIQLVHYHFQNVIPELVNSCPPNPSPDCDYNYLILVSSYAQAANLHL
      160      170      180      190      200      210

      180      190      200      210      220
Cry1Ac SVLRDVSVF---GQRWGFDA---ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG-
      : : : : : : : : : : : : : : : : : :
gi|216 TVLNQAVKFEAYLKNRQFVDYLEPLPTAIDYYPVLTKAIEDYTNVCTYKKGKLNLIKTT
      220      230      240      250      260      270

      230      240      250      260      270
Cry1Ac PDSR-----DWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLEN
      : : : : : : : : : : : : : : : : : :
gi|216 PDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYPIGVQSELTREIYQ--VL-N
      280      290      300      310      320      330

      280      290      300      310      320      330
Cry1Ac FDGS--FRG-SAQGIEGSI-RSPHLMIDILNSITITYDAHRG-EYYWSGHQIMASPVGFSGP
      : : : : : : : : : : : : : : : : : :
gi|216 FEESPYKYDFQYQEDSLTRRPHLFTWLDLSLNFYEKAQTPPNPFVTSHYNMFH-YTLDNI
      340      350      360      370      380      390

      340      350      360      370      380      390
Cry1Ac EFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL----YRRPFNIGINNQLSVLDGT
      : : : : : : : : : : : : : : : : : :
gi|216 SQKSSVFGNH--NVTDKLKSLG--LATNIYIFLLNVISLDNKYLNDYN--NISKMDFFITNGT
      400      410      420      430      440      450

      400      410      420      430      440
Cry1Ac -----EFAYGTSNLPASVYRKSGTVDSLDEIPPQNNNV--PPRGFVSHRLSHVSMFRSG
      : : : : : : : : : : : : : : : : : :

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gi|216 RLLEKELTAG-SGQITYDVNKNIFGLPILKRRENQGNPTLFPTYDNYSHILS----FIKS
      460      470      480      490      500

      450      460      470      480      490      500
Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNNGS-VISGPGFTGGDL
      : : : : : : : : : : : : : : : : : :
gi|216 LSPATYKTKQVYTFAWTHSSVDPKNTIYTHLTTQIPAVKANSGLTASVQVGGPGHTGGDL
      510      520      530      540      550      560

      510      520      530      540      550
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP-----IHLNVNWNQSSIFS
      : : : : : : : : : : : : : : : : : :
gi|216 IDF-----KDFHKITCQHSNFQSSYFIRIRYASNGSANTRAVINLSIP-GVAELGM
      570      580      590      600      610

      560      570      580      590      600      610
Cry1Ac NTVPA-TATSLDNLQSSDFGYFESANAFSSLG-NIVGVRNFSGT---AGVIIDRFEFIP
      : : : : : : : : : : : : : : : : : :
gi|216 ALNPTPSGTDYTNLKYKDFQYLEFSNEVKFAPNQNISLVFNRSVDVYTNVTVLIDKIEFLP
      620      630      640      650      660      670

      620      630      640      650      660
Cry1Ac VTATLEAEYN---LERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVYLSDEFCLDE
      : : : : : : : : : : : : : : : : : :
gi|216 ITRSIREDRKQKLETVQOIINTFYANPKNTLQSELTDYDIDQAANLVECTISEELYPKE
      680      690      700      710      720      730

      670      680      690      700      710      720
Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLN
      : : : : : : : : : : : : : : : : : :
gi|216 KMLLLDEVKNAKQLSQRNVLQNGDFESATL---GWTTSDNITIQEDDPIFKGHVLMHS
      740      750      760      770      780      790

      730      740      750      760      770      780
Cry1Ac GTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
      : : : : : : : : : : : : : : : : : :
gi|216 GARDIDGTIFPTYIFQKIDESKLPYTRYLVRFVGVSSKDELVSVRYGEEIDAIMNVPA
      800      810      820      830      840      850

      790      800      810      820      830
Cry1Ac T-GSLWPLSAQSPIGKCGEPNRC---AP-HLEWNPDLDCSCR--DGEK---CAHSHSHF
      : : : : : : : : : : : : : : : : : :
gi|216 DLNLYLPSTFD-----CEGSNRCETSAVPANIGNTSDMLYSQCYDTGKKHVVC-QDSHQF
      860      870      880      890      900

      840      850      860      870      880      890
Cry1Ac SLDIDVGCITDLNEDLVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      : : : : : : : : : : : : : : : : : :
gi|216 SFTITDGTALDITNENIGVWVWVFKISSPDGYASLDNLEVIIEGPDIDGALSRLVHMEKKWND
      910      920      930      940      950      960

      900      910      920      930      940      950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRVHSIREAYLPELS
      : : : : : : : : : : : : : : : : : :
gi|216 QMEAKRSETQQAYDVAKAIDALFTNVQDEALQFDITTLAQIQYAEYLVQSIPIVYNDWLS
      970      980      990      1000      1010      1020

      960      970      980      990      1000      1010
Cry1Ac VIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNVKGHVVDVEEQNNQRSVL

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gi|216 DVPGMNYDIYVELDARVAQARYLYDTRNIIKNGDFTQGVGMWHVTGNADVQ-QIDGVSVL
1030 1040 1050 1060 1070 1080

Cry1Ac VVPEWEAEVSEQEVRVCPGRGYILLRVYAYKEGYEGCVTIHEIENNTDELKFSNVCVEEIIY
. . . . .

gi|216 VLSNWSAGVSNVHLQHNGHYVLRVIAKKEGPGNGYVTLMDCEENQEKLTPFSCEE----
1090 1100 1110 1120 1130 1140

Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNR

gi|216 -----

Cry1Ac GYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
. . . . .

gi|216 -----GYITKTVDFPDTDRVRIEIGETEGSFYIESIELICMNE
1150 1160 1170 1180

>>gi|21685485|emb|CAD30148.1| pesticidal crystal protei (1180 aa)
initn: 1592 initl: 571 opt: 1112 Z-score: 1300.4 bits: 252.6 E(): 1.6e-63
Smith-Waterman score: 1714; 33.306% identity (59.393% similar) in 1219 aa overlap
(44-1182:70-1180)

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Cry1Ac CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFV--LGLVDIIWG-
. . . . .

gi|216 QSTNYKDWLNMCCQQNQYGGDFETFIDSGELSAYTIVGTVLTGFGFTTPLLGLALIGFGT
40 50 60 70 80 90

Cry1Ac ---IFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWE
. . . . .

gi|216 LIPVLFPAQDQSNWSDPITQTKNIIKKEIASTYISNANKILNRSFNVIYSTYHNLKWTWE
100 110 120 130 140 150

Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLLSVYVQAANLHL
. . . . .

gi|216 NNP-NPQNTQDVRTQIQLVHYHFQNVIPELVNSCPPNPDCDYNNILVSSYAQAANLHL
160 170 180 190 200 210

Cry1Ac SVLRDVSVF---GQRWGFDA---ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG-
. . . . .

gi|216 TVLNQAVKFEAYLKNNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVCVTTYKGLNLIKTT
220 230 240 250 260 270

Cry1Ac PDSR-----DWIRYQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLEN
. . . . .

gi|216 PDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGKYPIGVQSELTREIYQ--VL-N
280 290 300 310 320 330

Cry1Ac FDGS-FRG-SAQGIEGSI-RSPHLMIDILNSITITYDAHRG-EYYWSGHQIMASPVGFSGP

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gi|216 FEESPXYKYDFQYQEDSLTRRPHLFTWLDLNFYEKAQTPNPNFFTSYHNMFMH-YTLDNI
340 350 360 370 380 390

Cry1Ac EFTFPPLYGTMGNAAPQRIVAQLGQGVYRTLSTL-----YRRPFNIGINNQQLSVLDGT
. . . . .

gi|216 SQKSSVFGNH-NVTDKLLKSLG-LATNIYIFLLNVIISLDNKYLNDYN-NISKMDFFITNGT
400 410 420 430 440 450

Cry1Ac ----EFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNNV--PPRQGFSHRLSHVSMFRSG
. . . . .

gi|216 RLLEKELTAG-SGQITVDVKNKIFGLPILKRENQGNPTLFPPTYDNYSHILS----FIKS
460 470 480 490 500

Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDL
. . . . .

gi|216 LSIPTATYKTQVYTFAWTHSSVDPKNTIYTHLTTQIPAVKANSLGTASKVVGPGHTGGDL
510 520 530 540 550 560

Cry1Ac VRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYASVTP-----IHLNVHWGNSSIFS
. . . . .

gi|216 IDF-----KDFHKITCQHSNFQSQSYFIRIRYASNGSANTRAVINLSIP-GVAELGM
570 580 590 600 610

Cry1Ac NTVPA-TATSLDNLQSSDFGYFESANAFTSSLG-NIVGVNRFSGT---AGVIIDRFEFIP
. . . . .

gi|216 ALNPTFSGTDYTNLYKQDFQYLEFSNEVKFAPNQNISLVFNRSVDYVNTTVLIDKIEFLP
620 630 640 650 660 670

Cry1Ac VTATLEAEYN---LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDE
. . . . .

gi|216 ITRSIREDEKQKLETVQQIINTFYANPKNTLQSELTDYDIDQANLVECISEELYPKE
680 690 700 710 720 730

Cry1Ac KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGTTIQQGGDDVFKENYVTLN
. . . . .

gi|216 KMLLLDEVKNAKQLSQSRNVLQNGDFESATL---GWTSDNITIQEDDPIFKGHYLMHS
740 750 760 770 780 790

Cry1Ac GTFD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
. . . . .

gi|216 GARDIDGTIFPTYIFQKIDESKLPYTRYLVRGFGVSSKDELVVSRYGEEIDAIMNVPA
800 810 820 830 840 850

Cry1Ac T-GSLWPLSAQSPIGKCGEPNRC---AP-HLEWNPDLDCSCR--DGEK---CAHSHSHF
. . . . .

gi|216 DLNLYLPSTFD-----CEGSNRCETSAVPANIGNTSDMLYSCQYDTGKHKHVVC-QDSHQF
860 870 880 890 900

Cry1Ac 840 850 860 870 880 890

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Cry1Ac SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
gi|216 SFTIDTGDALDTNENIGVWVMFKISSPDGYASLDNLEVIEBEGPIDGEALSRVKHMEKKWND
910 920 930 940 950 960

900 910 920 930 940 950
Cry1Ac KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS
gi|216 QMEAKRSETQQAYDVAQKQIDALFTNVQDEALQFDTTLAQIQYAEYLVQSIPIVYNDWLS
970 980 990 1000 1010 1020

960 970 980 990 1000 1010
Cry1Ac VIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVL
gi|216 DVPGMNYDIYVELDARVAQARYLYDTRNLIKNGDFTQVGMGWHVTGNADVQ-QIDGVSVL
1030 1040 1050 1060 1070 1080

1020 1030 1040 1050 1060 1070
Cry1Ac VVPEWEAEVSVQEVRCVPGRGYILRVVTAYKEGYGEGCVTIEHIENNTDELKFSNCVVEEIIY
gi|216 VLSNWSAGVSNVHLQHNHGYVLRVIAKKEGPGNGYVTLMDCEEENQKLTPTSCEE----
1090 1100 1110 1120 1130 1140

1080 1090 1100 1110 1120 1130
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVVEEKSYSYDGRRENPCFNR
gi|216 -----

1140 1150 1160 1170 1180
Cry1Ac GYRDYTPLPVGVVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|216 -----GYITKTVDFPDTDRVRIEIGETEGSFYIESIELCMNE
1150 1160 1170 1180

>>gi|57639076|gb|AAW55474.1| delta-endotoxin [Bacillus t (1136 aa)
initt: 1760 initt1: 565 opt: 1107 Z-score: 1294.8 bits: 251.5 E(): 3.4e-63
Smith-Waterman score: 1918; 33.584% identity (62.155% similar) in 1197 aa overlap
(38-1182:43-1136)

10 20 30 40 50 60
Cry1Ac NPININECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVL----G
gi|576 GSIKNTNYKDWLAMCENNQQYGVNPAAINSSSVTALKVAGAILKFNPNPAGTVLTVLSA
20 30 40 50 60 70

70 80 90 100 110 120
Cry1Ac LVDIIWGFQPSQ---WDAFLVQIEQLINQRIEEFARNQAIARLEGLSNLYQIYAESFRE
gi|576 VLPILWPTNTPTPERVWVDFMTNTGNLIDQTVTAVVRTDANAKMTVVVKDYLDQYTTKFN
80 90 100 110 120 130

130 140 150 160 170
Cry1Ac WEADPTNPALREEMRIQFNDMNSALT-TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|576 WKREPNNQSYRTAVITQFNLTSAKLRETAVYFSNLVGYELLLLPIYAQVANFNLLIRDG
140 150 160 170 180 190

180 190 200 210 220 230

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Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
gi|576 LINAQEWLSARSAGDQLYNTMVQYTKKEYIAHSITWYNKGLDVLNRKNSGQWITFNDYKRE
200 210 220 230 240 250

240 250 260 270 280 290
Cry1Ac LTLTVLDIVSLFPNYSRTPYPIRTV-----SQLTREIYTNVPLENFDFGSRFGSAQGIE
gi|576 MTIQVLDLILALFASYPDRRYPADKIDNTKLSKTEFTREIYITALV----ESPSSKSIAALE
260 270 280 290 300

300 310 320 330 340 350
Cry1Ac GSI-RSPHMLDILNSITIIYTDARHGEYYSWGHQIMASPVGFGPEFTFPPLYGTMGNAAP
gi|576 AALTRDVLHFTWLKRVDFWNTTIYQDLRFLSANKIGFSYTNSSAMQES-GIYSSGFGSN
310 320 330 340 350 360

360 370 380 390 400 410
Cry1Ac QQRIVAQQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQT
gi|576 LTHQI-QLNSNVYKT-SITDTSPPSN-RVTKMDFYKIDGTLASYNISNITPTPEGLRTTFF
370 380 390 400 410 420

420 430 440 450 460 470
Cry1Ac VDSLDEIPPQNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNII
gi|576 GFSTNENTP---NQPTVNDYTHLSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQI
430 440 450 460 470

480 490 500 510 520
Cry1Ac ASDSTITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTST
gi|576 YTDAITQVPAVKSNSLNATAKVIKGPHTGGDLVALTSNGT-LSGRMEIQCKTISFNDPT
480 490 500 510 520 530

530 540 550 560 570 580
Cry1Ac R-YRVRVRYASVTPIHNLNVWGNSSIFSNTVPATATSL---DNLQSSDFGY--FESANAF
gi|576 RSYGLRIRIYAANSPIVLNVSYVLQGVSRGTTISTESTFSRPNNIIPTDLKYEEFVKDPF
540 550 560 570 580 590

590 600 610 620 630
Cry1Ac TS-----SLGNIVGV---RNFSGTAGVIIDRFEPVPTATL--EAE-YNLERAQKAVN
gi|576 DAIIVPMLSSNQLITTAIQPSNMTSNNQVIIDRIEIPITQSLDETENQNLESREVVN
600 610 620 630 640 650

640 650 660 670 680 690
Cry1Ac ALFTSNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDEERNLLQ
gi|576 ALFTNDAKDALNIGTDDYDIDQAAANPVECISEELYPKMKMLLLDEVKNKQLSQSRNVLQ
660 670 680 690 700 710

700 710 720 730 740
Cry1Ac DSNFKDINRQPERGWGGSGITIQGGDDVFKENYVTLSGTFD---ECYPTLYQKIDESK
gi|576 NGDFESAT----LGWTTSDNITIQEDDPIFKGHYLMHSGAREIDGTIFPTYIFQKIDESK
720 730 740 750 760 770

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510      520      530      540      550      560
Cry1Ac  VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP-----IHLNVNWNSSIFS
      510      520      530      540      550
gi|592  IDF-----KDHFKITCQHSNFQSYFIRIRYASNGSANTRAVINLSIP-GVAELGM
      570      580      590      600      610
Cry1Ac  NIVPA-TATSLDNLQSSDFGYFESANAFTSSLG-NIVGVRNFSGT---AGVIDRFEFIP
      560      570      580      590      600      610
gi|592  ALNPTFSGTDYTNLKYKDFQYLEFSEVNFAPNQNISLVFNRSVYTNNTVLIDKIEFLP
      620      630      640      650      660      670
Cry1Ac  VTATLAEAYN---LERAQKAVNALFTSTNQLGLKTNVTDYHDIQVSNLVTYLSDEFCLDE
      620      630      640      650      660
gi|592  ITRSIREDREKQKLETVQQIINTFYANPIKNTLQSELTDYDIDQAAANLVECISEELYPKE
      680      690      700      710      720      730
Cry1Ac  KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLN
      670      680      690      700      710      720
gi|592  KMLLLDEVKNAKQLSQSRNVLQNGDFESATL---GWTTSDNITIQEDDPIFKGHYHMS
      740      750      760      770      780      790
Cry1Ac  GTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
      730      740      750      760      770      780
gi|592  GARDIDGTIFPTYIFQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
      800      810      820      830      840      850
Cry1Ac  T-GSLWPLSAQSPIGKCGEPNRC---AP-HLEWNPDLDCSCR--DGEK---CAHSHHF
      790      800      810      820      830
gi|592  DLNLYPSTFD----CEGSNRCETSAPVANIINTSDMLYSQYDTGKKHVVC-QDSHQF
      860      870      880      890      900
Cry1Ac  SLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      840      850      860      870      880      890
gi|592  SFTIDTGALDTNENIGVWVWFKISSPDGYASLDNLEVEIEGPDIDGALSRLVHMEKKWND
      910      920      930      940      950      960
Cry1Ac  KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELS
      900      910      920      930      940      950
gi|592  QMEAKRSETQQAYDVAKQAIIDALFTNVQDEALQFDTTLAQIYAEYLVQSIPIYVYNDWLS
      970      980      990      1000      1010      1020
Cry1Ac  VIPGVNAAIFEELEGRIPTAFSLYDARNVIKNGDFNNGLSQWVNVKGVHDVEEQNNQRSVL
      960      970      980      990      1000      1010
gi|592  DVPGMNYDIYVELDARVAQARYLYDIRNIIKNGDFTQGVMGVHVTGNADVQ-QIDGVSVL
      1030      1040      1050      1060      1070      1080
Cry1Ac  VVPEWAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFNQVVEEIIY
      1020      1030      1040      1050      1060      1070

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gi|592  VLSNWSAGVSQNVHLQHNHGYVLGVIKKEGPGNGYVTLMDWEENQEKLTFTSCEE----
      1090      1100      1110      1120      1130      1140
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGRYNEAPSVPADYASVYEEKSYTDGRRENPCFN
      1080      1090      1100      1110      1120      1130
gi|592  -----
      1140      1150      1160      1170      1180
Cry1Ac  GYRDYTPLVGVYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      1140      1150      1160      1170      1180
gi|592  -----GYITKTVDVFPDTRVRIEIGETEGSFYIESIELICMNE
      1150      1160      1170      1180
>>gi|40352|emb|CAA68485.1| unnamed protein product [Baci (1180 aa)
      initn: 1565 init1: 570 opt: 1100 Z-score: 1286.3 bits: 250.0 E(): 1e-62
      Smith-Waterman score: 1704; 33.224% identity (59.229% similar) in 1219 aa overlap
      (44-1182:70-1180)
Cry1Ac  CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFV--LGLVDIIWG-
      20      30      40      50      60      70
gi|403  QSTNYKDWLNMCCQNNQYGGDFETFIDSGELSAYTIIVVGTVLTGFGFTPLGLALIGFT
      40      50      60      70      80      90
Cry1Ac  ---IFGPSQ----WDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWE
      80      90      100      110      120
gi|403  LIPVLVPAQDQSNQNTWSDFITQTKNIIKKEIASTYISNANKILNRSFNVISTYHNHLKTWE
      100      110      120      130      140      150
Cry1Ac  ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLLSVYQAANLHL
      130      140      150      160      170
gi|403  NNP-NPQNTQDVRTQIQLVHYHFQNVIPVPELVNSCPNPNSDCYYNLLVSSYAQAANLHL
      160      170      180      190      200      210
Cry1Ac  SVLRDVSVF---GQRWGFDA---ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG-
      180      190      200      210      220
gi|403  TVLNQAVKFEAYLKNNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVYCVTTYKGLNLIKTT
      220      230      240      250      260      270
Cry1Ac  PDSR----DWIRYNQFRRELTLTVDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVPLEN
      230      240      250      260      270
gi|403  PDSNLDGNINWNTYNTYRTKMTTAVLDVVAFPNYDVGKYPYIGVQSELREIYQ--VL-N
      280      290      300      310      320      330
Cry1Ac  FDGS-FRG-SAQGIIEGSI-RSPHLMIDILNSITTYTDAHRG-EYYWVSGHQIMASPVGFSGP
      280      290      300      310      320      330
gi|403  FEESPKYDYDFQYQEDSLTRRPHLFTWLDLNFYEKAQTTPNPNTTSHYNMFH-YTLDNI
      340      350      360      370      380      390
Cry1Ac  EPTFFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNNQLSVLGDT
      340      350      360      370      380      390

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gi|403 SQKSSVFGNH-NVTDKLSLG-LATNIYIFLLNVISLDNKYLNDYN-NISKMDFFITNGT
      400      410      420      430      440      450
Cry1Ac -----EFAYGTSSNLPASVYRKSQTVDLDEIPPQNNNV--PPRQGFSHRLSHVSMFRSG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 RLLEKELTAG-SGQITYDVNKNIFGLPILKRENOGNPTLFPYDNYSHILS----FIKS
      460      470      480      490      500
Cry1Ac -----FNSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNFS-VISGPGFTGGDL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 LSIPATYKTQVYTFAWTHSSVDPKNTIYTHLTTQIPAVKANS LGTAS KVVQPGHGTGGDL
      510      520      530      540      550      560
Cry1Ac -----VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP-----IHLNVNWNSSIFS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 IDF-----KDFHKITCQHSNFPQSYFIRIRYASNGSANTRAVINLSIP-GVAELGM
      570      580      590      600      610
Cry1Ac -----NIVPA-TATSLDNLQSSDFGYFESANAF TSSLG-NIVGVRNFSGT---AGVIIDRFEPFIP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 ALNPTFSGTDYTNLKYKDFQYLEFSEVVKFAPNQNI SLVFNRSVYVYNTNTVLIDKIEFLP
      620      630      640      650      660      670
Cry1Ac -----VTATLEAEYN---LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 ITRSIREDRKQKLETVQQIINTFYANPIKNTLQSELTDYDIDQAANLVECLSEELYPKE
      680      690      700      710      720      730
Cry1Ac -----KRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 KMLLLDEVKNAKQLSQRNVLQNGDFESATL---GWTSDNITIQEDDPIFKGHYHMS
      740      750      760      770      780      790
Cry1Ac -----GTFD---ECYPTTYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 GARDIDGTIFPTYIFQKIDESKLPYTRYLVRFVGS SKDVELVVSRYGEEIDAIMNVPA
      800      810      820      830      840      850
Cry1Ac -----T-GSLWPLSAQSPIGKCGEPNRC---AP-HLEWNPDLDCSCR--DGEK---CAHSHSHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 DLNLYPSTFD-----CEGSNRCETSAVPANIGNTSDMLYSQYDTGKKHVVVC-QDSHQF
      860      870      880      890      900
Cry1Ac -----SLDIDVGC TDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 SFTIDTGALDNTNENIGVWVMPKISSPDGYASLDNLEVIEEGPIDGEALSRVKHMEKKWND
      910      920      930      940      950      960
Cry1Ac -----KREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELS
      900      910      920      930      940      950

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      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 QMEAKRSEYQQAYDVAKQALDALFTNVQDEALQFDITTLAQIQYAEYLVQSIPIVYNDWLS
      970      980      990      1000      1010      1020
Cry1Ac -----VIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 DVPGMNYDIYVELDARVAQARYLYDIRNIKNGDFTQGVMGWHTGNADVQ-QIDGVSVL
      1030      1040      1050      1060      1070      1080
Cry1Ac -----VVPWEAEVSEQEVRVCPGRGYILRV TAYKEGYGEGCVTIHEIENNTDELKFSNCVEEEII
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 VLSNWSAGVSQNVHLQHNHGYVLGVIAKKEGPGNGYVTLMDWEEHQEKLTF TSCEE----
      1090      1100      1110      1120      1130      1140
Cry1Ac -----PNNTVTCNDYTVNQEEYGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFN
      1080      1090      1100      1110      1120      1130
gi|403 -----
      1140      1150      1160      1170      1180
Cry1Ac -----GYRDTPLPVGIVTKLEYFPETDKWIEIGETEGTFIVDSVELLLMEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|403 -----GYITKTVDFPDTDRVRIEIGETEGSFYIESIELICMNE
      1150      1160      1170      1180

>>gi|52145404|gb|AAU29411.1| Cry3Aa protein [Bacillus th (652 aa)
      initn: 749 initl: 470 opt: 1094 Z-score: 1283.0 bits: 248.5 E(): 1.5e-62
      Smith-Waterman score: 1098; 33.566% identity (67.308% similar) in 572 aa overlap
      (60-612:99-651)

      30      40      50      60      70      80
Cry1Ac -----GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|521 TTKDVIQKGISVVGDLGLVGVGFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      70      80      90      100      110      120
Cry1Ac -----90      100      110      120      130      140
      QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMMSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|521 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
      130      140      150      160      170      180
Cry1Ac -----150      160      170      180      190      200
      TAIPLFAVQNYQVPLLSVVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|521 NSMSPFAISGYEVLPLTTAQAANIHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
      190      200      210      220      230      240
Cry1Ac -----210      220      230      240      250      260
      YTDHAVRWYNTGLERWVGPDSRDWIRYQFRRELTTLTVLDIVSLFNPYDSRTYPIRTVSO
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|521 YTDHCVKWNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFLYDVRLYPKVEKTE
      250      260      270      280      290      300
Cry1Ac -----270      280      290      300      310
      LTREIYTNPVL--ENFDGSGFRGSAQIEGSIRSPHMDILNSITIYTDHRGEY-----

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gi|521 LTRDVLTPDIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTFRFRPGYGNDSFN
310 320 330 340 350 360

Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFNI
320 330 340 350 360 370
gi|521 YWSGVVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLFNP-GEKVYRAVANTNLAVWPSAV
370 380 390 400 410 420

Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQV--DSLDEIPPQNNVPPRQGFSD
380 390 400 410 420 430
gi|521 YSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPPEKGYSH
430 440 450 460 470

Cry1Ac RLSHVSMFRSFGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490
gi|521 QLNVMCFMLQGSRGTI-----PVLTWTHKSVDFNMDISKKITQLPLVKAYKQLQSGASV
480 490 500 510 520 530

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPPSTSTRYRVRVRYASVTPPIHLNVNWN
500 510 520 530 540 550
gi|521 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKHRARIHYASTSQITFTLSLDG
540 550 560 570 580

Cry1Ac SSIFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFI
560 570 580 590 600 610
gi|521 APFNQYFYDKTINKGDTLTYNFNLASFSTPFELSGNQLIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670
gi|521 PVN
650

>>gi|124263655|gb|ABM97547.1|Cry4A [Bacillus thuringien (1180 aa)
initn: 1541 initl: 570 opt: 1096 Z-score: 1281.6 bits: 249.1 E(): 1.8e-62
Smith-Waterman score: 1678; 34.319% identity (62.007% similar) in 1116 aa overlap
(44-1078:70-1148)

Cry1Ac CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFV--LGLVDIIWG-
20 30 40 50 60 70
gi|124 QSTNYKDWLNMCCQQNQYGGDFETFIDSGELSAIYIVVGTVLTFGFGFTPLGLALIGPFT
40 50 60 70 80 90

Cry1Ac ---IFGPSQ----WDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWE
80 90 100 110 120
gi|124 LIPVLPFAQDQNSWTSDFITQTKNIKKEIASTYISNANKILNRSFNWISTYHNLKQWTE
100 110 120 130 140 150

Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLLSVYVQAANLHL
130 140 150 160 170

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gi|124 NNP-NPQNTQDVRTQIQLVHYHFQNVIPELVNSCCPNPNSDCDYNNLLVSSYAHAANLHL
160 170 180 190 200 210

Cry1Ac SVLRDVSVF---GQRWGFDA---ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG-
180 190 200 210 220
gi|124 TVLNQAVKFEAYLKNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVCTTYKKGLNLIKTT
220 230 240 250 260 270

Cry1Ac PDSR----DWIRYNQFRRELTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPLEN
230 240 250 260 270
gi|124 PDSNLDGNINWNTYNTYRTKMTTAVLDVVALFPIDYVGVKYPIDVQSELTREIY--QVL-N
280 290 300 310 320 330

Cry1Ac FDGS-FRG-SAQGIEGSI-RSPHLMIDLNSITTYTDAHRG-EYYWSGHQIMASPVGFSGP
280 290 300 310 320 330
gi|124 FEESPYYDFQYQEDSLTRRPHLFTWLDLNFYEKAQTTPNFFTSHYNM---PHYTLTLD
340 350 360 370 380 390

Cry1Ac EFTFPLYGTMGNAAPQQRIVAQ-LGQGVYRTLSSSTL----YRRPFNIGINNQQLSVLDG
340 350 360 370 380
gi|124 NIS-QKSSVFGNHNVTDKLKGALATNIYIFLLNVISLDNKYLNNDYN-NISKMDFFITNG
400 410 420 430 440 450

Cry1Ac T-----EFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNV--PPRQGFSHRLSHVSMFRS
390 400 410 420 430 440
gi|124 TRLEKELTAG-SGQITYDVNKNIFGLPILKRRENQGNPTLFPTYDNYSHILS---FIK
460 470 480 490 500

Cry1Ac GFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGD
450 460 470 480 490 500
gi|124 SLSIPATYKTQVYTFAWTHSSVDPKNTIYTHLTTQIPAVKANSLGTASKVVGPGHTGGD
510 520 530 540 550 560

Cry1Ac LVRLNSSGNNIQNRGYIEVPIHFPPSTSTRYRVRVRYASVTP-----IHLNVNWNSSSIF
510 520 530 540 550
gi|124 LIDF-----KDHFKITCQHSNFQOQSYFIRIRFASNGSANTRAVINLSIP-GVAELG
570 580 590 600 610

Cry1Ac SNTVPA-TATSLDNLQSSDFGYFESANAFTSSLG-NIVGVRNFGT---AGVIIDRFEFI
560 570 580 590 600 610
gi|124 MALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPNQNISLVFNRSVYNTTTLVLDKIEFL
620 630 640 650 660 670

Cry1Ac PVTATLEAEYN--LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLD
620 630 640 650 660
gi|124 PITRSIREDKQKLETVQOIINTFYANPIKNTLQSELTDYDIDQAANLVECISELEYPK
680 690 700 710 720 730

Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLLSVYVQAANLHL
670 680 690 700 710 720

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Cry1Ac EKRELSSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFKENYVTL
gi|124 EKMLLLDEVKNAQLSKSRNVLQNGDFESATL---GWTTSNITIQEDDPIFKGHYLMH
740 750 760 770 780 790

730 740 750 760 770 780
Cry1Ac SGTGFD---ECYPTLYLQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVP
gi|124 SGARDIDGTIFPTYIFQKIDESKLPYTRYLVRGFGVSSKDVVSVRYGEEIDAIMHVP
800 810 820 830 840 850

790 800 810 820 830
Cry1Ac GT-GSLWPLSAQSPIGKCGEPNRC---AP-HLEWNPDLDCSCR--DGEK---CAHSHSH
gi|124 ADLNLYLPSTCD----CEASNRCE TSAVPANIGTSDMLYSCQYDTGKHHVVC-QDSHQ
860 870 880 890 900

840 850 860 870 880 890
Cry1Ac FSLDIDVGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWR
gi|124 FSFTLLDGTALDINENIGVWVMFKISSPDGYASLDNLEVEEGPIDGEALSRVKHMEKKWN
910 920 930 940 950 960

900 910 920 930 940 950
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPEL
gi|124 DQMEAKRSETQAYDVAKQADALFNTVQDEALQFDTTLAQIQYAEYLVQSPYVYNDWL
970 980 990 1000 1010 1020

960 970 980 990 1000 1010
Cry1Ac SVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSV
gi|124 SDVPMNNDIYVELDARVAQARYLYDIRNIKNGDFTQGVMGWHTGNADVQ-QIDGVSV
1030 1040 1050 1060 1070 1080

1020 1030 1040 1050 1060 1070
Cry1Ac LVPVEWAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCFVEEII
gi|124 LVLFNWSAGVSNVHLHNNHGYVLGVIKKEGPGNGYVTLMDWEENQEKLTFTSC--EEG
1090 1100 1110 1120 1130 1140

1080 1090 1100 1110 1120 1130
Cry1Ac YPNNVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFN
gi|124 YITKTVDFVPPDTRVRIEIGETEGSFYIESIDLICMNE
1150 1160 1170 1180

>>gi|29823396|emb|CAD88617.1| unnamed protein product [s (596 aa)
initn: 719 init1: 454 opt: 1086 Z-score: 1274.2 bits: 246.8 E(): 4.7e-62
Smith-Waterman score: 1090; 33.625% identity (67.075% similar) in 571 aa overlap
(60-612:44-595)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFQSPQWDAFLVQIEQLIN
gi|298 TTKDVIQKGISVVGDLGLGVVGFPGGALVVSFYTNFLNITWPSDEP--WKAFMEQVEALMD
20 30 40 50 60 70

90 100 110 120 130 140

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Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALT
gi|298 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRLFSQAESHFRN
80 90 100 110 120 130

150 160 170 180 190 200
Cry1Ac AIPLFVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRFDAATINSRYNDLTRLIGNY
gi|298 SMPSPFAISGYEVLFLTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRLKLTQEY
140 150 160 170 180 190

210 220 230 240 250 260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYSRTYPIRTVSQ
gi|298 TDHCVKWYVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLVDVRLYKPKTEL
200 210 220 230 240 250

270 280 290 300 310
Cry1Ac TREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHLMIDILNSITITYTDAHRGEY-----Y
gi|298 TRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFNY
260 270 280 290 300 310

320 330 340 350 360 370
Cry1Ac WSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQGVYRTLSST-LYRRPFNI-
gi|298 WSGNYVSTRPSIGSNDIITSPFYGNK-SSEPQNLFEFN-GEKVYRAVANTNLAVWPSAVY
320 330 340 350 360

380 390 400 410 420 430
Cry1Ac -GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHR
gi|298 SGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSHQ
370 380 390 400 410 420

440 450 460 470 480 490
Cry1Ac LSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
gi|298 LNYVMCFMLMQSGRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLQSGASVV
430 440 450 460 470

500 510 520 530 540 550
Cry1Ac SGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
gi|298 AGPRFTGDIQCTENGAATI--YVTPDVSY---SQYRARIRHYASTSQITFTSLDGA
480 490 500 510 520 530

560 570 580 590 600 610
Cry1Ac SIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNI-VGVRNFGTAGVIIDRFEFIP
gi|298 PFNQYVFDKTIKNGD'TLYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIP
540 550 560 570 580 590

620 630 640 650 660 670
Cry1Ac VTATLAEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRE
gi|298 VN

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>>gi|155689526|gb|ABU29255.1| Sequence 7 from patent US (596 aa)
initn: 719 initl: 454 opt: 1086 Z-score: 1274.2 bits: 246.8 E(): 4.7e-62
Smith-Waterman score: 1090; 33.625% identity (67.075% similar) in 571 aa overlap
(60-612:44-595)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGI FGP SQWDAFLVQIEQLIN
gi|155 TTKDVIQKGISVVGDLG VVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALTT
gi|155 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRELFSQAESHFRN
80 90 100 110 120 130

150 160 170 180 190 200
Cry1Ac AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAA TINSRYNDLTRLIGNY
gi|155 SMPSPFAISGYEVLFLTTYQAANTHLFLKDAQIYGE EWGYEKEDIAEFYKRLKLTQEY
140 150 160 170 180 190

210 220 230 240 250 260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT TLTVLDIVSLFPNYDSRTYPIRTVSQ L
gi|155 TDHCVKWYVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTEL
200 210 220 230 240 250

270 280 290 300 310
Cry1Ac TREIYTNPVL--ENFDGSRGSAQGI EGSIRSPHLM DILNSIT IYTD AHRGEY-----Y
gi|155 TRDVLTDPIVGNVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQGYGND SFNY
260 270 280 290 300 310

320 330 340 350 360 370
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI-
gi|155 WSGNYVSTRPSIGSNDIITSPFYGNK--SSEP VQNLEFN-GEKVYRAVANTNLAVWPSAVY
320 330 340 350 360

380 390 400 410 420 430
Cry1Ac -GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKS GTV--DSLDEIPQNNVPPRQGF SHR
gi|155 SGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSHQ
370 380 390 400 410 420

440 450 460 470 480 490
Cry1Ac LSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFN NI IASDSITQIPAVKGNFLFNG-SVI
gi|155 LNYVMCFMLQSGRGTI----PVL TWTHKSVDFNMIDSKITQLPLVKAYKLQSGASV V
430 440 450 460 470

500 510 520 530 540 550
Cry1Ac SGPFGTGGDLVRLNSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNWGNS
gi|155 AGPRFTGGDI IQCTENGSAATI--YVTPDVS Y---SQKYRAR IHYASTSQITFTTSLDGA
480 490 500 510 520 530

560 570 580 590 600 610
Cry1Ac SIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNI-VGVRNFGTAGVIIDRFEFIP
gi|155 PFNQYYFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIP
540 550 560 570 580 590
620 630 640 650 660 670
Cry1Ac VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
gi|155 VN

>>gi|158496871|gb|ABW60288.1| Sequence 7 from patent US (596 aa)
initn: 719 initl: 454 opt: 1086 Z-score: 1274.2 bits: 246.8 E(): 4.7e-62
Smith-Waterman score: 1090; 33.625% identity (67.075% similar) in 571 aa overlap
(60-612:44-595)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGI FGP SQWDAFLVQIEQLIN
gi|158 TTKDVIQKGISVVGDLG VVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALTT
gi|158 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRELFSQAESHFRN
80 90 100 110 120 130

150 160 170 180 190 200
Cry1Ac AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAA TINSRYNDLTRLIGNY
gi|158 SMPSPFAISGYEVLFLTTYQAANTHLFLKDAQIYGE EWGYEKEDIAEFYKRLKLTQEY
140 150 160 170 180 190

210 220 230 240 250 260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELT TLTVLDIVSLFPNYDSRTYPIRTVSQ L
gi|158 TDHCVKWYVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTEL
200 210 220 230 240 250

270 280 290 300 310
Cry1Ac TREIYTNPVL--ENFDGSRGSAQGI EGSIRSPHLM DILNSIT IYTD AHRGEY-----Y
gi|158 TRDVLTDPIVGNVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQGYGND SFNY
260 270 280 290 300 310

320 330 340 350 360 370
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI-
gi|158 WSGNYVSTRPSIGSNDIITSPFYGNK--SSEP VQNLEFN-GEKVYRAVANTNLAVWPSAVY
320 330 340 350 360

380 390 400 410 420 430
Cry1Ac -GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKS GTV--DSLDEIPQNNVPPRQGF SHR
gi|158 SGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSHQ
370 380 390 400 410 420

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```

      440      450      460      470      480      490
Cry1Ac LSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|158 LNYVMCFLMQGSRGTI----PVLTWTHKSVDFNFMIDSKKITQLPLVKAYKLQSGASVV
      430      440      450      460      470

```

```

      500      510      520      530      540      550
Cry1Ac SGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|158 AGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDGA
      480      490      500      510      520      530

```

```

      560      570      580      590      600      610
Cry1Ac SIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|158 PFNQYFDDKTIKNGDILTYSNLFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIP
      540      550      560      570      580      590

```

```

      620      630      640      650      660      670
Cry1Ac VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
      :
gi|158 VN

```

>>gi|111920198|gb|ABH70473.1| Sequence 7 from patent US (596 aa)  
 initn: 719 init1: 454 opt: 1086 Z-score: 1274.2 bits: 246.8 E(): 4.7e-62  
 Smith-Waterman score: 1090; 33.625% identity (67.075% similar) in 571 aa overlap  
 (60-612:44-595)

```

      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 TTKDVIQKGISVVGDLGVLGVPFPGALVSYFYNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

```

```

      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRELFSQAESHFRN
      80      90      100      110      120      130

```

```

      150      160      170      180      190      200
Cry1Ac AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 SMPSPFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQEQY
      140      150      160      170      180      190

```

```

      210      220      230      240      250      260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 TDHCWKVNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFLYDVRVLYPKEVKTEL
      200      210      220      230      240      250

```

```

      270      280      290      300      310
Cry1Ac TREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHMLDILNSITITYTDAHRGEY-----Y
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 TRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRPQPGYGGNDSFNY
      260      270      280      290      300      310

```

```

      320      330      340      350      360      370
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 WSGNYVSTRPSIGSNDIITSPFYGNK--SSEPQVQNLFEFN-GEKVYRAVANTNLAVWPSAVY
      320      330      340      350      360

```

```

      380      390      400      410      420      430
Cry1Ac -GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPQNNVPPRQGFSHR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 SGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTTDEPLEKGYSHQ
      370      380      390      400      410      420

```

```

      440      450      460      470      480      490
Cry1Ac LSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 LNYVMCFLMQGSRGTI----PVLTWTHKSVDFNFMIDSKKITQLPLVKAYKLQSGASVV
      430      440      450      460      470

```

```

      500      510      520      530      540      550
Cry1Ac SGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 AGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDGA
      480      490      500      510      520      530

```

```

      560      570      580      590      600      610
Cry1Ac SIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|111 PFNQYFDDKTIKNGDILTYSNLFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFIP
      540      550      560      570      580      590

```

```

      620      630      640      650      660      670
Cry1Ac VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
      :
gi|111 VN

```

>>gi|45934892|gb|AAS79487.1| insecticidal crystal protei (652 aa)  
 initn: 732 init1: 467 opt: 1086 Z-score: 1273.6 bits: 246.8 E(): 5.1e-62  
 Smith-Waterman score: 1090; 33.566% identity (67.133% similar) in 572 aa overlap  
 (60-612:99-651)

```

      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|459 TTKDVIQKGISVVGDLGVLGVPFPGALVSYFYNFLNTIWPSEDP--WKAFMEQVEALMD
      70      80      90      100      110      120

```

```

      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|459 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
      130      140      150      160      170      180

```

```

      150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|459 NSMPSPFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQEQY
      190      200      210      220      230      240

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```

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|459 YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
250      260      270      280      290      300

```

```

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSFRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----
gi|459 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTQFPGYGYGNSDFN
310      320      330      340      350      360

```

```

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLSST--LYRRPFNI
gi|459 YWSGNVYSTRPSIGSNDIITSPPFYGNK--SSEPQVQNLEFN--GEKVYRAVANTNLAVWPSAV
370      380      390      400      410      420

```

```

380      390      400      410      420      430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSSH
gi|459 YSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
430      440      450      460      470

```

```

440      450      460      470      480      490
Cry1Ac RLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|459 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLQSGASV
480      490      500      510      520      530

```

```

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN
gi|459 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSDLG
540      550      560      570      580

```

```

560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRNFSGTAGVIIDRFEFI
gi|459 APFNQYYFDKTIKGDITLYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

```

```

620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|459 PVN
650

```

```

>>gi|208153|gb|AAA73184.1| crystal toxin (597 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:44-596)

```

```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLIN
gi|208 TTKDVIQKGISVVGDLGVLGVPFPGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20      30      40      50      60      70

```

```

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|208 QKIADYAKNKALAEQLGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSAESHFR
80      90      100      110      120      130

```

```

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGPDAATINSRYNDLTRLIGN
gi|208 NSMPSFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQE
140      150      160      170      180      190

```

```

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|208 YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
200      210      220      230      240      250

```

```

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSFRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----
gi|208 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTQFPGYGYGNSDFN
260      270      280      290      300      310

```

```

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLSST--LYRRPFNI
gi|208 YWSGNVYSTRPSIGSNDIITSPPFYGNK--SSEPQVQNLEFN--GEKVYRAVANTNLAVWPSAV
320      330      340      350      360

```

```

380      390      400      410      420      430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSSH
gi|208 YSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
370      380      390      400      410      420

```

```

440      450      460      470      480      490
Cry1Ac RLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|208 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLQSGASV
430      440      450      460      470

```

```

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN
gi|208 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSDLG
480      490      500      510      520      530

```

```

560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRNFSGTAGVIIDRFEFI
gi|208 APFNQYYFDKTIKGDITLYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
540      550      560      570      580      590

```

```

620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|208 PVN

```

>>gi|111920197|gb|ABH70472.1| Sequence 4 from patent US (597 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:44-596)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|111 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLGLESLNYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|111 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
80 90 100 110 120 130

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLRLIGN
gi|111 NSMPFSAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
140 150 160 170 180 190

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTPYPIRTVSO
gi|111 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVEKTE
200 210 220 230 240 250

270 280 290 300 310
Cry1Ac LTREIYTNPVLP--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|111 LTRDVLTPDIVGNNLRG--YGTTFNSIENYIRKPHLFDYLHRIQPHTRFQPGYGYNDSFN
260 270 280 290 300 310

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTPSST--LYRRPFNI
gi|111 YWSGNVSTRPSIGSNDIITSPFYGNK--SSEPVQNLFPN--GEKVYRAVANTNLAVWPSAV
320 330 340 350 360

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
gi|111 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
370 380 390 400 410 420

440 450 460 470 480 490
Cry1Ac RLSHVSMSRSGFSNSVSIIRAPMPSWIHRSAEFNIIASDSITQIPAVKGNFLPFG--SV
gi|111 QLNVMCFMQLGSRGTI----PVLTTWTKSVDFNFMIIDSKITQLPLVKAYKLQSGASV
430 440 450 460 470

500 510 520 530 540 550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVYASVTPIHLMNVWGN
gi|111 VAGPRFTGGDIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSLDG
480 490 500 510 520 530

560 570 580 590 600 610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANFTSSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|111 APFNQYFFDKTINKGDTLTYSNFNLSFSTPPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI
540 550 560 570 580 590

620 630 640 650 660 670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|111 PVN

>>gi|158496870|gb|ABW60287.1| Sequence 4 from patent US (597 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:44-596)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|158 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLGLESLNYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|158 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
80 90 100 110 120 130

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLRLIGN
gi|158 NSMPFSAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
140 150 160 170 180 190

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTPYPIRTVSO
gi|158 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVEKTE
200 210 220 230 240 250

270 280 290 300 310
Cry1Ac LTREIYTNPVLP--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|158 LTRDVLTPDIVGNNLRG--YGTTFNSIENYIRKPHLFDYLHRIQPHTRFQPGYGYNDSFN
260 270 280 290 300 310

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTPSST--LYRRPFNI
gi|158 YWSGNVSTRPSIGSNDIITSPFYGNK--SSEPVQNLFPN--GEKVYRAVANTNLAVWPSAV
320 330 340 350 360

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
gi|158 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
370 380 390 400 410 420

```

          440      450      460      470      480      490
Cry1Ac RLSHVMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|158 QLNVMCFMLMQGSRGTI-----PVLTWTHKSVDFNFNMIIDSKKITQLPLVKAYKLQSGASV
          430      440      450      460      470

```

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          500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHILNVNWN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|158 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSDLG
          480      490      500      510      520      530

```

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          560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|158 APFNQYYFDKTIKGDITLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
          540      550      560      570      580      590

```

```

          620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
      : :
gi|158 PVN

```

>>gi|312848|emb|CAA50310.1| cryIIIA insect control prote (597 aa)  
 initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:44-596)

```

          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGFPGSQWDAFLVQIEQLIN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 TTKDVIQKGISVVGDLGVLGVPFPGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
          20      30      40      50      60      70

```

```

          90      100      110      120      130      140
Cry1Ac QRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
          80      90      100      110      120      130

```

```

          150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 NSMPSFAISGVEVFLFTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRLKLTQE
          140      150      160      170      180      190

```

```

          210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERWVGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTPYPIRTVQS
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 YTDHCVKWYVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALPFLYDVRLYPKVETKE
          200      210      220      230      240      250

```

```

          270      280      290      300      310
Cry1Ac LTRDIYTNVPL--ENFDGSRGSAQGIIEGSIKSPHMLDILNSITTYTDAHRGEY-----
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 LTRDVLTPDIVGVNLRG--YGTTFSNIEYIRKPHLFDYLRHQFTRFPQGGYGNDSFN
          260      270      280      290      300      310

```

```

          320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSPEPTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRFPNI
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 YWSGNVSTRPSIGSNDIITSPFYGNK--SSEPQVQNLFEFN-GEKVYRAVANTNLAVWPSAV
          320      330      340      350      360

```

```

          380      390      400      410      420      430
Cry1Ac --GINNQLSVL-DGTEFAYGTSSNLPASVYRKSQTV--DSLDEIPQNNNVPPRQGF
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
          370      380      390      400      410      420

```

```

          440      450      460      470      480      490
Cry1Ac RLSHVMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 QLNVMCFMLMQGSRGTI-----PVLTWTHKSVDFNFNMIIDSKKITQLPLVKAYKLQSGASV
          430      440      450      460      470

```

```

          500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHILNVNWN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSDLG
          480      490      500      510      520      530

```

```

          560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|312 APFNQYYFDKTIKGDITLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
          540      550      560      570      580      590

```

```

          620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
      : :
gi|312 PVN

```

>>gi|29823393|emb|CAD88616.1| unnamed protein product [s (597 aa)  
 initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:44-596)

```

          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGFPGSQWDAFLVQIEQLIN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|298 TTKDVIQKGISVVGDLGVLGVPFPGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
          20      30      40      50      60      70

```

```

          90      100      110      120      130      140
Cry1Ac QRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|298 QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
          80      90      100      110      120      130

```

```

          150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|298 NSMPSFAISGVEVFLFTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRLKLTQE
          140      150      160      170      180      190

```

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```

      210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERLVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVEKTE
      200      210      220      230      240      250

```

```

      270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRFRGSAQIEGSIKIRSPHMLDILNSITIYTDHRGEY-----
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 LTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQPHTRFPQPGYYGNDSEFN
      260      270      280      290      300      310

```

```

      320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLEFN-GEKVYRAVANTNLAVWPSAV
      320      330      340      350      360

```

```

      380      390      400      410      420      430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
      370      380      390      400      410      420

```

```

      440      450      460      470      480      490
Cry1Ac RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 QLNIVMCFMLQGSRTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKQLQSGASV
      430      440      450      460      470

```

```

      500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
      480      490      500      510      520      530

```

```

      560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNI-VGVRNFSGTAGVIIDRFEFI
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|298 APFNQYYFDKTIKGDTLTYNSFNLSASFSTPFELSGNNLQIGVGTGLSAGDKVYIDKIEFI
      540      550      560      570      580      590

```

```

      620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
      ::
gi|298 PVN

```

>>gi|155689525|gb|ABU29254.1| Sequence 4 from patent US (597 aa)  
 initn: 732 initl: 467 opt: 1084 Z-score: 1271.8 bits: 246.3 E(): 6.4e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:44-596)

```

      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFIPGPSQWDAFLVQIEQLIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTKDVIQKGISVVGDLLGVVGFPGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

```

```

      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISRLBGLNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
      ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QKIADYAKNKALAEQLQQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRRELFPSQAESHFR
      80      90      100      110      120      130

```

```

      150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NSMPSFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQE
      140      150      160      170      180      190

```

```

      210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERLVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVEKTE
      200      210      220      230      240      250

```

```

      270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRFRGSAQIEGSIKIRSPHMLDILNSITIYTDHRGEY-----
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 LTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQPHTRFPQPGYYGNDSEFN
      260      270      280      290      300      310

```

```

      320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLEFN-GEKVYRAVANTNLAVWPSAV
      320      330      340      350      360

```

```

      380      390      400      410      420      430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
      370      380      390      400      410      420

```

```

      440      450      460      470      480      490
Cry1Ac RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QLNIVMCFMLQGSRTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKQLQSGASV
      430      440      450      460      470

```

```

      500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
      :::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
      480      490      500      510      520      530

```

```

      560      570      580      590      600      610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNI-VGVRNFSGTAGVIIDRFEFI
      ::: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 APFNQYYFDKTIKGDTLTYNSFNLSASFSTPFELSGNNLQIGVGTGLSAGDKVYIDKIEFI
      540      550      560      570      580      590

```

```

      620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
      ::
gi|155 PVN

```



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```

420      430      440      450      460      470
Cry1Ac  440      450      460      470      480      490
RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-SV
gi|155  QLNIVMCFMLMQSGRGTI-----PVLTWTHKSVDFNMDISKITQLPLVKAYKLSGASV
480      490      500      510      520

```

```

500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|155  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSDLG
530      540      550      560      570      580

```

```

560      570      580      590      600      610
Cry1Ac  SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFI
gi|155  APFNQYYFDKTIKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

```

```

620      630      640      650      660      670
Cry1Ac  PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDFCLDEKR
gi|155  PVN

```

>>gi|158496869|gb|ABW60286.1| Sequence 2 from patent US (644 aa)  
 initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:91-643)

```

30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|158  TTKDVIQKGISVVGDLGLVGVGPFPGALVSYFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100      110

```

```

90      100     110     120     130     140
Cry1Ac  QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|158  QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
120     130     140     150     160     170

```

```

150     160     170     180     190     200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|158  NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
180     190     200     210     220     230

```

```

210     220     230     240     250     260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVVSQ
gi|158  YTDHCVKWYVGLDKLRGSSYSWVFNRYRREMTLTVLDLIALPPLYDVRLYPKVKTE
240     250     260     270     280     290

```

```

270     280     290     300     310
Cry1Ac  LTREIYTNPVL--ENFDGSRGSAQIEGSIKIRPHLMDILNITITYTDAHRGEY-----
gi|158  LTRDVLTPDIVGNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFQPGYGNDSFN

```

```

300      310      320      330      340      350
Cry1Ac  320      330      340      350      360      370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLSSST-LYRRPFNI
gi|158  YWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSAV
360      370      380      390      400      410

```

```

380      390      400      410      420      430
Cry1Ac  --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH
gi|158  YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420      430      440      450      460      470

```

```

440      450      460      470      480      490
Cry1Ac  RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-SV
gi|158  QLNIVMCFMLMQSGRGTI-----PVLTWTHKSVDFNMDISKITQLPLVKAYKLSGASV
480      490      500      510      520

```

```

500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|158  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSDLG
530      540      550      560      570      580

```

```

560      570      580      590      600      610
Cry1Ac  SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFI
gi|158  APFNQYYFDKTIKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

```

```

620      630      640      650      660      670
Cry1Ac  PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDFCLDEKR
gi|158  PVN

```

>>gi|83322340|gb|ABC03740.1| Sequence 2 from patent US 6 (644 aa)  
 initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:91-643)

```

30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|833  TTKDVIQKGISVVGDLGLVGVGPFPGALVSYFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100     110

```

```

90      100     110     120     130     140
Cry1Ac  QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|833  QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
120     130     140     150     160     170

```

```

150     160     170     180     190     200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|833  NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

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180      190      200      210      220      230
Cry1Ac  210      220      230      240      250      260
YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTPYPIRTVVSQ
gi|833  YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTLVLDLIALFPLYDVRLYPKVEVKTE
240      250      260      270      280      290

```

```

Cry1Ac  270      280      290      300      310
LTREIYTNPVL--ENFDGSGFRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|833  LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSEFN
300      310      320      330      340      350

```

```

Cry1Ac  320      330      340      350      360      370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|833  YWSGNYVSTRPSIGSNDIITSFYGK--SSEPVQNLFEFN--GEKVVAVANTNLAVWPSAV
360      370      380      390      400      410

```

```

Cry1Ac  380      390      400      410      420      430
--GINNQQLSVL--DGTEFAYGTSSNLPNAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
gi|833  YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
420      430      440      450      460      470

```

```

Cry1Ac  440      450      460      470      480      490
RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|833  QLNVMCFMLMQGSRGTI----PVLTWTHKSVDFNMISSKIKITQLPLVKAYKQLQSGASV
480      490      500      510      520

```

```

Cry1Ac  500      510      520      530      540      550
ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNVNWN
gi|833  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSLDG
530      540      550      560      570      580

```

```

Cry1Ac  560      570      580      590      600      610
SSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|833  APFNQYDFDKTINKGDTLTYSNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

```

```

Cry1Ac  620      630      640      650      660      670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|833  PVN

```

>>gi|270236|gb|AAA01896.1| Sequence 2 from Patent US 485 (644 aa)  
 initn: 732 init1: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62  
 Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:91-643)

```

30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIGWIFGFSQWDAFLVQIEQLIN
gi|270  TTKDVIQKGISVVGDLGVLGVPFPGALVSVFYTNFLNTIWPSEDP--WKAFMEQVEALMD

```

```

70      80      90      100      110
Cry1Ac  90      100      110      120      130      140
QRIIEFARNQAIISREGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMMSALT
gi|270  QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
120      130      140      150      160      170

```

```

Cry1Ac  150      160      170      180      190      200
TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGN
gi|270  NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEWEGYKEDI AEFYKRLKLTQQ
180      190      200      210      220      230

```

```

Cry1Ac  210      220      230      240      250      260
YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTPYPIRTVVSQ
gi|270  YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTLVLDLIALFPLYDVRLYPKVEVKTE
240      250      260      270      280      290

```

```

Cry1Ac  270      280      290      300      310
LTREIYTNPVL--ENFDGSGFRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|270  LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSEFN
300      310      320      330      340      350

```

```

Cry1Ac  320      330      340      350      360      370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|270  YWSGNYVSTRPSIGSNDIITSFYGK--SSEPVQNLFEFN--GEKVVAVANTNLAVWPSAV
360      370      380      390      400      410

```

```

Cry1Ac  380      390      400      410      420      430
--GINNQQLSVL--DGTEFAYGTSSNLPNAVYRKSQTV--DSLDEIPPQNNVPPRQGFSSH
gi|270  YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
420      430      440      450      460      470

```

```

Cry1Ac  440      450      460      470      480      490
RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|270  QLNVMCFMLMQGSRGTI----PVLTWTHKSVDFNMISSKIKITQLPLVKAYKQLQSGASV
480      490      500      510      520

```

```

Cry1Ac  500      510      520      530      540      550
ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNVNWN
gi|270  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSLDG
530      540      550      560      570      580

```

```

Cry1Ac  560      570      580      590      600      610
SSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|270  APFNQYDFDKTINKGDTLTYSNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

```

```

Cry1Ac  620      630      640      650      660      670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR

```

Regulatory Product Characterization Team

gi|270 PVN

>>gi|143082|gb|AAA22541.1| insecticidal crystal protein (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLIN
gi|143 TTKDVIQKGISVVGDLGLVGVGPFPGALVSYFTNLFNTIWPSEDP--WKAFMEQVEALMD

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|143 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFPSQAESHFR

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|143 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|143 YTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALPPLYDVRLYPKVKTE

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHLMIDLNSITITYTDAHRGEY-----
gi|143 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFPQGGYGNDSFN

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLST-LYRRPFNI
gi|143 YWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSAV

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQGV--DSLDEIPPQNNVPPRQGFSSH
gi|143 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH

440 450 460 470 480 490
Cry1Ac RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|143 QLNVMCFMQLGSRGTI----PVLTWTHKSVDFFNMIDSKITQLPLVKAYKQLSGASV

500 510 520 530 540 550
Cry1Ac ISGPFGTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN

gi|143 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

560 570 580 590 600 610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|143 APFNQYYFDKTIKNGDGLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI

620 630 640 650 660 670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|143 PVN

>>gi|111920196|gb|ABH70471.1| Sequence 2 from patent US (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLIN
gi|111 TTKDVIQKGISVVGDLGLVGVGPFPGALVSYFTNLFNTIWPSEDP--WKAFMEQVEALMD

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|111 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFPSQAESHFR

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|111 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|111 YTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALPPLYDVRLYPKVKTE

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHLMIDLNSITITYTDAHRGEY-----
gi|111 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFPQGGYGNDSFN

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLST-LYRRPFNI
gi|111 YWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSAV

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQGV--DSLDEIPPQNNVPPRQGFSSH

Regulatory Product Characterization Team

gi|111 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490

gi|111 QLNVMCFMLMQGSRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLGSGASV
480 490 500 510 520

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHILNVNWN
500 510 520 530 540 550

gi|111 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
560 570 580 590 600 610

gi|111 APFNQYFFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|111 PVN

>>gi|592649|gb|AAA54256.1| Sequence 2 from Patent WO 880 (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFVQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|592 TTKDVIQKGISVVGDLGVLVGGVFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
90 100 110 120 130 140

gi|592 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFQAESHFR
120 130 140 150 160 170

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
150 160 170 180 190 200

gi|592 NSMPSFAISGYEVFLFTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRLKLTQE
180 190 200 210 220 230

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
210 220 230 240 250 260

gi|592 YTDHCVKWYVGLDKLRGSSYESWVFNRYRREMTTLVLDLIALFPLYDVRVLPKREKTE
240 250 260 270 280 290

Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQGIIEGSRSPHMLDILNITITYTDAHRGEY-----
270 280 290 300 310

gi|592 LTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFPQGGYGNDSFN
300 310 320 330 340 350

Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLSS-TLYRRPFNI
320 330 340 350 360 370

gi|592 YWSGNVSTRPSIGSNDIITSPFYGNK--SSEPQVNLFEF-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPASVYRKSQTV--DSLDEIPPQNNVPPRQGFHS
380 390 400 410 420 430

gi|592 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490

gi|592 QLNVMCFMLMQGSRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLGSGASV
480 490 500 510 520

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHILNVNWN
500 510 520 530 540 550

gi|592 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
560 570 580 590 600 610

gi|592 APFNQYFFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|592 PVN

>>gi|2490714|gb|AAB78850.1|I62690 Sequence 2 from patent (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFVQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|249 TTKDVIQKGISVVGDLGVLVGGVFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
90 100 110 120 130 140

gi|249 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFQAESHFR
120 130 140 150 160 170

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
150 160 170 180 190 200

Regulatory Product Characterization Team

gi|249 NSMPSFAISGYEVLFLTTTAAQANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
180 190 200 210 220 230

Cry1Ac 210 220 230 240 250 260
YTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ

gi|249 YTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240 250 260 270 280 290

Cry1Ac 270 280 290 300 310
LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----

gi|249 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFPQGYGNSDFN
300 310 320 330 340 350

Cry1Ac 320 330 340 350 360 370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI

gi|249 YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLFEF--GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac 380 390 400 410 420 430
--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH

gi|249 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac 440 450 460 470 480 490
RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV

gi|249 QLNVMCFMLQGSRTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLSGASV
480 490 500 510 520

Cry1Ac 500 510 520 530 540 550
ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN

gi|249 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac 560 570 580 590 600 610
SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI

gi|249 APFNQYFDFKTIKGDITLYNSFNLSAFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac 620 630 640 650 660 670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR

gi|249 PVN

>>gi|514312|gb|AAC43266.1| CryIIIA (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac 30 40 50 60 70 80
GERIETGYTPIDISLTLQFLLSEFVPGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLIN

gi|514 TTKDVIQKGISVVGDLGLVGVGFFPGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac 90 100 110 120 130 140
QRIEEFARNQAIARLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT

gi|514 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELSQAESHFR
120 130 140 150 160 170

Cry1Ac 150 160 170 180 190 200
TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGN

gi|514 NSMPSFAISGYEVLFLTTTAAQANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
180 190 200 210 220 230

Cry1Ac 210 220 230 240 250 260
YTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ

gi|514 YTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240 250 260 270 280 290

Cry1Ac 270 280 290 300 310
LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----

gi|514 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFPQGYGNSDFN
300 310 320 330 340 350

Cry1Ac 320 330 340 350 360 370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI

gi|514 YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLFEF--GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac 380 390 400 410 420 430
--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH

gi|514 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac 440 450 460 470 480 490
RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV

gi|514 QLNVMCFMLQGSRTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLSGASV
480 490 500 510 520

Cry1Ac 500 510 520 530 540 550
ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWN

gi|514 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac 560 570 580 590 600 610
SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI

gi|514 APFNQYFDFKTIKGDITLYNSFNLSAFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac 620 630 640 650 660 670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR



Regulatory Product Characterization Team

gi|160 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac RLSHVSMPFRSGFSNVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490

gi|160 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGASV
480 490 500 510 520

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNWNWGN
500 510 520 530 540 550

gi|160 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNI-VGVRNFSGTAGVIIDRFEFI
560 570 580 590 600 610

gi|160 APFNQYYFDKTIKGDITLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|160 PVN

>>gi|142736|gb|AAA50255.1| crystal protein [Bacillus thu (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIFGSPQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|142 TTKDVIQKGISVVGDLGVLVGGFPPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac QRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
90 100 110 120 130 140

gi|142 QKIADYAKNKALAEQLQGNVVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
120 130 140 150 160 170

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
150 160 170 180 190 200

gi|142 NSMPSFAISGYEVLFLTTYAQAAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQKLTQEQE
180 190 200 210 220 230

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTPYRTVVSQ
210 220 230 240 250 260

gi|142 YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALPFLYDVRVLPKVEKTE
240 250 260 270 280 290

Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQIEGSIIRSPHMLDILNSITITYTDAHRGEY-----
270 280 290 300 310

gi|142 LTRDVLTDPIVGVNMLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRPQPGYYGNDSFN
300 310 320 330 340 350

Cry1Ac YWSGHQIMASPVGFSGPEPTFFPLYGTMGNAAPQQRIVAQLGQGVYRVLST-LYRRPFNI
320 330 340 350 360 370

gi|142 YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLEFN-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac --GINNQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPQNNVPPRQGFSH
380 390 400 410 420 430

gi|142 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac RLSHVSMPFRSGFSNVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490

gi|142 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGASV
480 490 500 510 520

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNWNWGN
500 510 520 530 540 550

gi|142 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFSTSLGNI-VGVRNFSGTAGVIIDRFEFI
560 570 580 590 600 610

gi|142 APFNQYYFDKTIKGDITLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|142 PVN

>>gi|14707|emb|CAA00116.1| 66 kDa protein from B.thuring (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIFGSPQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|147 TTKDVIQKGISVVGDLGVLVGGFPPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac QRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
90 100 110 120 130 140

gi|147 QKIADYAKNKALAEQLQGNVVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
120 130 140 150 160 170

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
150 160 170 180 190 200

Regulatory Product Characterization Team

gi|147 NSMPSFAISGVEVLFLLTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
180 190 200 210 220 230

Cry1Ac 210 220 230 240 250 260
YTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVQSQ

gi|147 YTDHCVKWYVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240 250 260 270 280 290

Cry1Ac 270 280 290 300 310
LTREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----

gi|147 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFPQGYGNDSPFN
300 310 320 330 340 350

Cry1Ac 320 330 340 350 360 370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI

gi|147 YWSGNVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEF-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac 380 390 400 410 420 430
--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFHS

gi|147 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac 440 450 460 470 480 490
RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV

gi|147 QLNVMCFMLQGSRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLQSGASV
480 490 500 510 520

Cry1Ac 500 510 520 530 540 550
ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN

gi|147 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac 560 570 580 590 600 610
SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIDRFEFI

gi|147 APFNQYYFDKTIKNGDITLYNSFNLASFSTPFELSGNNLQIGVGTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac 620 630 640 650 660 670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR

gi|147 PVN

>>gi|3995646|gb|AAC89074.1|AR013196 Sequence 2 from pate (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac 30 40 50 60 70 80
GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN

gi|399 TTKDVIQKGISVVGDLGLGVVGFPGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110

Cry1Ac 90 100 110 120 130 140
QRIEEFARNQAIISRLBGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT

gi|399 QKIADYAKNKALAEQQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
120 130 140 150 160 170

Cry1Ac 150 160 170 180 190 200
TAIPLFAVQNYQVPLLSVYVQANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGN

gi|399 NSMPSFAISGVEVLFLLTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
180 190 200 210 220 230

Cry1Ac 210 220 230 240 250 260
YTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVQSQ

gi|399 YTDHCVKWYVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240 250 260 270 280 290

Cry1Ac 270 280 290 300 310
LTREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----

gi|399 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFPQGYGNDSPFN
300 310 320 330 340 350

Cry1Ac 320 330 340 350 360 370
YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI

gi|399 YWSGNVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEF-GEKVYRAVANTNLAVWPSAV
360 370 380 390 400 410

Cry1Ac 380 390 400 410 420 430
--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFHS

gi|399 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
420 430 440 450 460 470

Cry1Ac 440 450 460 470 480 490
RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV

gi|399 QLNVMCFMLQGSRGTI----PVLTWTHKSVDFNMDISKKITQLPLVKAYKLQSGASV
480 490 500 510 520

Cry1Ac 500 510 520 530 540 550
ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN

gi|399 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
530 540 550 560 570 580

Cry1Ac 560 570 580 590 600 610
SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIDRFEFI

gi|399 APFNQYYFDKTIKNGDITLYNSFNLASFSTPFELSGNNLQIGVGTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

Cry1Ac 620 630 640 650 660 670

Regulatory Product Characterization Team

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|399 PVN
>>gi|40253|emb|CAA68482.1| unnamed protein product [Baci (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIGIFGSPQWDAFLVQIEQLIN
gi|402 TTKDVIQKGISVVGDLLGVVGFPPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|402 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGN
gi|402 NSMPSFAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|402 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTE

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQIEGSI RSPHMLDILNSITTYTDAHRGEY-----
gi|402 LTRDVLTDPIVGVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQGGYGNDSFN

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|402 YWSGNYVSTRPSIGSNDIITSPFYGNK--SSEP VQNLEFN--GEKVYRAVANTNLAVWPSAV

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKS GTV--DSLDEIPPQNNVPPRQGF SH
gi|402 YSGVTKVEFSQYNDQTD EAA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH

440 450 460 470 480 490
Cry1Ac RLSHVS MFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|402 QLNIVMCFMLMQSRGTI----PVL TWTHKSVDFNFN MIDSKKITQLPLVKAKYKLSGASV

500 510 520 530 540 550

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|402 VAGPRFTGGDIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLGD
530 540 550 560 570 580

560 570 580 590 600 610
Cry1Ac SSI FNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|402 APFNQYFDFKTI NKGDTLTYN SFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI

620 630 640 650 660 670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|402 PVN

>>gi|594203|gb|AAA55810.1| Sequence 9 from Patent EP 031 (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIGIFGSPQWDAFLVQIEQLIN
gi|594 TTKDVIQKGISVVGDLLGVVGFPPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|594 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGN
gi|594 NSMPSFAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|594 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTE

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQIEGSI RSPHMLDILNSITTYTDAHRGEY-----
gi|594 LTRDVLTDPIVGVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQGGYGNDSFN

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|594 YWSGNYVSTRPSIGSNDIITSPFYGNK--SSEP VQNLEFN--GEKVYRAVANTNLAVWPSAV

380 390 400 410 420 430

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Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPsAVYRKSgTV--DSLDEIPPQNNVPPRQGFSh
gi|594 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH

Cry1Ac RLSHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-SV
gi|594 QLNVMCFLMQGSRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGASV

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|594 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVLIIDRFEFI
gi|594 APFNQYYFDKTIINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|594 PVN

>>gi|29823391|emb|CAD88615.1| unnamed protein product [B (644 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.3 bits: 246.4 E(): 6.8e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:91-643)

Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|298 TTKDVIQKGISVVGDLGLVGVGFPFGALVSYFNTFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|298 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGN
gi|298 NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTTLVLDIVSLFPNYSRTPYPIRTVVSQ
gi|298 YTDHCVKWYNVGLDKLRSSYESWVNFNRYREMTLTVLIDLALFPLYDVRLYPKVKTE

270 280 290 300 310

Cry1Ac LTREIYTNPVL--ENFDGSFRGSAQGIIEGSIRSPHMLDILNSITIYTDahrGEY-----
gi|298 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQHFTRFPQGYGNDsfN

Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRtLSST-LYRRPFNI
gi|298 YWSGNYVSTRPSIGSNDIITSPPYGNK-SSEPvQNLefN-GEKVYRAVANTnLAWpSAV

Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPsAVYRKSgTV--DSLDEIPPQNNVPPRQGFSh
gi|298 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH

Cry1Ac RLSHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG-SV
gi|298 QLNVMCFLMQGSRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGASV

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|298 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVLIIDRFEFI
gi|298 APFNQYYFDKTIINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|298 PVN

>>gi|4688623|emb|CAB41411.1| Cry3Aa protein [Bacillus th (652 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.2 bits: 246.4 E(): 6.9e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:99-651)

Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|468 TTKDVIQKGISVVGDLGLVGVGFPFGALVSYFNTFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|468 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR

150 160 170 180 190 200

Regulatory Product Characterization Team

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Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|468 NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEEWGYEKEDIAEFYKRQLKTQE
190      200      210      220      230      240

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|468 YTDHCVKYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
250      260      270      280      290      300

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLMIDLNSITITYTDAHRGEY-----
gi|468 LTRDVLTDPIVGVNLRG--YGTTFNINIENYIRKPHLFDYLHRIQFTRFPQGYGNDISFN
310      320      330      340      350      360

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|468 YWSGNYVSTRPSIGSNDIITSFPYGNK--SSEPVQNLFEF--GEKVYRAVANTNLAVWPSAV
370      380      390      400      410      420

380      390      400      410      420      430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|468 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
430      440      450      460      470

440      450      460      470      480      490
Cry1Ac RLSHVSMPFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|468 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMIDSKITQLPLVKAYKQLQSGASV
480      490      500      510      520      530

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|468 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
540      550      560      570      580

560      570      580      590      600      610
Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|468 APFNQYYFDKTIKGDTLTYNSFNLFASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKR
gi|468 PVN
650

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>>gi|12810107|gb|AAE44022.1| Sequence 113 from patent US (652 aa)
initn: 732 init1: 467 opt: 1084 Z-score: 1271.2 bits: 246.4 E(): 6.9e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:99-651)

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30      40      50      60      70      80

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Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|128 TTKDVIQKGISVVGDLGLVGVGFFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100      110      120

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMMSALT
gi|128 QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
130      140      150      160      170      180

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|128 NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEEWGYEKEDIAEFYKRQLKTQE
190      200      210      220      230      240

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
gi|128 YTDHCVKYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
250      260      270      280      290      300

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLMIDLNSITITYTDAHRGEY-----
gi|128 LTRDVLTDPIVGVNLRG--YGTTFNINIENYIRKPHLFDYLHRIQFTRFPQGYGNDISFN
310      320      330      340      350      360

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
gi|128 YWSGNYVSTRPSIGSNDIITSFPYGNK--SSEPVQNLFEF--GEKVYRAVANTNLAVWPSAV
370      380      390      400      410      420

380      390      400      410      420      430
Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|128 YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSH
430      440      450      460      470

440      450      460      470      480      490
Cry1Ac RLSHVSMPFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|128 QLNVMCFMLMQSGRGTI----PVLTWTHKSVDFNMIDSKITQLPLVKAYKQLQSGASV
480      490      500      510      520      530

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|128 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
540      550      560      570      580

560      570      580      590      600      610
Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|128 APFNQYYFDKTIKGDTLTYNSFNLFASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI
590      600      610      620      630      640

600      610      620      630      640      650
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
gi|128 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
540      550      560      570      580

560      570      580      590      600      610
Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|128 APFNQYYFDKTIKGDTLTYNSFNLFASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI
590      600      610      620      630      640

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Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|128 PVN
650

>>gi|40188420|gb|AAR75945.1| Sequence 113 from patent US (652 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.2 bits: 246.4 E(): 6.9e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:99-651)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
gi|401 TTKDVIQKGISVVGDLLGVVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110 120

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|401 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
130 140 150 160 170 180

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRFDAATINSRYNDLTRLIGN
gi|401 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
190 200 210 220 230 240

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVVSQ
gi|401 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALPFLYDVRLYPKYKTE
250 260 270 280 290 300

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQIEGSIKSPHLMIDLNSITIIYTDHARGEY-----
gi|401 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQPHTRFPQGGYNDGSFN
310 320 330 340 350 360

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFNI
gi|401 YWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQNLFEF--GKQVYRAVANTNLAVWPSAV
370 380 390 400 410 420

380 390 400 410 420 430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQGV--DSLDEIPPQNNVPPRQGFSSH
gi|401 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWSDIDQLPPEPTTDEPLEKGYSH
430 440 450 460 470

440 450 460 470 480 490
Cry1Ac RLSHVSMFRSFGSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|401 QLNVMCFMLMQGSRGTI-----PVLTWTHKSVDFNFNMDISKITQLPLVKAYKQLQSGASV
480 490 500 510 520 530

500 510 520 530 540 550
Cry1Ac ISGPGTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNWNWGN
gi|401 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYKARIRIHASTSQITFTLSLDG
540 550 560 570 580

560 570 580 590 600 610
Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSSLGNI--VGNRFNSGTAGVIIDRFEFI
gi|401 APFNQYFFDKTINKGDTLTYSNFNLSAFSTPFELSGNNLQIGVGTGLSAGDKVYIDKIEFI
590 600 610 620 630 640

620 630 640 650 660 670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|401 PVN
650

>>gi|155684780|gb|ABU27035.1| Sequence 113 from patent U (652 aa)
initn: 732 initl: 467 opt: 1084 Z-score: 1271.2 bits: 246.4 E(): 6.9e-62
Smith-Waterman score: 1088; 33.566% identity (66.958% similar) in 572 aa overlap
(60-612:99-651)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
gi|155 TTKDVIQKGISVVGDLLGVVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70 80 90 100 110 120

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|155 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
130 140 150 160 170 180

150 160 170 180 190 200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRFDAATINSRYNDLTRLIGN
gi|155 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
190 200 210 220 230 240

210 220 230 240 250 260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVVSQ
gi|155 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALPFLYDVRLYPKYKTE
250 260 270 280 290 300

270 280 290 300 310
Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQIEGSIKSPHLMIDLNSITIIYTDHARGEY-----
gi|155 LTRDVLTDPIVGVNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQPHTRFPQGGYNDGSFN
310 320 330 340 350 360

320 330 340 350 360 370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFNI
gi|155 YWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQNLFEF--GKQVYRAVANTNLAVWPSAV
370 380 390 400 410 420



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150      160      170      180      190      200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGN
gi|401  NSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
190      200      210      220      230      240

210      220      230      240      250      260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|401  YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
250      260      270      280      290      300

270      280      290      300      310
Cry1Ac  LTREIYTNPVL--ENFDGSFRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----
gi|401  LTRDVLTDPIVGVNLRG-YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNSFSN
310      320      330      340      350      360

320      330      340      350      360      370
Cry1Ac  YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-LYRRPFNI
gi|401  YWSGNVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSAV
370      380      390      400      410      420

380      390      400      410      420      430
Cry1Ac  --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|401  YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
430      440      450      460      470

440      450      460      470      480      490
Cry1Ac  RLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|401  QLNVMCFMQGSRGTI-----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLQSGASV
480      490      500      510      520      530

500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|401  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
540      550      560      570      580

560      570      580      590      600      610
Cry1Ac  SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|401  APFNQYYFDKTIKGDITLTYNSFNLFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac  PVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDEFCLDEKR
gi|401  PVN
650

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>>gi|594327|gb|AAA55934.1| Sequence 14 from Patent EP 02 (644 aa)  
 initn: 731 initl: 467 opt: 1083 Z-score: 1270.1 bits: 246.1 E(): 7.9e-62  
 Smith-Waterman score: 1087; 33.566% identity (66.958% similar) in 572 aa overlap  
 (60-612:91-643)

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30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI IWGIFGPSQWDAFLVQIEQLIN
gi|594  TTKDVIQKGISVVGDLGLVGVFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100      110

90      100      110      120      130      140
Cry1Ac  QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|594  QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSAQESHFR
120      130      140      150      160      170

150      160      170      180      190      200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGN
gi|594  NSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|594  YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac  LTREIYTNPVL--ENFDGSFRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----
gi|594  LTRDVLTDPIVGVNLRG-YGTTFNSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNSFSN
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac  YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-LYRRPFNI
gi|594  YWSGNVSTRPSIGSNDIITSPPFYGNK-SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSAV
360      370      380      390      400      410

380      390      400      410      420      430
Cry1Ac  --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSH
gi|594  YSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
420      430      440      450      460      470

440      450      460      470      480      490
Cry1Ac  RLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|594  ELNYVMCFMQGSRGTI-----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLQSGASV
480      490      500      510      520

500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|594  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
530      540      550      560      570      580

560      570      580      590      600      610
Cry1Ac  SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|594  APFNQYYFDKTIKGDITLTYNSFNLFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

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          380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGF
gi|298 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
          370      380      390      400      410      420

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          440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSFGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|298 HQLNYVMCFMLQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLGSGAS
          430      440      450      460      470

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          500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWG
gi|298 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHASTSQITFTLSLD
          480      490      500      510      520      530

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          560      570      580      590      600
Cry1Ac NSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRFNSGTAGVIIDRFEF
gi|298 GAPFNQYYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEF
          540      550      560      570      580      590

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          610      620      630      640      650      660
Cry1Ac IPVTTALEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
gi|298 IPVNV

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>>gi|111920199|gb|ABH70474.1| Sequence 9 from patent US (598 aa)  
 initn: 732 initl: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.7e-62  
 Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap  
 (60-612:44-597)

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          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|111 TTKDVIQKGISVVGDLGAVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
          20      30      40      50      60      70

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          90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
gi|111 QKIADYAKNKALAEQLQGNVVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF
          80      90      100      110      120      130

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          150      160      170      180      190      200
Cry1Ac TTAIPLFVAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLTRLIG
gi|111 RNSMPSFAISGYEVLFLTYAQAANTHLFLLKDAQIYGEWEWYKEDIAEFYKRQLKLTQ
          140      150      160      170      180      190

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          210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLVLDIVSLFPNYSRTPYIRTVS
gi|111 EYTDHCVKWINVGLDKLRGSSYESWVNFNRYRREMTLVLDLIALFLPFLYDVRLYPKVKVT
          200      210      220      230      240      250

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          270      280      290      300      310
Cry1Ac QLTREIYTNVPL--ENFDGSRGSAQIEGSIKSPHLMIDLNSITTYTDAHRGEY-----
gi|111 ELTRDVLTDPIVGVNLRG--YGTTFSNIEYIRKPHLFDYLHRIQFHTRFPQGYGNDSEF
          260      270      280      290      300      310

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          320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFFN
gi|111 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEFPVQNLEFN--GEKVYRAVANTNLAVWPSA
          320      330      340      350      360

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          380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGF
gi|111 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
          370      380      390      400      410      420

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          440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSFGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|111 HQLNYVMCFMLQGSRGTI-----PVLTWTHKSVDFFNMIDSKKITQLPLVKAYKLGSGAS
          430      440      450      460      470

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          500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWG
gi|111 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHASTSQITFTLSLD
          480      490      500      510      520      530

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          560      570      580      590      600
Cry1Ac NSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRFNSGTAGVIIDRFEF
gi|111 GAPFNQYYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEF
          540      550      560      570      580      590

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          610      620      630      640      650      660
Cry1Ac IPVTTALEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
gi|111 IPVNV

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>>gi|158496872|gb|ABW60289.1| Sequence 9 from patent US (598 aa)  
 initn: 732 initl: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.7e-62  
 Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap  
 (60-612:44-597)

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          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|158 TTKDVIQKGISVVGDLGAVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
          20      30      40      50      60      70

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          90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
gi|158 QKIADYAKNKALAEQLQGNVVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF
          80      90      100      110      120      130

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      150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 RNSMPFSAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ
      140      150      160      170      180      190

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      210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFNPYDSRTYPIRTVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 EYTDHCVKWYNVGLDKLRGSSYESVWNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT
      200      210      220      230      240      250

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      270      280      290      300      310
Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQGIIEGSIKSPHMLDILNSITIIYTDHRGEY-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 ELTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFPQGYGNDSF
      260      270      280      290      300      310

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      320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQVNLQFN--GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

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      380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYG
      370      380      390      400      410      420

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      440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 HQLNYVMCFLMQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLQSGAS
      430      440      450      460      470

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      500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLD
      480      490      500      510      520      530

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      560      570      580      590      600
Cry1Ac NSSIFSNVTPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 GAPFNQYYFDKTIKGDTLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEF
      540      550      560      570      580      590

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      610      620      630      640      650      660
Cry1Ac IPVTATLEAEYNLERAQKAVNALFTSTNQLGLKNTVTDYHIDQVSNLVTYLSDEFCLDEK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 IPVNV

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>>gi|111920203|gb|ABH70478.1| Sequence 17 from patent US (600 aa)
  initn: 663 initl: 454 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.7e-62
Smith-Waterman score: 1086; 33.565% identity (67.130% similar) in 575 aa overlap
(60-612:44-599)

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      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFIPGSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 TTKDVIQKGISVVGDLGLLVGVGFFPGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

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      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISRLRGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALTT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRELFSQAESHFPN
      80      90      100      110      120      130

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      150      160      170      180      190      200
Cry1Ac AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 SMPFSAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQEY
      140      150      160      170      180      190

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      210      220      230      240      250      260
Cry1Ac TDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFNPYDSRTYPIRTVSQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 TDHCVKWYNVGLDKLRGSSYESVWNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKTEL
      200      210      220      230      240      250

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      270      280      290      300      310
Cry1Ac TREIYTNPVL--ENFDGSRGSAQGIIEGSIKSPHMLDILNSITIIYTDHRGEY-----Y
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 TRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFPQGYGNDSFNY
      260      270      280      290      300      310

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      320      330      340      350      360      370
Cry1Ac WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 WSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQVNLQFN--GEKVYRAVANTNLAVWPSAVY
      320      330      340      350      360

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      380      390      400      410      420      430
Cry1Ac -GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSSHR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 SGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSHQ
      370      380      390      400      410      420

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      440      450      460      470      480      490
Cry1Ac LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 LNYVMCFLMQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLQSGASVV
      430      440      450      460      470

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      500      510      520      530      540      550
Cry1Ac SGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 AGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDGA
      480      490      500      510      520      530

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      560      570      580      590      600
Cry1Ac SIFSNTVPP---ATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVNRFSGTAGVIIDRF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 PNFQYAAPFYFDKTIKGDTLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKI

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320      330      340      350      360
Cry1Ac  380      390      400      410      420      430
-GINNQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHR
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  SGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSHQ
370      380      390      400      410      420

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```

440      450      460      470      480      490
Cry1Ac  LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  LNYVMCFLMQGSRGTI----PVLTWTHKSVDFNMIIDSKITQLPLVKAYKLQSGASVV
430      440      450      460      470

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500      510      520      530      540      550
Cry1Ac  SGPFGTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  AGPRFTGGDIIQCTENGAATI--YVTPDVSY--SQYRARIHYASTSQITFTLSDGA
480      490      500      510      520      530

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560      570      580      590      600
Cry1Ac  SIFSNTVP----ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  PFNQYAAPFYFDKTLINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKI
540      550      560      570      580      590

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610      620      630      640      650      660
Cry1Ac  EFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLD
: . . . . .
gi|158  EFIPVN
600

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>>gi|155689531|gb|ABU29260.1| Sequence 17 from patent US (600 aa)  
 initn: 663 init1: 454 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.7e-62  
 Smith-Waterman score: 1086; 33.565% identity (67.130% similar) in 575 aa overlap  
 (60-612:44-599)

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30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFQSDWDAFLVQIEQLIN
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  TTKDVIQKGISVVGDLGVLVGFVPGAGFVLGLVDIIWGFQSDWDAFLVQIEQLIN
20      30      40      50      60      70

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90      100     110     120     130     140
Cry1Ac  QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQ--FNDMNSALTT
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPAAPFPHSQGRIRELFSQAESHFRN
80      90      100     110     120     130

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150     160     170     180     190     200
Cry1Ac  AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNY
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  SMPSPFAISGYEVLFTTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQEQY
140     150     160     170     180     190

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210     220     230     240     250     260
Cry1Ac  TDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVLSFPNYDSRTYPIRTVSQL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  TDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFLYDVRLYPKVEVKTEL

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200      210      220      230      240      250
Cry1Ac  270      280      290      300      310
TREIYTNPVL--ENFDGFSFRGSAQGIIEGSIIRSPHMLDILNSITIIYTDHARGEY-----Y
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  TRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYGGNDSFNY
260      270      280      290      300      310

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320      330      340      350      360      370
Cry1Ac  WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRVLTSST-LYRRPFNI-
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  WSGNYVSTRPISGNDIITSPFYGNK-SSEPQNLQEFN-GEKVYRAVANTNLAVWPSAVY
320      330      340      350      360

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```

380      390      400      410      420      430
Cry1Ac  -GINNQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHR
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  SGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPETTDEPLEKGYSHQ
370      380      390      400      410      420

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440      450      460      470      480      490
Cry1Ac  LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVI
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  LNYVMCFLMQGSRGTI----PVLTWTHKSVDFNMIIDSKITQLPLVKAYKLQSGASVV
430      440      450      460      470

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500      510      520      530      540      550
Cry1Ac  SGPFGTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNS
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  AGPRFTGGDIIQCTENGAATI--YVTPDVSY--SQYRARIHYASTSQITFTLSDGA
480      490      500      510      520      530

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560      570      580      590      600
Cry1Ac  SIFSNTVP----ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRF
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  PFNQYAAPFYFDKTLINKGDTLTYNFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKI
540      550      560      570      580      590

```

```

610      620      630      640      650      660
Cry1Ac  EFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLD
: . . . . .
gi|155  EFIPVN
600

```

>>gi|158496873|gb|ABW60290.1| Sequence 11 from patent US (606 aa)  
 initn: 732 init1: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.8e-62  
 Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap  
 (60-612:52-605)

```

30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFQSDWDAFLVQIEQLIN
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  TTKDVIQKGISVVGDLGVLVGFVPGAGFVLGLVDIIWGFQSDWDAFLVQIEQLIN
30      40      50      60      70

```

```

90      100     110     120     130     140
Cry1Ac  QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158  QKIADYAKNKALAEQLQNNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF

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      80      90      100      110      120      130
Cry1Ac 150      160      170      180      190      200
      TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
      . . . . .
gi|158 RNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQ
      140      150      160      170      180      190
Cry1Ac 210      220      230      240      250      260
      NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS
      . . . . .
gi|158 EYTDHCVKWYNVGLDKLRGSSYSEWVNFNRYRREMTLVLDLIALFPLVDVRLYPKEVKT
      200      210      220      230      240      250
Cry1Ac 270      280      290      300      310
      QLTREIYTNPVL--ENFDGSRGSAQGIIEGSIKPHLMDILNSITTYDAHRGEY----
      . . . . .
gi|158 ELTRDVLTDPIVGVNLRG--YGTTFSNIEYIRKPHLFDYLHRIQFHTRFQPGYGNDSF
      260      270      280      290      300      310
Cry1Ac 320      330      340      350      360      370
      -YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN
      . . . . .
gi|158 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSA
      320      330      340      350      360      370
Cry1Ac 380      390      400      410      420      430
      I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      . . . . .
gi|158 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
      380      390      400      410      420      430
Cry1Ac 440      450      460      470      480      490
      HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
      . . . . .
gi|158 HQLNVMCFMQSGRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKQLQSGAS
      440      450      460      470      480
Cry1Ac 500      510      520      530      540      550
      VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW
      . . . . .
gi|158 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD
      490      500      510      520      530      540
Cry1Ac 560      570      580      590      600
      NSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
      . . . . .
gi|158 GAPFNQYFYDKTINKGDTLTYNLNFASFSTPFELSGNQLIGVGLSAGDKVYIDKIEF
      550      560      570      580      590      600
Cry1Ac 610      620      630      640      650      660
      IPVTTAEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEK
      . . . . .
gi|158 IPVNV

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>>gi|155689528|gb|ABU29257.1| Sequence 11 from patent US (606 aa)
  initn: 732 init1: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.8e-62

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Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap
(60-612:52-605)

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      30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIWIWGFPGSQWDAFLVQIEQLIN
      . . . . .
gi|155 TTKDVIQKGISVVGDLGLVGVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      30      40      50      60      70
Cry1Ac 90      100      110      120      130      140
      QRIIEFARNQAIKSRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
      . . . . .
gi|155 QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPAPFRNPHSQGRIRELFSQAESHF
      80      90      100      110      120      130
Cry1Ac 150      160      170      180      190      200
      TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
      . . . . .
gi|155 RNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQ
      140      150      160      170      180      190
Cry1Ac 210      220      230      240      250      260
      NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS
      . . . . .
gi|155 EYTDHCVKWYNVGLDKLRGSSYSEWVNFNRYRREMTLVLDLIALFPLVDVRLYPKEVKT
      200      210      220      230      240      250
Cry1Ac 270      280      290      300      310
      QLTREIYTNPVL--ENFDGSRGSAQGIIEGSIKPHLMDILNSITTYDAHRGEY----
      . . . . .
gi|155 ELTRDVLTDPIVGVNLRG--YGTTFSNIEYIRKPHLFDYLHRIQFHTRFQPGYGNDSF
      260      270      280      290      300      310
Cry1Ac 320      330      340      350      360      370
      -YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN
      . . . . .
gi|155 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPVQNLFEFN-GEKVYRAVANTNLAVWPSA
      320      330      340      350      360      370
Cry1Ac 380      390      400      410      420      430
      I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      . . . . .
gi|155 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
      380      390      400      410      420      430
Cry1Ac 440      450      460      470      480      490
      HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
      . . . . .
gi|155 HQLNVMCFMQSGRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKQLQSGAS
      440      450      460      470      480
Cry1Ac 500      510      520      530      540      550
      VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW
      . . . . .
gi|155 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD
      490      500      510      520      530      540
Cry1Ac 560      570      580      590      600
      NSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
      . . . . .

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gi|155 GAPFNQYYFDKTIKNGD... 550 560 570 580 590 600

Cry1Ac IPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK

gi|155 IPVN

>>gi|111920200|gb|ABH70475.1| Sequence 11 from patent US (606 aa)
initn: 732 initl: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.8e-62
Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap
(60-612:52-605)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN

gi|111 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL

gi|111 QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF

Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIG

gi|111 RNSMPSFAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQ

Cry1Ac NYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS

gi|111 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT

Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHLMIDLNSITITYTDAHRGEY----

gi|111 ELTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSF

Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN

gi|111 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLEFN--GEKVYRAVANINLAVWPSA

Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPYSAVYRKSQTV--DSLDEIPPQNNVPPRQGF

gi|111 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY

Cry1Ac HRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--S

gi|111 HQLNVYMCFLMQSGRGTI-----PVLTWTHKSVDFNMDSKITQLPLVKAYKLQSGAS

Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWG

gi|111 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD

Cry1Ac NSSIFSNTVPATATSLDNLQSSDFGYFESANAFSTSLGNI--VGVNRFSGTAGVIDRFEF

gi|111 GAPFNQYYFDKTIKNGD... 550 560 570 580 590 600

Cry1Ac IPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK

gi|111 IPVN

>>gi|29823400|emb|CAD88619.1| unnamed protein product [s (606 aa)
initn: 732 initl: 467 opt: 1082 Z-score: 1269.4 bits: 245.9 E(): 8.8e-62
Smith-Waterman score: 1086; 33.508% identity (66.841% similar) in 573 aa overlap
(60-612:52-605)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN

gi|298 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL

gi|298 QKIADYAKNKALAEQLQGNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF

Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIG

gi|298 RNSMPSFAISGVEVLFLLTYAQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQ

Cry1Ac NYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS

gi|298 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKEVKT

Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHLMIDLNSITITYTDAHRGEY----

gi|298 ELTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSF

Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN

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gi|298 NYWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLEFN--GEKVYRAVANTNLAVWPSA
320 330 340 350 360 370

Cry1Ac I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
380 390 400 410 420 430

gi|298 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
380 390 400 410 420 430

Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
440 450 460 470 480 490

gi|298 HQLNYVMCFMLQGSRTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGAS
440 450 460 470 480

Cry1Ac VISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNWN
500 510 520 530 540 550

gi|298 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD
490 500 510 520 530 540

Cry1Ac NSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
560 570 580 590 600

gi|298 GAPFNQYYFDKTIKNGDTLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIE
550 560 570 580 590 600

Cry1Ac IPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
610 620 630 640 650 660

gi|298 IPVN

>>gi|155689529|gb|ABU29258.1| Sequence 13 from patent US (597 aa)
initn: 732 init1: 467 opt: 1081 Z-score: 1268.3 bits: 245.7 E(): 1e-61
Smith-Waterman score: 1085; 33.566% identity (66.608% similar) in 572 aa overlap
(60-612:44-596)

Cry1Ac GERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|155 TTKDVIQKGISVVGDLGVLGVPFPGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
90 100 110 120 130 140

gi|155 QKIADYAKNKALAEQLQGNVVEYVLSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
80 90 100 110 120 130

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
150 160 170 180 190 200

gi|155 NSMPBSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEAFYKRQKLTQE
140 150 160 170 180 190

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRITYPIRTVSQ
210 220 230 240 250 260

gi|155 YTDHCVKWNVGLDLKLRGSSYESWVFNFRYRREMTLTVLIDLIALFLYDVRLYPKVKTE
200 210 220 230 240 250

Cry1Ac LTRREIYTNPVL--ENFDGSRGSAQIEGSIIRSPHMLDILNSITTYTDAHRGEY-----
270 280 290 300 310

gi|155 LTRDLVLTDPVIGVNNLRG--YGTTFNSNIENYIRKPHLFDYLHRIQPHTRFPQPGYGNDSFN
260 270 280 290 300 310

Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAVQLQGQGVYRTLSST-LYRRFPNI
320 330 340 350 360 370

gi|155 YWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLEFN--GEKVYRAVANTNLAVWPSAV
320 330 340 350 360

Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
380 390 400 410 420 430

gi|155 YSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
370 380 390 400 410 420

Cry1Ac RLSHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
440 450 460 470 480 490

gi|155 QLNHYVMCFMLQGSRTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGSGASV
430 440 450 460 470

Cry1Ac ISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNWN
500 510 520 530 540 550

gi|155 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
480 490 500 510 520 530

Cry1Ac SSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
560 570 580 590 600 610

gi|155 APAAPFYFDKTIKNGDTLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
540 550 560 570 580 590

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|155 PVN

>>gi|111920201|gb|ABH70476.1| Sequence 13 from patent US (597 aa)
initn: 732 init1: 467 opt: 1081 Z-score: 1268.3 bits: 245.7 E(): 1e-61
Smith-Waterman score: 1085; 33.566% identity (66.608% similar) in 572 aa overlap
(60-612:44-596)

Cry1Ac GERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIGWIFGSPQWDAFLVQIEQLIN
30 40 50 60 70 80

gi|111 TTKDVIQKGISVVGDLGVLGVPFPGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
20 30 40 50 60 70

Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
90 100 110 120 130 140



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Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFI
gi|298 APAAPFYFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|298 PVN

>>gi|158496874|gb|ABW60291.1| Sequence 13 from patent US (597 aa)
initn: 732 initl: 467 opt: 1081 Z-score: 1268.3 bits: 245.7 E(): 1e-61
Smith-Waterman score: 1085; 33.566% identity (66.608% similar) in 572 aa overlap
(60-612:44-596)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLIN
gi|158 TTKDVIQKGISVVGDLGVLVGGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|158 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSAQESHFR

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|158 NSMPSFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQE

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTV SQ
gi|158 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR LYPKEVKTE

Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLM DILNSITTYTDAHRGEY-----
gi|158 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFPQPGYGNDSFN

Cry1Ac YWSGHQIMASPVGFSGPEFTPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
gi|158 YWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPVQNL EFN-GEKVYRAVANTNLAVWPSAV

Cry1Ac --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKS GTV--DSLDEIPPQNNVPPRQGF SH
gi|158 YSGVTKEVFSQYNDQTD EEA--STQTYDSK--RNVGAVSWDSIDQLPPE TTDDEPLEKGYSH

Cry1Ac 440 450 460 470 480 490

Cry1Ac RLSHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|158 QLNLYVMCFLMQSSRGTI-----PVLTWTHKSVDFN MIDSKITQLPLVKAYKLGSGASV

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN G
gi|158 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTTSLD G

Cry1Ac SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFI
gi|158 APAAPFYFDKTINKGDTLTYNFNLASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIEFI

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|158 PVN

>>gi|155689530|gb|ABU29259.1| Sequence 15 from patent US (601 aa)
initn: 676 initl: 467 opt: 1080 Z-score: 1267.0 bits: 245.5 E(): 1.2e-61
Smith-Waterman score: 1084; 33.507% identity (67.014% similar) in 576 aa overlap
(60-612:44-600)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLIN
gi|155 TTKDVIQKGISVVGDLGVLVGGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|155 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRELFSAQESHFR

Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|155 NSMPSFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRLKLTQE

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTV SQ
gi|155 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVR LYPKEVKTE

Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIRSPHLM DILNSITTYTDAHRGEY-----
gi|155 LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFPQPGYGNDSFN

Cry1Ac 320 330 340 350 360 370



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Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|158 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
      80          90          100          110          120          130

      150          160          170          180          190          200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|158 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
      140          150          160          170          180          190

      210          220          230          240          250          260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVVSQ
gi|158 YTDHCWKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
      200          210          220          230          240          250

      270          280          290          300          310
Cry1Ac LTRREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|158 LTRDVLTDPIVGVNLRG--YGTTFSNIEYIRKPHLFDYLHRIQPHTRFPQGGYGNDSFN
      260          270          280          290          300          310

      320          330          340          350          360          370
Cry1Ac YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST--LYRRPFNI
gi|158 YWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQNLLEFN--GEKVYRAVANTNLAVWPSAV
      320          330          340          350          360

      380          390          400          410          420          430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH
gi|158 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
      370          380          390          400          410          420

      440          450          460          470          480          490
Cry1Ac RLSHVMFRRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|158 QLNIVMCFMLMQSRGTI----PVLTWTHKSVDFNMDISKITQLPLVKAYKLGSGASV
      430          440          450          460          470

      500          510          520          530          540          550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|158 VAGPRFTGGDIIQCTENGAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
      480          490          500          510          520          530

      560          570          580          590          600
Cry1Ac SSIFNTVP---ATATSLDNLQSSDFGYFESANFTSSLGNI--VGVRFNSGTAGVIIDR
gi|158 APFNQYAAPFFYDKTINKGDTLTYSFNLASFTSTPELFGNNLQIGVTGLSAGDKVYIDK
      540          550          560          570          580          590

      610          620          630          640          650          660
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCL
gi|158 IEFIPVN
      600

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>>gi|111920202|gb|ABH70477.1| Sequence 15 from patent US (601 aa)
initn: 676 initl: 467 opt: 1080 Z-score: 1267.0 bits: 245.5 E(): 1.2e-61
Smith-Waterman score: 1084; 33.507% identity (67.014% similar) in 576 aa overlap
(60-612:44-600)

      30          40          50          60          70          80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|111 TTKDVIQKGISVVGDLGLVGVGFPFGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20          30          40          50          60          70

      90          100          110          120          130          140
Cry1Ac QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|111 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
      80          90          100          110          120          130

      150          160          170          180          190          200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|111 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
      140          150          160          170          180          190

      210          220          230          240          250          260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVVSQ
gi|111 YTDHCWKWYNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
      200          210          220          230          240          250

      270          280          290          300          310
Cry1Ac LTRREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|111 LTRDVLTDPIVGVNLRG--YGTTFSNIEYIRKPHLFDYLHRIQPHTRFPQGGYGNDSFN
      260          270          280          290          300          310

      320          330          340          350          360          370
Cry1Ac YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST--LYRRPFNI
gi|111 YWSGNYVSTRPSIGSNDIITSPPFYGNK--SSEPQNLLEFN--GEKVYRAVANTNLAVWPSAV
      320          330          340          350          360

      380          390          400          410          420          430
Cry1Ac --GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH
gi|111 YSGVTKVEFSQYNDQTEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH
      370          380          390          400          410          420

      440          450          460          470          480          490
Cry1Ac RLSHVMFRRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--SV
gi|111 QLNIVMCFMLMQSRGTI----PVLTWTHKSVDFNMDISKITQLPLVKAYKLGSGASV
      430          440          450          460          470

      500          510          520          530          540          550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
gi|111 VAGPRFTGGDIIQCTENGAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLDG
      480          490          500          510          520          530

      560          570          580          590          600
Cry1Ac SSIFNTVP---ATATSLDNLQSSDFGYFESANFTSSLGNI--VGVRFNSGTAGVIIDR
gi|111 APFNQYAAPFFYDKTINKGDTLTYSFNLASFTSTPELFGNNLQIGVTGLSAGDKVYIDK
      540          550          560          570          580          590

      610          620          630          640          650          660
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCL
gi|111 IEFIPVN
      600

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          560          570          580          590          600
Cry1Ac SSIFNTVP---ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 APFNQYAAPFFYDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDK
          540          550          560          570          580          590

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          610          620          630          640          650          660
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDEFCL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 IEFIPVN
          600

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>>gi|143084|gb|AAA22542.1| insect control protein (644 aa)  
 initn: 725 init1: 467 opt: 1080 Z-score: 1266.6 bits: 245.5 E(): 1.3e-61  
 Smith-Waterman score: 1084; 33.798% identity (67.073% similar) in 574 aa overlap  
 (60-612:91-643)

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          30          40          50          60          70          80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGFSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 TTKDVIQKGISVVGDLLGVVGFPPFGALVSFYTNFLNTIWPSED--WKAFMEQVEALMD
          70          80          90          100          110

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          90          100          110          120          130          140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 QKIADYAKNKALAEQLQLQNNVEDYVSALSSWQKNPVRNPHSQGRIRELFSQAESHFR
          120          130          140          150          160          170

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          150          160          170          180          190          200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 NSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWEYKEDIAEFYKRLKLTQE
          180          190          200          210          220          230

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          210          220          230          240          250          260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVSQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 YTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLDVRLYPKEVKTE
          240          250          260          270          280          290

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          270          280          290          300          310
Cry1Ac LTREIYTNPVL--ENFDGSRFGSAQGIIEGSIKSPHMLDILNSITIYTDHAHGEY-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 LTRDVLTDPIVGVNLRG-YGTFNSNIENYIRKPHLFDYLRHQFHTRFQPGYYGNDVSN
          300          310          320          330          340          350

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          320          330          340          350          360          370
Cry1Ac YWSGHQIMASPVFGSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 YWSGNYVSTRSIGSNDIITSPFYGNK--SSEPVQNLFPN-GEKVYRAVANTNLAVWPSAV
          360          370          380          390          400          410

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          380          390          400          410          420          430
Cry1Ac --GINNQLSVL-DGTEFAYGTSSNLPASAVYRKSQV--DSLDEIPPQNNVPPRQGFHS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 YSGVTKVEFSQYNDQTDAA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGYSH
          420          430          440          450          460          470

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          440          450          460          470          480          490
Cry1Ac RLSHVSFMFRSGFSNSVSIIRAPMFVSIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 QLNVMCFMLQGGSRGTI-----PVLTWTHKSVDFNMIDSKKITQLPLVKAYKLGSGASV
          480          490          500          510          520

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          500          510          520          530          540
Cry1Ac ISGPGFTGGDLVRL--NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 VAGPRFTGGDIIQCTENASAATI---YVTPDVSY---SQKYRARIHVASTSQITFTLSL
          530          540          550          560          570

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          550          560          570          580          590          600
Cry1Ac GNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 DGAPFNQYFDKTINKGDTLTYNSFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIE
          580          590          600          610          620          630

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          610          620          630          640          650          660
Cry1Ac FIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDEFCLDE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|143 FIPVN
          640

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>>gi|111920205|gb|ABH70480.1| Sequence 21 from patent US (597 aa)  
 initn: 732 init1: 467 opt: 1079 Z-score: 1265.9 bits: 245.2 E(): 1.4e-61  
 Smith-Waterman score: 1083; 33.508% identity (66.492% similar) in 573 aa overlap  
 (60-612:44-597)

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          30          40          50          60          70          80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIGWIFGFSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 TTKDVIQKGISVVGDLLGVVGFPPFGALVSFYTNFLNTIWPSED--WKAFMEQVEALMD
          20          30          40          50          60          70

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          90          100          110          120          130          140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 QKIADYAKNKALAEQLQLQNNVEDYVSALSSWQKNPAPFRNPHSQGRIRELFSQAESHF
          80          90          100          110          120          130

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          150          160          170          180          190          200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 RNSMPSFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEWEYKEDIAEFYKRLKLTQ
          140          150          160          170          180          190

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          210          220          230          240          250          260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 EYTDHCVKWNVGLDKLRGSSYESWVFNRYRREMTLTVLDLIALFPLDVRLYPKEVKTE
          200          210          220          230          240          250

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          270          280          290          300          310
Cry1Ac QLTREIYTNPVL--ENFDGSRFGSAQGIIEGSIKSPHMLDILNSITIYTDHAHGEY-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|111 ELTRDVLTDPIVGVNLRG-YGTFNSNIENYIRKPHLFDYLRHQFHTRFQPGYYGNDVSN
          260          270          280          290          300          310

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320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN
      . . . . .
gi|111 NYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPQVQNLEFN-GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

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380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      . . . . .
gi|111 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
      370      380      390      400      410      420

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440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
      . . . . .
gi|111 HQLNYVMCFMQLGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGSGAS
      430      440      450      460      470

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500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNW
      . . . . .
gi|111 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD
      480      490      500      510      520      530

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560      570      580      590      600
Cry1Ac NSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
      . . . . .
gi|111 GAPAAPFYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIE
      540      550      560      570      580      590

```

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610      620      630      640      650      660
Cry1Ac IPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
      . . .
gi|111 IPV

```

>>gi|29823410|emb|CAD88624.1| unnamed protein product [s (597 aa)  
 initn: 732 init1: 467 opt: 1079 Z-score: 1265.9 bits: 245.2 E(): 1.4e-61  
 Smith-Waterman score: 1083; 33.508% identity (66.492% similar) in 573 aa overlap  
 (60-612:44-597)

```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLIN
      . . . . .
gi|298 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

```

```

90      100      110      120      130      140
Cry1Ac QRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPT----NPALREEMRIQFNDMNSAL
      . . . . .
gi|298 QKIADYAKNKALAEIQGLQNNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF
      80      90      100      110      120      130

```

```

150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFGRWGFDAATINSRYNDLTRLIG
      . . . . .
gi|298 RNSMSPFAISGYEVLFLTYAQAANTHLFLKDAQIYGEWEVYKEDIAEFYKRLKLTQ
      140      150      160      170      180      190

```

```

210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVS
      . . . . .
gi|298 EYTDHCVKWYNVGLDKLRGSSYSEWVNFNRYRREMLTTLVLDLIALFPPLYDVRLYPKVEKT
      200      210      220      230      240      250

```

```

270      280      290      300      310
Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITITYTDAHRGEY----
      . . . . .
gi|298 ELTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFPQGYGND
      260      270      280      290      300      310

```

```

320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFN
      . . . . .
gi|298 NYWSGNYVSTRPSIGSNDIITSPFYGNK-SSEPQVQNLEFN-GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

```

```

380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
      . . . . .
gi|298 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY
      370      380      390      400      410      420

```

```

440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
      . . . . .
gi|298 HQLNYVMCFMQLGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGSGAS
      430      440      450      460      470

```

```

500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNW
      . . . . .
gi|298 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD
      480      490      500      510      520      530

```

```

560      570      580      590      600
Cry1Ac NSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRF
      . . . . .
gi|298 GAPAAPFYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTLGSLAGDKVYIDKIE
      540      550      560      570      580      590

```

```

610      620      630      640      650      660
Cry1Ac IPVTTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
      . . .
gi|298 IPV

```

>>gi|158496878|gb|ABW60295.1| Sequence 21 from patent US (597 aa)  
 initn: 732 init1: 467 opt: 1079 Z-score: 1265.9 bits: 245.2 E(): 1.4e-61  
 Smith-Waterman score: 1083; 33.508% identity (66.492% similar) in 573 aa overlap  
 (60-612:44-597)

```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLIN
      . . . . .
gi|158 TTKDVIQKGISVVGDLGVLVGFPPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

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90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT----NPALREEMRIQFNDMNSAL
gi|158 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF
      80      90      100      110      120      130

150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
gi|158 RNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRLKLTQ
      140      150      160      170      180      190

210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS
gi|158 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVKVT
      200      210      220      230      240      250

270      280      290      300      310
Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQGI EGSIRSPHLMIDLNSITTYTDAHRGEY----
gi|158 ELTRDVLTDPIVGVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQPGYGNDSF
      260      270      280      290      300      310

320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRP FN
gi|158 NYWSGNYVSTRPSIGSNDIITSPFYGNK--SSEPVQNLEFN--GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF S
gi|158 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY S
      370      380      390      400      410      420

440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|158 HQLNYVMCFMQGSRGTI-----PVL TWTHKSVDFNMI DSKKITQLPLVKAYKQLQSGAS
      430      440      450      460      470

500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWG
gi|158 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIH YASTSQITFTLSLD
      480      490      500      510      520      530

560      570      580      590      600
Cry1Ac NSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNI--VGVRFNSGTAGVIIDRF EF
gi|158 GAPAAPFYFDKTIINKGDTLTYN SFNLASFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEF
      540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac IPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
gi|158 IPV

```

```

>>gi|155689533|gb|ABU29262.1| Sequence 21 from patent US (597 aa)
  initn: 732 initl: 467 opt: 1079 Z-score: 1265.9 bits: 245.2 E(): 1.4e-61
  Smith-Waterman score: 1083; 33.508% identity (66.492% similar) in 573 aa overlap
  (60-612:44-597)

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30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI I WGFGPSQWDAFLVQIEQLIN
gi|155 TTKDVIQKGISVVGDL LGVGVFPFGGALV SFYTNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT----NPALREEMRIQFNDMNSAL
gi|155 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPAAPFRNPHSQGRIRELFSQAESHF
      80      90      100      110      120      130

150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
gi|155 RNSMPSFAISGYEVLFLTTYQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRLKLTQ
      140      150      160      170      180      190

210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVS
gi|155 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFPLYDVRLYPKVKVT
      200      210      220      230      240      250

270      280      290      300      310
Cry1Ac QLTREIYTNPVL--ENFDGSRGSAQGI EGSIRSPHLMIDLNSITTYTDAHRGEY----
gi|155 ELTRDVLTDPIVGVNLRG--YGTTF SNIENYIRKPHLFDYLHRIQFHTRFPQPGYGNDSF
      260      270      280      290      300      310

320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRP FN
gi|155 NYWSGNYVSTRPSIGSNDIITSPFYGNK--SSEPVQNLEFN--GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL--DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGF S
gi|155 VYSGVTKVEFSQYNDQTDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGY S
      370      380      390      400      410      420

440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|155 HQLNYVMCFMQGSRGTI-----PVL TWTHKSVDFNMI DSKKITQLPLVKAYKQLQSGAS
      430      440      450      460      470

500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWG
gi|155 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIH YASTSQITFTLSLD
      480      490      500      510      520      530

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          560      570      580      590      600
Cry1Ac NSSIFSNTV PATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEF
..          : .. : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|155 GAPAAPFYFDKTIKNGD560TLTYNSFN570LN580ASFSTPF590FELSGNNLQIGVTGLSAGDKVYIDKIEF
          540      550      560      570      580      590

```

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          610      620      630      640      650      660
Cry1Ac IPV610TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
          : : :
gi|155 IPV

```

>>gi|29823408|emb|CAD88623.1| unnamed protein product [s (602 aa)  
 initn: 676 initl: 467 opt: 1078 Z-score: 1264.7 bits: 245.0 E(): 1.6e-61  
 Smith-Waterman score: 1082; 33.449% identity (66.898% similar) in 577 aa overlap  
 (60-612:44-601)

```

          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI30IWGFGPSQWDAFLVQIEQLIN
          : .. : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 TTKDVIQKGISVVG40DLLGVVGF50FFGGALV60FSYTNFLN70TIW80PS80EDP--WKAFMEQVEALMD
          20      30      40      50      60      70

```

```

          90      100     110     120     130     140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 QKIADYAKNKALAE90LQGLQNNVEDYV100SALSSWQKNP110APFRNPHS120OGRIRELFSQAESHF
          80      90      100     110     120     130

```

```

          150     160     170     180     190     200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS150VFGQRWGFDAATINSRYNDLTRLIG
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 RNSMPSFAISG160YEVLF170LT180TYAQAANTHL190FLKDAQIYGE200EWG200EYKEDIAE200FKRQLKLTQ
          140     150     160     170     180     190

```

```

          210     220     230     240     250     260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL210TLTVLDIVSLFPNYDSRTYPIRTVS
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRRE220MTLVLDLIALFPLYDVRLYPKEVKT
          200     210     220     230     240     250

```

```

          270     280     290     300     310
Cry1Ac QLTREIYTNPVL--ENFDG270SFRGSAQGI280EGSIRSPH290LMDILNSIT300IYTD310AHRGEY----
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 ELTRDVLTDPIVGVN270NRG-YG280TTF290SNIENY300IRKPHL310FDYLHRIQ310PHTRFQPGYGNDSF
          260     270     280     290     300     310

```

```

          320     330     340     350     360     370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ320QRIVAQLGQGVYRTLSST-LYRRP370FN
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 NYWSGNYVSTRPSIGSNDIITS320PFYGNK--SSE330PVQ340NLEFN-GEK350VYRAVANTLAVW360PSA
          320     330     340     350     360

```

```

          380     390     400     410     420     430
Cry1Ac I--GINNQ380LSVL-DGTEFAYGTSSNLP390SAVYR400KSGTV--DSLDEI410PPQNNV420PPRQ430GS
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 VYSGVTKVEFSQYNDQ380TDEA--STQ390TYDSK--R400NVGAVSWDSIDQL410PPET420TDEPLEK430GS
          370     380     390     400     410     420

```

```

          440     450     460     470     480     490
Cry1Ac HRLSHVSMFRSFGFSN440SVSII450RAPMFSWI460HRS470AEFN480NIASDSITQIPAVKGNFL490NG-S
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 HQLN440YVMCF450LMQGS460RGTI----P470VL480TW490THKSVDF490NMIDSKKITQ490LPLVKAYKLQ490SGAS
          430     440     450     460     470

```

```

          500     510     520     530     540     550
Cry1Ac VISGPGFTGGDLVRLN500SSGNNIQNRGYIEV510PIHFP520STSTRYRVRVRYASV530TP540IHLNVN550WG
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--S500QYRARIHYASTSQIT510FT520FLSLD
          480     490     500     510     520     530

```

```

          560     570     580     590     600
Cry1Ac NSSIFSNTV560---ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIID
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 GAPFNQYAAPFYFDKTIKNGD560TLTYNSFN570LN580ASFSTPF590FELSGNNLQIGVTGLSAGDKVYID
          540     550     560     570     580     590

```

```

          610     620     630     640     650     660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|298 KIEFIPVN
          600

```

>>gi|158496877|gb|ABW60294.1| Sequence 19 from patent US (602 aa)  
 initn: 676 initl: 467 opt: 1078 Z-score: 1264.7 bits: 245.0 E(): 1.6e-61  
 Smith-Waterman score: 1082; 33.449% identity (66.898% similar) in 577 aa overlap  
 (60-612:44-601)

```

          30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDI30IWGFGPSQWDAFLVQIEQLIN
          : .. : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|158 TTKDVIQKGISVVG40DLLGVVGF50FFGGALV60FSYTNFLN70TIW80PS80EDP--WKAFMEQVEALMD
          20      30      40      50      60      70

```

```

          90      100     110     120     130     140
Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|158 QKIADYAKNKALAE90LQGLQNNVEDYV100SALSSWQKNP110APFRNPHS120OGRIRELFSQAESHF
          80      90      100     110     120     130

```

```

          150     160     170     180     190     200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS150VFGQRWGFDAATINSRYNDLTRLIG
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|158 RNSMPSFAISG160YEVLF170LT180TYAQAANTHL190FLKDAQIYGE200EWG200EYKEDIAE200FKRQLKLTQ
          140     150     160     170     180     190

```

```

          210     220     230     240     250     260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL210TLTVLDIVSLFPNYDSRTYPIRTVS
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|158 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRRE220MTLVLDLIALFPLYDVRLYPKEVKT
          200     210     220     230     240     250

```

```

          270     280     290     300     310
Cry1Ac QLTREIYTNPVL--ENFDG270SFRGSAQGI280EGSIRSPH290LMDILNSIT300IYTD310AHRGEY----
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|158 ELTRDVLTDPIVGVN270NRG-YG280TTF290SNIENY300IRKPHL310FDYLHRIQ310PHTRFQPGYGNDSF
          260     270     280     290     300     310

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320 330 340 350 360 370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFN
gi|158 NYWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPQVQNFN-GEKVYRAVANTNLAVWPSA

380 390 400 410 420 430
Cry1Ac I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFN
gi|158 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYN

440 450 460 470 480 490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|158 HQLNYVMCFMLQGSRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGQSGAS

500 510 520 530 540 550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNNG
gi|158 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD

560 570 580 590 600
Cry1Ac NSSIFSNVTP----ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIID
gi|158 GAPFNQYAAPFYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYID

610 620 630 640 650 660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFN
gi|158 KIEFIPVN
600

>>gi|111920204|gb|ABH70479.1| Sequence 19 from patent US (602 aa)
initn: 676 initl: 467 opt: 1078 Z-score: 1264.7 bits: 245.0 E(): 1.6e-61
Smith-Waterman score: 1082; 33.449% identity (66.898% similar) in 577 aa overlap
(60-612:44-601)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLIN
gi|111 TTKDVIQKGISVVGDLGVLVGFVGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

90 100 110 120 130 140
Cry1Ac QRIEEFARNQAI SRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
gi|111 QKIADYAKNKALAEQLQGNVVEDYVLSLSSWQKNPAAPFRNPHSQGRIRELFSQAESHF

150 160 170 180 190 200
Cry1Ac TTAIPLFVAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGWGFDATINSRYNDLTRLIG
gi|111 RNSMPSFALISGYEVLFLTYAQAANTHLFLLKDAQIYGEWEVYKEDIAEFYKRQLKLTQ

210 220 230 240 250 260
Cry1Ac NYTDHAVRWYNTGLERVWVGFSDSRDWIRYNOQFRRELTTLVLDIVSLFPNYDSRTYPIRTVS
gi|111 EYTDHCVKYNVGLDKLRGSSYSEVWVNFNRYRREMTLTVLDLIALFPLVDVRLYPKEVKT

270 280 290 300 310
Cry1Ac QLTREIYTNVPL--ENFDGSRGSAQIEGSIKSPHMLDILNSITIYTDHRGEY----
gi|111 ELTRDVLTDPIVGVNMLRG-YGTTFSNIENYIRKPHLFDYLHRIQPHTRFQPGYGNDSF

320 330 340 350 360 370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSST-LYRRPFN
gi|111 NYWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPQVQNFN-GEKVYRAVANTNLAVWPSA

380 390 400 410 420 430
Cry1Ac I--GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFN
gi|111 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYN

440 450 460 470 480 490
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|111 HQLNYVMCFMLQGSRGTI----PVLTWTHKSVDFNMIIDSKKITQLPLVKAYKLGQSGAS

500 510 520 530 540 550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNNG
gi|111 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLSLD

560 570 580 590 600
Cry1Ac NSSIFSNVTP----ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIID
gi|111 GAPFNQYAAPFYFDKTIKNGDITLTYNSFNLFASFSTPFELSGNNLQIGVTGLSAGDKVYID

610 620 630 640 650 660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFN
gi|111 KIEFIPVN
600

>>gi|155689532|gb|ABU29261.1| Sequence 19 from patent US (602 aa)
initn: 676 initl: 467 opt: 1078 Z-score: 1264.7 bits: 245.0 E(): 1.6e-61
Smith-Waterman score: 1082; 33.449% identity (66.898% similar) in 577 aa overlap
(60-612:44-601)

30 40 50 60 70 80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLIN
gi|155 TTKDVIQKGISVVGDLGVLVGFVGGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD

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90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSAL
gi|155 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPAAPFRNPHSQGRIRRELFSSQAESHF
      80      90      100      110      120      130

150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
gi|155 RNSMPSPFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQ
      140      150      160      170      180      190

210      220      230      240      250      260
Cry1Ac NYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVS
gi|155 EYTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFLPLYDVRLYPKVKVT
      200      210      220      230      240      250

270      280      290      300      310
Cry1Ac QLTRREIYTNPVL--ENFDGSRFGSAQGLEGSIRSPHLMIDILNSITITYDAHRGEY----
gi|155 ELTRDVLTDPIVGVNMLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYYGNDSF
      260      270      280      290      300      310

320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQGVYRTLSST-LYRRPFN
gi|155 NYWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPQVNLFEFN-GEKVYRAVANTNLAVWPSA
      320      330      340      350      360

380      390      400      410      420      430
Cry1Ac I--GINNQQLSVL-DGTEFAYGTSNLSAVYRKSGTV--DSLDEIPPQNNVPPRQGF
gi|155 VYSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPEPTTDEPLEKGY
      370      380      390      400      410      420

440      450      460      470      480      490
Cry1Ac HRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-S
gi|155 HQLNVMCFMQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGSGAS
      430      440      450      460      470

500      510      520      530      540      550
Cry1Ac VISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWG
gi|155 VVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLD
      480      490      500      510      520      530

560      570      580      590      600
Cry1Ac NSSIFSNTVP----ATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIID
gi|155 GAPFNQYAAPFYFDKTIKNGDTLTYNSFNLSASFSTPFELSGNNLQIGVTLGAGDKVYIID
      540      550      560      570      580      590

610      620      630      640      650      660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVNSLVTYLSDFEC
gi|155 KIEFIPVN

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600
>>gi|2490715|gb|AAB78851.1|I62691 Sequence 4 from patent (645 aa)
initn: 732 initl: 467 opt: 1077 Z-score: 1263.1 bits: 244.8 E(): 2e-61
Smith-Waterman score: 1077; 33.101% identity (66.725% similar) in 574 aa overlap
(60-612:92-644)

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGFIPGSPQWDAFLVQIEQLIN
gi|249 TTKDVIQKGISVVGDLGVLGVGFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVREALMD
      70      80      90      100      110

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMNSALT
gi|249 QKIADYAKNKALAE LQGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRRELFSSQAESHFR
      120      130      140      150      160      170

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|249 NSMPSPFAISGYEVLFLTTYAQAANTHLFLLKDAQIYGEEWGYEKEDIAEFYKRQLKLTQE
      180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|249 YTDHCVKWYNVGLDKLRGSSYESWVNFNRYRREMTLTVLDLIALFLPLYDVRLYPKVKTE
      240      250      260      270      280      290

270      280      290      300      310
Cry1Ac LTRREIYTNPVL--ENFDGSRFGSAQGLEGSIRSPHLMIDILNSITITYDAHRGEY----
gi|249 LTRDVLTDPIVGVNMLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRXXXXXGNDSFN
      300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQGVYRTLSSTLYRRPFNIG
gi|249 YWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPQVNLFEFN-GEKVYRAVANT-----NLA
      360      370      380      390      400      410

380      390      400      410      420      430
Cry1Ac INNQQL-SVLDGTEFA-YGTSSNLSA-VY---RKSQTV--DSLDEIPPQNNVPPRQGF
gi|249 VXXSAVXSGVTKVEFSQYNDQTDDEASTQTYDSXRNVGAVSWDSIDQLPPEPTTDEPLEKGY
      420      430      440      450      460      470

440      450      460      470      480
Cry1Ac SHRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-
gi|249 SHQLNVMCFMQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKLGSGA
      480      490      500      510      520

490      500      510      520      530      540
Cry1Ac SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNW
gi|249 SVVAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSL

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530      540      550      560      570      580
550      560      570      580      590      600
Cry1Ac  GNSSIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGNI-VGVRNFSGTAGVIIDRFE
      . . . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|249  DGAPFNQYYFDKTIKNGDITLYNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIE
      590      600      610      620      630      640

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610      620      630      640      650      660
Cry1Ac  FIPVVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
      : : : :
gi|249  FIPVN

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>>gi|593596|gb|AAA55203.1| Sequence 5 from Patent EP 035 (610 aa)  
 initn: 723 initl: 458 opt: 1075 Z-score: 1261.1 bits: 244.4 E(): 2.5e-61  
 Smith-Waterman score: 1079; 33.392% identity (66.958% similar) in 572 aa overlap  
 (60-612:44-596)

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30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFFGSPQWDAFLVQIEQLIN
      : . . . . : : : : : : : : : . . . : . . . : . . . : . . . :
gi|593  TTKDVIQKGISVVGDLLGVVGFPPFGGALVSYFNFLNTIWPSEDP--WKAFMEQVEALMD
      20      30      40      50      60      70

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90      100     110     120     130     140
Cry1Ac  QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
      : : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  QKIADYAKNKALAEQLQGNVEDYVLSWQKNPVSSRNPHSQGRIRELFSQAESHFR
      80      90      100     110     120     130

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150     160     170     180     190     200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  NSMPSFAISGYEVLFLTTYQAANTNLFLLKDAQIYGEWEYKEDIAEFYKRQLKLTQE
      140     150     160     170     180     190

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210     220     230     240     250     260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVQSQ
      : : : : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  YTDHCVKWYNVGLDKLRGSSYESWVFNRYRREMTLVLDLIALFPLYDVRLYPKEVKTE
      200     210     220     230     240     250

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270     280     290     300     310
Cry1Ac  LTRREIYTNPVL--ENFDGSRFRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGEY-----
      : : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFN
      260     270     280     290     300     310

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320     330     340     350     360     370
Cry1Ac  YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPFNI
      : : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  YWSGNVSTRPSIGSNDIITSPPFYGNK--SSEPQVQLFEN--GKVKYRAVANTNLAVWPSAV
      320     330     340     350     360

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380     390     400     410     420     430
Cry1Ac  --GINNQQLSVL-DGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFHSH
      : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  YSGVTKVEFSQYNDQTDDEA--STQTYDSK--RNVGAVSWDSIDQLPPETTDEPLEKGYSH

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370      380      390      400      410      420
440      450      460      470      480      490
Cry1Ac  RLSHVMFMRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
      : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  QLNIVMCFMLMQSGRGTI-----PVLTWTHKSVDFNMDSSKITQLPLVKAYKLSGASV
      430      440      450      460      470

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500      510      520      530      540      550
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGN
      : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY--SQKYRARIHYASTSQITFTLSLDG
      480      490      500      510      520      530

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560      570      580      590      600      610
Cry1Ac  SSIIFSNTVPATATSLDNLQSSDFGYFESANAFSSSLGNI-VGVRNFSGTAGVIIDRFEFI
      . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|593  APFNQYYFDKTIKNGDITLYNSFNLSFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
      540      550      560      570      580      590

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620      630      640      650      660      670
Cry1Ac  PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
      : :
gi|593  PVNLRSPGTELEFIDI
      600      610

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>>gi|162767645|emb|CAP58826.1| unnamed protein product [ (465 aa)  
 initn: 840 initl: 425 opt: 1072 Z-score: 1259.3 bits: 243.7 E(): 3.2e-61  
 Smith-Waterman score: 1072; 42.474% identity (67.629% similar) in 485 aa overlap  
 (168-624:1-465)

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140     150     160     170     180     190
Cry1Ac  FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRY
      : : : : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|162  AANLHLAILRDSVIFGERWGLTTINVNENY
      10      20      30

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200     210     220     230     240     250
Cry1Ac  NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSR
      : : : : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|162  NRLIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTVLDIAAFFPNYDNR
      40      50      60      70      80      90

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260     270     280     290     300     310
Cry1Ac  TYPPIRTVSQLTREIYTNPVLNFDGSRFRGSAQ-----IEGS-IRSPHLMIDLNSITTYT
      : : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|162  RYPIQPVGLTREVYTDPLI-NFNPQLQSVQQLPTFNVMESSAIRNPHLFDILNLIPTI
      100     110     120     130     140

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320     330     340     350     360
Cry1Ac  DAHR-GE-YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST
      : : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|162  DWFSVGRNFYWGGRVIVSLIG--GGNITSPIYGREANQEPFRSFT--FNGPVFRTLSNP
      150     160     170     180     190     200

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370     380     390     400     410     420
Cry1Ac  LYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPP
      : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|162  TLRLLQQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRGTVDSLTELPEPNDVSP

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210      220      230      240      250
Cry1Ac  RQGFSHRLSHVSMF-RSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNF
gi|162  REGYSHRLCHATFVQRSQTPFLTTGVV---FSWTHRSATLNTIDPERINQIPLVKGFR
260      270      280      290      300      310
Cry1Ac  LFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIH
gi|162  VMGGTSVITGPGFTGGDLRRNTFGDFVS---LQVNNSPITQ-RYRLRFYASSRDAR
320      330      340      350      360      370
Cry1Ac  LNVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIVGVRN-
gi|162  VIVLTGAASTGVGGQVSVNMPLQKTMIEIGENLTSRTFRYTDPSNPFSSFRANPDIIGISEQ
380      390      400      410      420      430
Cry1Ac  --F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|162  PLFGAGSISSELYIDKIEIILADATFEAESDLER
440      450      460
Cry1Ac  IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
650      660      670      680      690      700

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>>gi|58826238|gb|AAW82872.1| Cry3 delta endotoxin [Bacil (644 aa)  
 initn: 724 initl: 467 opt: 1068 Z-score: 1252.4 bits: 242.9 E(): 7.7e-61  
 Smith-Waterman score: 1072; 33.217% identity (66.608% similar) in 572 aa overlap  
 (60-612:91-643)

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30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|588  TTKDVIQKGISVVGDLGLGVVGFPPFGALVVSFYTNFLNTSWPSEDP--WKAFMEQVEALMD
70      80      90      100     110
Cry1Ac  QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|588  QKIADYAKNKALAEQLQGNVVDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESYFR
120     130     140     150     160     170

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150     160     170     180     190     200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLRLIGN
gi|588  NSMPSFAISGYEVLFLTTYQAANTHLFLKDAQIYGEWGYEKEDIAEFYKRQLKLTQE
180     190     200     210     220     230

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210     220     230     240     250     260
Cry1Ac  YTHAVRWYNTGLERVWGPDSRDWIRYNQFRELTTLVLDIVSLFPNYSRTPYPIRTVVSQ
gi|588  YTDHCVKWYNVGLDKLRSSYSWVNFNRYREMTLTVLDDLALPPLYDVRLYPKEVKTE
240     250     260     270     280     290

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270     280     290     300     310

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Cry1Ac  LTREIYTNPVL--ENFDGSFRGSAQGIIEGSIRSPHMLDILNSITIYTDahrgey-----
gi|588  LTRDVLTDPIVGVNLRG-YGTTFSNIENYIRKPHLFLNLRRIQPHTRFPQGYGNDSFN
300     310     320     330     340     350
Cry1Ac  YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRtLSSST-LYRRPFNI
gi|588  YWSGNYVSTRPSIGSNDIITSPPFYGNK-SSEPQNLLEFN-GEKVYRAVANTNLAWPSSAV
360     370     380     390     400     410
Cry1Ac  --GINNQQLSVL-DGTEFAYGTSSNLPsAVYRKSgTV--DSLDEIPPQNNVPPRQGFSh
gi|588  YSGVTKVEFSQYNDQIDEA--STQTYDSK--RNVGAVSWDSIDQLPPETDDEPLEKGYSH
420     430     440     450     460     470
Cry1Ac  RLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|588  QLNyVMCFLMQGSRGTI----PVLTWTHKSVDFNMIDSKKITQLPLVKAYKLQSGASV
480     490     500     510     520
Cry1Ac  ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHlNVNWN
gi|588  VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQKYRARIHYASTSQITFTLLSLDG
530     540     550     560     570     580
Cry1Ac  SSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFI
gi|588  APFNQYYFDKTIKNGDTLTYNSFNLASFSTPFELSGNNLQIGVTLGSAGDKYIDKIEIFI
590     600     610     620     630     640
Cry1Ac  PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
gi|588  PVN

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>>gi|31698148|gb|AAP63846.1| Sequence 2 from patent US 6 (644 aa)  
 initn: 704 initl: 440 opt: 1065 Z-score: 1248.9 bits: 242.2 E(): 1.2e-60  
 Smith-Waterman score: 1068; 33.217% identity (65.734% similar) in 572 aa overlap  
 (60-612:91-643)

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30      40      50      60      70      80
Cry1Ac  GERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLIN
gi|316  TTKDVIQKGISVVGDLGLGVVGFPPFGALVVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100     110
Cry1Ac  QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT--NPALREEMRIQFNDMNSALT
gi|316  QKIADYAKNKALAEQLQGNVVDYVSALSSWQKNPVSSRNPHSQGRIRELFSQAESHFR
120     130     140     150     160     170

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150     160     170     180     190     200
Cry1Ac  YTHAVRWYNTGLERVWGPDSRDWIRYNQFRELTTLVLDIVSLFPNYSRTPYPIRTVVSQ
gi|316  YTDHCVKWYNVGLDKLRSSYSWVNFNRYREMTLTVLDDLALPPLYDVRLYPKEVKTE
240     250     260     270     280     290

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270     280     290     300     310

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Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|316 NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEEWGYKKEDIAEFLKRQLKLTQE
180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|316 YTDHVFQWYVGLDKIRGSFYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|316 LTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFN
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPF
gi|316 YWSGNYVSTRPSIGSNDIITSFYGK--SSEPVQNLGFN--GEKVYRAVANTNLAVWPSAV
360      370      380      390      400      410

380      390      400      410      420      430
Cry1Ac NIGINNQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH
gi|316 NSGVTKVKFSQYNDQTEA---STQTSKRNKRVGAVSWDSIDQLPPEATDEPLEKGYSH
420      430      440      450      460      470

440      450      460      470      480      490
Cry1Ac RLSHVSMPFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|316 QLNVMCFMLQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKQLQSGASV
480      490      500      510      520

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWGN
gi|316 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
530      540      550      560      570      580

560      570      580      590      600      610
Cry1Ac SSIFSNTPATATSLDNLQSSDFGFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|316 APFNQYYFDKTIKGDTLTYNSFNLFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKR
gi|316 PVN

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>>gi|56626137|gb|AAW05659.1| Sequence 2 from patent US 6 (644 aa)
initn: 704 init1: 440 opt: 1065 Z-score: 1248.9 bits: 242.2 E(): 1.2e-60
Smith-Waterman score: 1068; 33.217% identity (65.734% similar) in 572 aa overlap
(60-612:91-643)

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30      40      50      60      70      80

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Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFIPGSPQWDAFLVQIEQLIN
gi|566 TTKDVIQKGISVVDLGLVGVFPFGALVSFYTNFLNTIWPSEDP--WKAFMEQVEALMD
70      80      90      100      110

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAIISREGLSNLYQIYAESFREWEADPT---NPALREEMRIQFNDMMSALT
gi|566 QKIADYAKNKALAEQLQGLQNNVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESHFR
120      130      140      150      160      170

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|566 NSMPSFAISGYEVLFLTTYAQAANTHLFLKDAQIYGEEWGYKKEDIAEFLKRQLKLTQE
180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|566 YTDHVFQWYVGLDKIRGSFYESWVFNRYRREMTLTVLDLIALFPLYDVRLYPKVKTE
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSRGSAQIEGSIKSPHMLDILNSITTYDAHRGEY-----
gi|566 LTRDVLTDPIVGVNLRG--YGTTFNSIENYIRKPHLFDYLHRIQFHTRFQPGYGNDSFN
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQGVYRTLSST--LYRRPF
gi|566 YWSGNYVSTRPSIGSNDIITSFYGK--SSEPVQNLGFN--GEKVYRAVANTNLAVWPSAV
360      370      380      390      400      410

380      390      400      410      420      430
Cry1Ac NIGINNQLSVL-DGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQNNVPPRQGFSH
gi|566 NSGVTKVKFSQYNDQTEA---STQTSKRNKRVGAVSWDSIDQLPPEATDEPLEKGYSH
420      430      440      450      460      470

440      450      460      470      480      490
Cry1Ac RLSHVSMPFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SV
gi|566 QLNVMCFMLQGSRGTI----PVLTWTHKSVDFNMDSKKITQLPLVKAYKQLQSGASV
480      490      500      510      520

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWGN
gi|566 VAGPRFTGGDIIQCTENGSAATI--YVTPDVSY---SQYRARIHYASTSQITFTLSLDG
530      540      550      560      570      580

560      570      580      590      600      610
Cry1Ac SSIFSNTPATATSLDNLQSSDFGFESANAFTSSLGNI--VGVNRFSGTAGVIIDRFEFI
gi|566 APFNQYYFDKTIKGDTLTYNSFNLFSTPFELSGNNLQIGVTGLSAGDKVYIDKIEFI
590      600      610      620      630      640

620      630      640      650      660      670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKR
gi|566 PVN

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>>gi|56626137|gb|AAW05659.1| Sequence 2 from patent US 6 (644 aa)
initn: 704 init1: 440 opt: 1065 Z-score: 1248.9 bits: 242.2 E(): 1.2e-60
Smith-Waterman score: 1068; 33.217% identity (65.734% similar) in 572 aa overlap
(60-612:91-643)

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30      40      50      60      70      80

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Regulatory Product Characterization Team

Cry1Ac 620 630 640 650 660 670
PVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKR
gi|566 PVN

>>gi|40145967|gb|AAR61472.1| Sequence 50 from patent US (652 aa)
initn: 1025 initl: 457 opt: 1064 Z-score: 1247.6 bits: 242.0 E(): 1.4e-60
Smith-Waterman score: 1133; 34.983% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEM
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRNPHSQGRI

Cry1Ac 140 150 160 170 180 190
RIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSSEDVA

Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRREMTLTVLDLIVLFFPY

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIRSPHLMIDILNSITIYTDA
gi|401 DVRLYPKGVKTELTRDIFTDPIFSLNLTQIEYGPFTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTITSPFFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNGKVVYLVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRVDFNTIDA EKITQLPV

Cry1Ac 490 500 510 520 530
VKGNFLENG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac 540 550 560 570 580 590
VTPIHLLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|401 TTNLRLFLVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSKDNELIIGAESF

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL

>>gi|12810088|gb|AAE44003.1| Sequence 50 from patent US (652 aa)
initn: 1025 initl: 457 opt: 1064 Z-score: 1247.6 bits: 242.0 E(): 1.4e-60
Smith-Waterman score: 1133; 34.983% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|128 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEM
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRNPHSQGRI

Cry1Ac 140 150 160 170 180 190
RIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSSEDVA

Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|128 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRREMTLTVLDLIVLFFPY

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIRSPHLMIDILNSITIYTDA
gi|128 DVRLYPKGVKTELTRDIFTDPIFSLNLTQIEYGPFTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|128 QPGYFGKDSFNYSWGNVETRPSIGSSKTITSPFFYGDK-STEPVQKLSFD-GQKVYRTIA

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Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYKSGTV---DSLDEIPPQ
gi|128 NTDVAAWPNGKVKVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFPTWTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKGNFLENG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VTPIHNLVNWGNSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|128 TTNLRLVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 VSNEKIYIDKIEFIPVQL
640 650

>>gi|155684761|gb|ABU27016.1| Sequence 50 from patent US (652 aa)
initn: 1025 initl: 457 opt: 1064 Z-score: 1247.6 bits: 242.0 E(): 1.4e-60
Smith-Waterman score: 1133; 34.983% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
60 70 80 90 100

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPT---NPALREEM
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRNPHSQGRI
110 120 130 140 150 160

Cry1Ac 140 150 160 170 180 190
RIQFNDMSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPFAVSKFEVLFVLPYQAANTHLLKDAQVFGEEWYSSDVA
170 180 190 200 210 220

Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRRELTLTVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVFNFRPREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIRSPHMLDILNSITIIYTD
gi|155 DVRLYPKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLOGIEFHPTL
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 QPGYFGKDSFNYSWGNVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYKSGTV---DSLDEIPPQ
gi|155 NTDVAAWPNGKVKVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFPTWTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKGNFLENG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

>>gi|40188401|gb|AAR75926.1| Sequence 50 from patent US (652 aa)
initn: 1025 initl: 457 opt: 1064 Z-score: 1247.6 bits: 242.0 E(): 1.4e-60
Smith-Waterman score: 1133; 34.983% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40188401|gb|AAR75926.1| Sequence 50 from patent US (652 aa)
initn: 1025 initl: 457 opt: 1064 Z-score: 1247.6 bits: 242.0 E(): 1.4e-60
Smith-Waterman score: 1133; 34.983% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
60 70 80 90 100

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPT---NPALREEM
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRNPHSQGRI
110 120 130 140 150 160

Regulatory Product Characterization Team

Cry1Ac 140 150 160 170 180 190
RIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac 200 210 220 230 240 250
SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
gi|401 EFYHRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNVPLE-NFDGSFRGSAQGIIEGSIKPHLMDILNSITITYTDA
gi|401 DVRLYPKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSIENSIKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGGQVYRTLS
gi|401 QPGYFKDGSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VPIHLNVNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40188404|gb|AAR75929.1| Sequence 56 from patent US (651 aa)
initn: 1027 initl: 445 opt: 1058 Z-score: 1240.6 bits: 240.7 E(): 3.5e-60
Smith-Waterman score: 1127; 34.820% identity (66.895% similar) in 583 aa overlap
(55-612:82-649)

Cry1Ac 30 40 50 60 70 80
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIIGWIFGPSQWDAF
gi|401 SSTEVLNDSVTKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWPSEDP--WKAF
60 70 80 90 100

Cry1Ac 90 100 110 120 130
LVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQ
gi|401 MAQVEVLIDKKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRNPHSQGRIREL
110 120 130 140 150 160

Cry1Ac 140 150 160 170 180 190
FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRY
gi|401 FSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSSEDVAEFY
170 180 190 200 210 220

Cry1Ac 200 210 220 230 240 250
NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSR
gi|401 HRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDIR
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300 310
TYPVRTVSQLTREIYTNVPLE-NFDGSFRGSAQGIIEGSIKPHLMDILNSITITYTDAHRG
gi|401 LYSKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSIENSIKPHLFDYLGQIEFHTRLQPG
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGGQVYRTLSST-
gi|401 YFGKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQNNN
gi|401 VAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPEPTD
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
gi|401 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEEKITQLPVVKA
470 480 490 500 510

Cry1Ac 490 500 510 520 530 540
NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTP
gi|401 YALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
520 530 540 550 560 570

Cry1Ac 550 560 570 580 590
IHLNVNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
gi|401 LRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
580 590 600 610 620 630



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370      380      390      400      410      420
Cry1Ac LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQNNN
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 VAAWPNGKVYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPETTD
      410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTRSVDFNTIDAEEKITQLPVVKA
      470      480      490      500      510

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490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 YALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      520      530      540      550      560      570

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550      560      570      580      590
Cry1Ac IHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSLGN-IVGVRNFSGT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 LRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
      580      590      600      610      620      630

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600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 EKIIYIDKIEFIPVQL
      640      650

```

>>gi|12810091|gb|AAE44006.1| Sequence 56 from patent US (651 aa)  
 initn: 1027 initl: 445 opt: 1058 Z-score: 1240.6 bits: 240.7 E(): 3.5e-60  
 Smith-Waterman score: 1127; 34.820% identity (66.895% similar) in 583 aa overlap  
 (55-612:82-649)

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30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGSPQWDAF
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWPSEDP--WKAF
      60      70      80      90      100

```

```

90      100      110      120      130
Cry1Ac LVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPT---NPALREEMRIQ
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 MAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRNPHSQGRIREL
      110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRY
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 FSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVGEWGYSSSDVAEYF
      170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTTLTVLDIVSLFPNYDSR
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 HRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFRFRREMTLTVLDLIVLFPFYDIR
      230      240      250      260      270      280

```

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260      270      280      290      300      310
Cry1Ac TYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGIIEGSIIRSPHMLDILNSITTYTDAHRG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 LYSKGVKTELTRDIFTDPIFSLNTLQEQYGTFFLSIENSIRKPHLFDYQLQGIIEFHTRLQPG
      290      300      310      320      330      340

```

```

320      330      340      350      360
Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 YFGKDSFNYSWNGYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD
      350      360      370      380      390      400

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370      380      390      400      410      420
Cry1Ac LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQNNN
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 VAAWPNGKVYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPETTD
      410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTRSVDFNTIDAEEKITQLPVVKA
      470      480      490      500      510

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490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 YALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      520      530      540      550      560      570

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550      560      570      580      590
Cry1Ac IHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSLGN-IVGVRNFSGT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 LRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
      580      590      600      610      620      630

```

```

600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 EKIIYIDKIEFIPVQL
      640      650

```

>>gi|40145965|gb|AAR61471.1| Sequence 48 from patent US (652 aa)  
 initn: 1012 initl: 444 opt: 1054 Z-score: 1235.9 bits: 239.8 E(): 6.5e-60  
 Smith-Waterman score: 1123; 34.983% identity (67.235% similar) in 586 aa overlap  
 (55-612:82-650)

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30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGSPQ---W
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIIN---PSDADPW
      60      70      80      90      100

```

```

80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRNPHSQGRIREL
      110      120      130      140      150      160

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350      360      370      380      390      400
Cry1Ac  370      380      390      400      410      420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQ
gi|155  NTDVAAWPngkVYLgVTKVDFsQYDDQK---NETSTQTYDSKRnNGHVsAQDSIDQLPPE
410      420      430      440      450      460

370      380      390      400      410      420
Cry1Ac  430      440      450      460      470      480
NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIASDSITQIPA
gi|155  TTDEPLEKAYsHQLNYAEcFLMQDRRGTI----PFFTWTHRsVDFFNtIDAEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  490      500      510      520      530
VKGNFLFNG-SVIsGPGFTGGDLVRLNssGNNIqNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155  VKAYALSSGAsIIEGPGFTGGNLLFLKESsNSIAK---FKVTLNSAALLQRyRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  540      550      560      570      580      590
VTPIHLNVNWGNssSIFsNTVPATATSLDNL--QSSDFGyFESANAFTSSLGN-IVGVRNF
gi|155  TTNLRLfVQNSnNDFLViyINKTMNKDDDLTYQTfDLATtNSNMGFsGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEyNLERAQKAVNALFTSTnQLGLKtNVDYHIDQVSNL
gi|155  VSNEKIYIDKIEFIpVQL
640      650

>>gi|155684768|gb|ABU27023.1| Sequence 64 from patent US (652 aa)
initn: 1012 initl: 444 opt: 1053 Z-score: 1234.7 bits: 239.6 E(): 7.5e-60
Smith-Waterman score: 1122; 34.983% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac  30      40      50      60      70
VEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAG---FVLGLVDIIWGIgFgPSQ---W
gi|155  SSTEVLdNSTVKDAVGTGISVVGQILgVVGVpFAGALtsfYQsFLNtIW---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac  80      90      100      110      120      130
DAFLVQIEQLINQRIEEFARNQAIsrLEGLsNLYQIYAESfREWEADPTN-PALREEMRI
gi|155  KAFMAQVEVLIDKKIEEYAKSkALAEQLQNNfEDYvNALNSWkKtPLSLRSKRsqDRI
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac  140      150      160      170      180      190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLsVLRDVsVfQRGWfDAATIN
gi|155  RELfSQAEShFRNSMpsFAVskFEVLfLPTyAQAAntHLLlLKDAQVfGEEngYssEDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  200      210      220      230      240      250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGpDSRDWIRYNQfRRELTlTVLDIVSLfPny
gi|155  EFYHRQLKLTQYTDHCvNwYVGLNGLRGsTYDAWkFNRFREEMTLTVLDLIVLFPFY

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230      240      250      260      270      280
Cry1Ac  260      270      280      290      300      310
DSRTYPIRTVSQLTREIYTNpVLE-NFDGSGFRGSAQIEGSIRsPHLMDILNsITTYTDA
gi|155  DVRLYPKGVKTELTRDIFTDPIfSLNtlQeYgPTfLSIENSIRKPHLFDyLQGIeFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  320      330      340      350      360
HRGEY-----YWSGHQIMASpVGFSGPEFTfPLYGTMGNAAPQRIVAQlGQGVYRTLS
gi|155  RPYGfGKDSFNyWsgNYVETRPSIGsSKTITsPFYgDK-STEPVQKLSFD-GQKVVRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  370      380      390      400      410      420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQ
gi|155  NTDVAAWPngkVYLgVTKVDFsQYDDQK---NETSTQTYDSKRnNGHVsAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  430      440      450      460      470      480
NNNVPPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIASDSITQIPA
gi|155  TTDEPLEKAYsHQLNYAEcFLMQDRRGTI----PFFTWTHRsVDFFNtIDAEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  490      500      510      520      530
VKGNFLFNG-SVIsGPGFTGGDLVRLNssGNNIqNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155  VKAYALSSGAsIIEGPGFTGGNLLFLKESsNSIAK---FKVTLNSAALLQRyRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  540      550      560      570      580      590
VTPIHLNVNWGNssSIFsNTVPATATSLDNL--QSSDFGyFESANAFTSSLGN-IVGVRNF
gi|155  TTNLRLfVQNSnNDFLViyINKTMNKDDDLTYQTfDLATtNSNMGFsGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEyNLERAQKAVNALFTSTnQLGLKtNVDYHIDQVSNL
gi|155  VSNEKIYIDKIEFIpVQL
640      650

>>gi|40188408|gb|AAR75933.1| Sequence 64 from patent US (652 aa)
initn: 1012 initl: 444 opt: 1053 Z-score: 1234.7 bits: 239.6 E(): 7.5e-60
Smith-Waterman score: 1122; 34.983% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac  30      40      50      60      70
VEVLGGERIETGYTPIDISLSLTQFLlSEfVPGAG---FVLGLVDIIWGIgFgPSQ---W
gi|401  SSTEVLdNSTVKDAVGTGISVVGQILgVVGVpFAGALtsfYQsFLNtIW---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac  80      90      100      110      120      130
DAFLVQIEQLINQRIEEFARNQAIsrLEGLsNLYQIYAESfREWEADPTN-PALREEMRI
gi|401  KAFMAQVEVLIDKKIEEYAKSkALAEQLQNNfEDYvNALNSWkKtPLSLRSKRsqDRI

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110      120      130      140      150      160
Cry1Ac  140      150      160      170      180      190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401  RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401  EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQGIIEGSIKPHLMDILNSITTYDA
gi|401  DVRLYPKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401  RPYGFKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401  NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATNNSMGFGSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401  VSNEKIYIDKIEFIPVQL
640      650

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>>gi|12810095|gb|AAE44010.1| Sequence 64 from patent US (652 aa)  
initn: 1012 initl: 444 opt: 1053 Z-score: 1234.7 bits: 239.6 E(): 7.5e-60

Smith-Waterman score: 1122; 34.983% identity (67.235% similar) in 586 aa overlap  
(55-612:82-650)

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30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
gi|128  SSTEVLNDSITVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac  DAFVLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|128  KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|128  RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|128  EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQGIIEGSIKPHLMDILNSITTYDA
gi|128  DVRLYPKGVKTELTRDIFTDPIFSLNTLQEYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|128  RPYGFKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|128  NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|128  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|128  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATNNSMGFGSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128  VSNEKIYIDKIEFIPVQL
640      650

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gi|155 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFFYGDK--STEPVQKLSFD--GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgtv---DSLDEIPpQ
370 380 390 400 410 420

gi|155 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRsvDFNNTIDAEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESsNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNwGSSIFsNTVPATATSLDNL--QSSDFGYFESANAFtSSLGN-IVGVRNF
540 550 560 570 580 590

gi|155 TTNLRlFVQNSNNDFlVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810086|gb|AAE44001.1| Sequence 46 from patent US (652 aa)
initn: 1013 initl: 445 opt: 1052 Z-score: 1233.5 bits: 239.4 E(): 8.7e-60
Smith-Waterman score: 1121; 34.812% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
30 40 50 60 70

gi|128 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQsFLNTIw---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIsrLEGLSNLYQIYAESFREWEADPT---NPALREEM
80 90 100 110 120 130

gi|128 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRNPHSQGRI
110 120 130 140 150 160

Cry1Ac RIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSvFGQRWGFDAATIN
140 150 160 170 180 190

gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|128 EfyHRKlKLTQQYTDHCVNwYNVGLNGLRGSTYDAWVKFNRRFRREMTLLVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTvsQLTREIYTNpVLE-NFDGSFRGSAQGIeGSIRsPHLMDILNSITiyTDA
260 270 280 290 300 310

gi|128 DIRLYSKGVKTELTRDIFTDPIFSLNTLQeYGTPLSLIENSIRKPHLFDYLQGIeFhTRL
290 300 310 320 330 340

Cry1Ac HRGEY----YWSGHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQLGQGVYRTLS
320 330 340 350 360

gi|128 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFFYGDK--STEPVQKLSFD--GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgtv---DSLDEIPpQ
370 380 390 400 410 420

gi|128 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPRQGFsHRLSHVSMFRSGFSNssVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRsvDFNNTIDAEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNssGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESsNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNwGSSIFsNTVPATATSLDNL--QSSDFGYFESANAFtSSLGN-IVGVRNF
540 550 560 570 580 590

gi|128 TTNLRlFVQNSNNDFlVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|128 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40145963|gb|AAR61470.1| Sequence 46 from patent US (652 aa)
initn: 1013 initl: 445 opt: 1052 Z-score: 1233.5 bits: 239.4 E(): 8.7e-60
Smith-Waterman score: 1121; 34.812% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
30 40 50 60 70

gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQsFLNTIw---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIsrLEGLSNLYQIYAESFREWEADPT---NPALREEM
80 90 100 110 120 130



Regulatory Product Characterization Team

Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL

>>gi|12810089|gb|AAE44004.1| Sequence 52 from patent US (651 aa)
initn: 1014 initl: 432 opt: 1048 Z-score: 1228.8 bits: 238.5 E(): 1.6e-59
Smith-Waterman score: 1117; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-649)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWPSEDP--WKAF

Cry1Ac LVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRIQ--
gi|128 MAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRIREL

Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRY
gi|128 FSQAESHFRNSMPSFAVSKFEVLFPLTYQAANTHLLLLKDAQVFGEEWGYSSSEDVAEYF

Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSR
gi|128 HRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWKFNFRREMTLVLDLIVLFPFYDIR

Cry1Ac TYPVRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIIRPHLMDILNSITTYDAHRG
gi|128 LYSKGVKTELTRDIFTDPIFSLNTLQEQYPTFLSIENSIRKPHLFDYLGQIEFHTRLQPG

Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQGLGQGVYRTLSST-
gi|128 YFGKDSFNYWSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD

Cry1Ac LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQVTV---DSLDEIPPQNNN
gi|128 VAAWPNKGVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPETTD

430 440 450 460 470 480

Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
gi|128 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTSRVDFVNTIDAEEKITQLPVVKA

Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPTSTSTRYRVRVRYASVTP
gi|128 YALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN

Cry1Ac IHLNVNWNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
gi|128 LRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN

Cry1Ac AGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|128 EKIIYIDKIEFIPVQL

>>gi|40188402|gb|AAR75927.1| Sequence 52 from patent US (651 aa)
initn: 1014 initl: 432 opt: 1048 Z-score: 1228.8 bits: 238.5 E(): 1.6e-59
Smith-Waterman score: 1117; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-649)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWPSEDP--WKAF

Cry1Ac LVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRIQ--
gi|401 MAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRIREL

Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRY
gi|401 FSQAESHFRNSMPSFAVSKFEVLFPLTYQAANTHLLLLKDAQVFGEEWGYSSSEDVAEYF

Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSR
gi|401 HRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWKFNFRREMTLVLDLIVLFPFYDIR

Cry1Ac TYPVRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIIRPHLMDILNSITTYDAHRG
gi|401 LYSKGVKTELTRDIFTDPIFSLNTLQEQYPTFLSIENSIRKPHLFDYLGQIEFHTRLQPG

320 330 340 350 360

Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-

gi|401 YFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD
350 360 370 380 390 400

Cry1Ac LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGV---DSLDEIPPQNNN

gi|401 VAAWPNKGYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNHVSQAQSDIDQLPETTD
410 420 430 440 450 460

Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG

gi|401 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPVVKA
470 480 490 500 510

Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP

gi|401 YALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
520 530 540 550 560 570

Cry1Ac IHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT

gi|401 LRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
580 590 600 610 620 630

Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY

gi|401 EKIIYDKIEFIPVQL
640 650

>>gi|155684762|gb|ABU27017.1| Sequence 52 from patent US (651 aa)
initn: 1014 initl: 432 opt: 1048 Z-score: 1228.8 bits: 238.5 E(): 1.6e-59
Smith-Waterman score: 1117; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-649)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF

gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFINTIWPSEDP--WKAF
60 70 80 90 100

Cry1Ac LVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRIQ--

gi|155 MAQVEVLIDKKEIEYAKSKALAELOGLQNNFEDYVNALSNWKKTPLSLRSKRSQDRIREL
110 120 130 140 150 160

Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRY

gi|155 FSOAESHRFNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWYSSDEDVAEYF
170 180 190 200 210 220

200 210 220 230 240 250

Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFRELTLTVLDIVSLFPNYDSR

gi|155 HRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFYDIR
230 240 250 260 270 280

Cry1Ac TYPVRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIIRSPHMLDILNSITTYDAHRG

gi|155 LYSKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLQGIIEFHRLQPG
290 300 310 320 330 340

Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-

gi|155 YFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD
350 360 370 380 390 400

Cry1Ac LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGV---DSLDEIPPQNNN

gi|155 VAAWPNKGYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNHVSQAQSDIDQLPETTD
410 420 430 440 450 460

Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG

gi|155 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPVVKA
470 480 490 500 510

Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP

gi|155 YALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
520 530 540 550 560 570

Cry1Ac IHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT

gi|155 LRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
580 590 600 610 620 630

Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY

gi|155 EKIIYDKIEFIPVQL
640 650

>>gi|40145969|gb|AAR61473.1| Sequence 52 from patent US (651 aa)
initn: 1014 initl: 432 opt: 1048 Z-score: 1228.8 bits: 238.5 E(): 1.6e-59
Smith-Waterman score: 1117; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-649)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQWDAF

gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFINTIWPSEDP--WKAF
60 70 80 90 100

90 100 110 120 130





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Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
. . . . .
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

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Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
. . . . .
gi|401 NTDVAAWPNGKVVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

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Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
. . . . .
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

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Cry1Ac 490 500 510 520 530
VKG NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
. . . . .
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

```

```

Cry1Ac 540 550 560 570 580 590
VTP IHLNWNWGNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . .
gi|401 TTNLRLVFNQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

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Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . .
gi|401 VSNEKIYIDKIEFIPVQL
640 650

```

>>gi|155684741|gb|ABU26996.1| Sequence 10 from patent US (652 aa)  
 initn: 1003 initl: 435 opt: 1045 Z-score: 1225.2 bits: 237.8 E(): 2.5e-59  
 Smith-Waterman score: 1114; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
. . . . .
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTI W---PSDADPW
60 70 80 90 100

```

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Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIE EFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
. . . . .
gi|155 KAFMAQVEVLIDKKEIEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSDRI
110 120 130 140 150 160

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Cry1Ac 140 150 160 170 180 190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
. . . . .
gi|155 RELFSQAESHFRNSMPSFAVSKFEVFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

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Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
. . . . .
gi|155 EFNQRQLKLTQQYSDHCVNWYNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

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Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGIIEGSIRSPHMDILNSITITYTDA
. . . . .
gi|155 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEQYGPFTFLSIENSIKPKHFLDYLOGIEFHPTRL
290 300 310 320 330 340

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```

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
. . . . .
gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

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Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
. . . . .
gi|155 NTDVAAWPNGKVVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

```

```

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
. . . . .
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

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Cry1Ac 490 500 510 520 530
VKG NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
. . . . .
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

```

```

Cry1Ac 540 550 560 570 580 590
VTP IHLNWNWGNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . .
gi|155 TTNLRLVFNQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

```

```

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . .
gi|155 VSNEKIYIDKIEFIPVQL
640 650

```

>>gi|155684769|gb|ABU27024.1| Sequence 66 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1045 Z-score: 1225.2 bits: 237.8 E(): 2.5e-59  
 Smith-Waterman score: 1114; 34.983% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
. . . . .
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTI W---PSDADPW
60 70 80 90 100

```



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540      550      560      570      580      590
Cry1Ac VPIIHLNVNWGNSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 TTNLRFLVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

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600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 VSNEKIYIDKIEFIPVQL
640      650

```

>>gi|40188381|gb|AAR75906.1| Sequence 10 from patent US (652 aa)  
 initn: 1003 init1: 435 opt: 1045 Z-score: 1225.2 bits: 237.8 E(): 2.5e-59  
 Smith-Waterman score: 1114; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW
60      70      80      90      100

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80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 EFYNRQLKLTQQYSDHCNVNWNVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

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260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLN-NFDGSRFRGSAQIEGSIIRSPHLMIDLNSITIIYTD
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

```

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350      360      370      380      390      400
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
350      360      370      380      390      400

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370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSQGTV---DSLDEIPPQ
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 NTDVAAWPNKGVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNGHVSQAQSDIDQLPPE
410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWHRSDVFFNTIDAEEKITQLPV
470      480      490      500      510

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490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VKAYALSSGASIEEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

```

>>gi|12810096|gb|AAE44011.1| Sequence 66 from patent US (652 aa)  
 initn: 1000 init1: 432 opt: 1045 Z-score: 1225.2 bits: 237.8 E(): 2.5e-59  
 Smith-Waterman score: 1114; 34.983% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

530      540      550      560      570      580      590
Cry1Ac VPIIHLNVNWGNSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTNLRFLVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VSNEKIYIDKIEFIPVQL
640      650

```

```

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW
60      70      80      90      100

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80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

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260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFRGSAQIEGSIIRSPHLMIDLNSITIIYTD
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128 DIRLYSKGVKTELTRDIFTDPIFLLNTLQEQYGTFLSIENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

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          320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGGQVYRRLS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
          350      360      370      380      390      400

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          370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NTDVAAWPNKGKLVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
          410      420      430      440      450      460

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          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSDVFFNTIDA EKITQLPV
          470      480      490      500      510

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          490      500      510      520      530
Cry1Ac VKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

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          540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

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          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|155684766|gb|ABU27021.1| Sequence 60 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1044 Z-score: 1224.1 bits: 237.6 E(): 2.9e-59  
 Smith-Waterman score: 1113; 34.812% identity (67.235% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPFAGALTSFYQSFLNTIWIW---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFRWEADPTN-PALREEMRI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR
          110      120      130      140      150      160

```

```

          140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFVFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDA
          170      180      190      200      210      220

```

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          200      210      220      230      240      250
Cry1Ac SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVLSLFPNY
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 EPHYRKLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAVVKFNRFRREMTLTLVLDIVLFFPFY
          230      240      250      260      270      280

```

```

          260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIIRSPHLMIDLNSITIYTDA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DIRLYSKGVKTELTRDIFTDPIFTLNTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
          290      300      310      320      330      340

```

```

          320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGGQVYRRLS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
          350      360      370      380      390      400

```

```

          370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NTDVAAWPNKGKLVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
          410      420      430      440      450      460

```

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          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSDVFFNTIDA EKITQLPV
          470      480      490      500      510

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

```

```

          540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|40188406|gb|AAR75931.1| Sequence 60 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1044 Z-score: 1224.1 bits: 237.6 E(): 2.9e-59  
 Smith-Waterman score: 1113; 34.812% identity (67.235% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPFAGALTSFYQSFLNTIWIW---PSDADPW
          60      70      80      90      100

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290      300      310      320      330      340
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155  QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|155  NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLHSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|155  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTWTRSVDFNTIDAEDITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155  VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VPIHLNVNWNWSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155  TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155  VSNEKIYIDKIEFIPVQL
640      650

>>gi|40188389|gb|AAR75914.1| Sequence 26 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIHWGIFGPSQ---W
gi|401  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIWIW---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401  KAFMAQVEVLIDKKEIYAKSKALAEQLQGNFEDYVNALNSWKKTPLSRSKRSQDRI
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQRWGFDAATIN
gi|401  RELFSQAESHFRNSMPSFAVSKFEVLFVLPYTAQAANTHLLLLKDAQVFGEEWGYSSDVA

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170      180      190      200      210      220
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERLVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|401  EFYHRQLKLTQQYTDHCVNWNVGNLNLGRGSTDYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQGIIEGSIIRSPHMLDILNSITTYTDA
gi|401  DIRLYSKGVKTELTRDIFTDPIFALNTLDEYGTFLSIENSIKPKHFLDYQLQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401  QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|401  NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLHSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTWTRSVDFNTIDAEDITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401  VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VPIHLNVNWNWSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401  TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401  VSNEKIYIDKIEFIPVQL
640      650

>>gi|40145947|gb|AAR61460.1| Sequence 26 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIHWGIFGPSQ---W
gi|401  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIWIW---PSDADPW
60      70      80      90      100

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60      70      80      90      100
Cry1Ac 80      90      100      110      120      130
DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110     120     130     140     150     160

140     150     160     170     180     190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFREMTLTLVLDLIVLFPFY
230     240     250     260     270     280

260     270     280     290     300     310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQIEGSIRSPHLMIDILNSITIYTDA
gi|401 DIRLYSGVKTELTRDIFTDPIFALNTLDEYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290     300     310     320     330     340

320     330     340     350     360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350     360     370     380     390     400

370     380     390     400     410     420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLP SAVA YRKS GTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410     420     430     440     450     460

430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFFTWTTHRSVDFNTIDA EKITQLPV
470     480     490     500     510

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALS SGAIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRIRYAS
520     530     540     550     560     570

540     550     560     570     580     590
Cry1Ac VTIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAF TSSLGN-IVGVRNF
gi|401 TTNLRLFQNSNNDPLVIYINKTMNKDDDLTYQTFDLAT TSNMFGSGDKNELIIGAESF
580     590     600     610     620     630

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. . . . .

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gi|401 VSNEKIYIDKIEFIPVQL
640     650

>>gi|40188398|gb|AAR75923.1| Sequence 44 from patent US (652 aa)
initn: 1000 init1: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLDNSTVKDAVGTGISVVGQLLGVVGVFPFAGALTSFYQSFLNTIW---PSDADPW
60      70      80      90      100

80      90      100     110     120     130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR
110     120     130     140     150     160

140     150     160     170     180     190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFREMTLTLVLDLIVLFPFY
230     240     250     260     270     280

260     270     280     290     300     310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQIEGSIRSPHLMIDILNSITIYTDA
gi|401 DIRLYSGVKTELTRDIFTDPIFALNTLDEYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290     300     310     320     330     340

320     330     340     350     360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350     360     370     380     390     400

430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFFTWTTHRSVDFNTIDA EKITQLPV
470     480     490     500     510

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALS SGAIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRIRYAS
520     530     540     550     560     570

540     550     560     570     580     590
Cry1Ac VTIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAF TSSLGN-IVGVRNF
gi|401 TTNLRLFQNSNNDPLVIYINKTMNKDDDLTYQTFDLAT TSNMFGSGDKNELIIGAESF
580     590     600     610     620     630

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. . . . .

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gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|401 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40145961|gb|AAR61469.1| Sequence 44 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGIERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGFPGSQ---W

gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI

gi|401 KAFMAQVEVLIDKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSQGR1
110 120 130 140 150 160

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAATIN

gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGFEEWYSSSEDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY

gi|401 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

260 270 280 290 300 310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSIKPHLMDILNSITITYTDA

gi|401 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTLSIENSIRKPHLFDYQGIIEFHTRL
290 300 310 320 330 340

320 330 340 350 360
Cry1Ac HRGEY-----YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYRTLS

gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

370 380 390 400 410 420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSNLPASVYRKSQGTV---DSLDEIPPQ

gi|401 NTDVAAPWNGKVVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

430 440 450 460 470 480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRSDVFFNTIDAEEKITQLPV
470 480 490 500 510

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|401 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|155684749|gb|ABU27004.1| Sequence 26 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGIERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGFPGSQ---W

gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI

gi|155 KAFMAQVEVLIDKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDR1
110 120 130 140 150 160

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAATIN

gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGFEEWYSSSEDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY

gi|155 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

260 270 280 290 300 310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSIKPHLMDILNSITITYTDA

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gi|155 DIRLYSKGVKTELTRDIFTDPIFALNLTLEDEYGPTFLSIENSIRKPHLFDYLQGIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
370 380 390 400 410 420

gi|155 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIHNLNWNWGNSSIFSNTV PATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|155 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810085|gb|AAE44000.1| Sequence 44 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTI W---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|128 KAFMAQVEVLIDDKIEEYAKSALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR I
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

gi|128 RELFSQAESHFRNSMPFSAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|128 EBYHRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAVVKFNFRFREMRTLVLVDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIRSPHMDILNSITIYTDA
260 270 280 290 300 310

gi|128 DIRLYSKGVKTELTRDIFTDPIFSLNLTLEQYGTFLSIENSIRKPHLFDYLQGIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|128 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
370 380 390 400 410 420

gi|128 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIHNLNWNWGNSSIFSNTV PATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|128 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|128 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810076|gb|AAE43991.1| Sequence 26 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1043 Z-score: 1222.9 bits: 237.4 E(): 3.4e-59
Smith-Waterman score: 1112; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70



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gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNMGNSISFNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|401 TTNLRLRFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|155684778|gb|ABU27033.1| Sequence 111 from patent U (652 aa)
initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
30 40 50 60 70
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVLSPFNY
200 210 220 230 240 250
gi|155 EFYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDDIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLN-NFDGSRFGSAQIEGSIRSPHMLDILNSITIIYTD
260 270 280 290 300 310
gi|155 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIEENSIRKPHFLDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360
gi|155 QPGYFGKDSFNYSWGNVYETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINQQLSVLDGTEFAYGTSSNLPASAVYRKSQGV---DSLDEIPQ
370 380 390 400 410 420

gi|155 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPA
430 440 450 460 470 480

gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWHRSDVFFNTIDAEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVLSGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRVRYAS
490 500 510 520 530

gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNMGNSISFNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590
gi|155 TTNLRLRFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650
gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40146001|gb|AAR61489.1| Sequence 111 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
30 40 50 60 70
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVLSPFNY
200 210 220 230 240 250
gi|401 EFYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDDIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLN-NFDGSRFGSAQIEGSIRSPHMLDILNSITIIYTD
260 270 280 290 300 310

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: : : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 DIRLSKGVKTELTRDIFTDPIFSLNLTLEQYGTFLSLIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYR TLS
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 NTDVAAWPNGKVVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVFFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANFTSSLGN-IVGVRNF
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40145979|gb|AAR61478.1| Sequence 62 from patent US (652 aa)
initn: 1001 initl: 438 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.983% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTI W---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSQGR I
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN

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: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 RELFSQAESHFRNSMPFSAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 EPHYRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAVVKFNRFRREMTTLVLDIVLFPF Y
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIRSPHMDILNSITIIYTD A
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 DVRLYPKGVKTELTRDIFDPIFAVNTLWEYGTFLSLIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYR TLS
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 RPYGFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 NTDVAAWPNGKVVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVFFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANFTSSLGN-IVGVRNF
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810105|gb|AAE44020.1| Sequence 111 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W

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      :: :: : .... :: ... :
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLLNTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIKPHLMDILNSITITDPA
      : : : . . . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|128 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTFLSIENSIRKPHLFDYLGIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . : : . . . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NTDVAAWPNGKVVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTRSVDFNFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
      : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRVRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTNLRLFVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650

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Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . : : : : : :
gi|128 VSNEKIYIDKIEFIPVQL
      640      650

>>gi|34423484|gb|AAQ68937.1| Sequence 2 from patent US 5 (652 aa)
      initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLLNTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIKPHLMDILNSITITDPA
      : : : . . . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|344 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTFLSIENSIRKPHLFDYLGIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIKPHLMDILNSITITDPA
      : : : . . . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|344 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTFLSIENSIRKPHLFDYLGIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . : : . . . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|344 NTDVAAWPNGKVVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTRSVDFNFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
      : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRVRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344 TTNLRLFVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      490      500      510      520      530

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Regulatory Product Characterization Team

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|344 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|344 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|344 VSNEKIYIDKIEFIPVQL

>>gi|155684754|gb|ABU27009.1| Sequence 36 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGI FGP SQ---W
gi|155 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSF LNTI W---PSDADPW

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNFRREMTLVLDLIVLFPFY

260 270 280 290 300 310
Cry1Ac DSRTYPIRITVSQLTRREIYTNVPLENFDGSRGSA-QGIEGIRS PHLMDILNSITITYTDA
gi|155 DIRLYSKGVKTELTRDIFTDPIFSLVNLVMVYGP TPLSIENSIRKPHLFDYLOGIEFHTRL

320 330 340 350 360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQGVYRTLS
gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

370 380 390 400 410 420

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPQP
gi|155 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVS AQDSIDQLPPE

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSFGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNVAECFLMQDRRTI-----PFFTWT HRSVDFNTIDA EKITQLPV

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL

>>gi|40145950|gb|AAR61462.1| Sequence 30 from patent US (652 aa)
initn: 998 initl: 430 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.983% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGI FGP SQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSF LNTI W---PSDADPW

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNFRREMTLVLDLIVLFPFY

260 270 280 290 300 310

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFRGSAQGIIEGSRSPHLMIDLNSITTYTDA

gi|401 DIRLYSGVKTELTRDIFLNTLQEYGPFLSISIENSIKRPFLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

gi|401 QPGYFGKDSFNWYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ

gi|401 NTDVAAWPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEDITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTPHILNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|401 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL

>>gi|40188407|gb|AAR75932.1| Sequence 62 from patent US (652 aa)
initn: 1001 initl: 438 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.983% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIHWGIFGSPQ---W

gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIIV---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI

gi|401 KAFMAQVEVLIDKKIEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSRKRSGRRI

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATIN

gi|401 RBLFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEWYSSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY

gi|401 EPYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSRSPHLMIDLNSITTYTDA

gi|401 DVRLYPKGVKTELTRDIFAVNTLWEYGPFLSISIENSIKRPFLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

gi|401 RPYGFGKDSFNWYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ

gi|401 NTDVAAWPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEDITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTPHILNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|401 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL

>>gi|12810081|gb|AAE43996.1| Sequence 36 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL





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      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGIIEGSIIRSPHLMIDLNSITIIYTD
gi|155 DIRLYSKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSIEINSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

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      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 QPGYFGKDSFNYSWGNVYETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

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      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|155 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

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      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRVDFNTIDA EKITQLPV
      470      480      490      500      510

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      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac VTIHLNWNWGNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

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      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|155684767|gb|ABU27022.1| Sequence 62 from patent US (652 aa)  
 initn: 1001 initl: 438 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59  
 Smith-Waterman score: 1111; 34.983% identity (66.894% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGSPQ---W
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIW---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac DAFVLQIEQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRKRKRSQGR
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWYSSSEDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCVNWYVNLNGLRGSTYDAVVKFNRFRREMTLVLVDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGIIEGSIIRSPHLMIDLNSITIIYTD
gi|155 DVRLYPKGVKTELTRDIDTDPIFAVNTLWEYGTFLSIEINSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

```

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      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 RPYGFGKDSFNYSWGNVYETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|155 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRVDFNTIDA EKITQLPV
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac VTIHLNWNWGNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

```

```

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|40145955|gb|AAR61465.1| Sequence 36 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59  
 Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSA-QGIEGSIRSPHLMIDLNSITTYTDA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 DIRLYSKGVKTELTRDIFTDPIFSLVNLVMVYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

```

```

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNNTIDAEEKITQLPVP
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 TTNLRLFLVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

```

```

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|40188394|gb|AAR75919.1| Sequence 36 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59  
 Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSA-QGIEGSIRSPHLMIDLNSITTYTDA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 DIRLYSKGVKTELTRDIFTDPIFSLVNLVMVYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

```

```

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNNTIDAEEKITQLPVP
      470      480      490      500      510

```









```

230      240      250      260      270      280
Cry1Ac 260      270      280      290      300      310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQIEGSIKPHLMDILNSITIIYTD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 DIRLYSKGVKTELTRDIFTDPIFSLNLTQEQYGTPLFSIENSIRKPHLFDYLQIEFHTRL
290      300      310      320      330      340
Cry1Ac 320      330      340      350      360
HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400
Cry1Ac 370      380      390      400      410      420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510
Cry1Ac 490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570
Cry1Ac 540      550      560      570      580      590
VTPIHNLVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFGSGDKNELIIGAESF
580      590      600      610      620      630
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 VSNEKIYIDKIEFIPVQL
640      650
>>gi|155684751|gb|ABU27006.1| Sequence 30 from patent US (652 aa)
initn: 998 init1: 430 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59
Smith-Waterman score: 1111; 34.983% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGFQPSQ---W
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SSTEVLNDSNVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
60      70      80      90      100
Cry1Ac 80      90      100      110      120      130
DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KAFMAQVEVLIDDKIEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI

```

```

110      120      130      140      150      160
Cry1Ac 140      150      160      170      180      190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQQRWGFDAATIN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RFLFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170      180      190      200      210      220
Cry1Ac 200      210      220      230      240      250
SRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFRRELTTLVLDIVSLFPNY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 EPHYRRLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280
Cry1Ac 260      270      280      290      300      310
DSRTYPIRTVSQLTREIYTNPV-LENFDGSGFRGSAQIEGSIKPHLMDILNSITIIYTD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DIRLYSKGVKTELTRDIFTDPIFLLNLTQEQYGTPLFSIENSIRKPHLFDYLQIEFHTRL
290      300      310      320      330      340
Cry1Ac 320      330      340      350      360
HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400
Cry1Ac 370      380      390      400      410      420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460
Cry1Ac 430      440      450      460      470      480
NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510
Cry1Ac 490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570
Cry1Ac 540      550      560      570      580      590
VTPIHNLVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFGSGDKNELIIGAESF
580      590      600      610      620      630
Cry1Ac 600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VSNEKIYIDKIEFIPVQL
640      650
>>gi|12810078|gb|AAE43993.1| Sequence 30 from patent US (652 aa)
initn: 998 init1: 430 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59

```



Regulatory Product Characterization Team

```

... : ..... : ... :... :... : : .....
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVFFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      : : : : ..... : : : : ..... : : : : .....
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      : : : : ..... : : : : ..... : : : : .....
gi|128 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . : : : : :
gi|128 VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|114210119|emb|CAL40964.1| unnamed protein product [ (652 aa)  
 initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59  
 Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 RELFSQAESHFRNSMPFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 EFYHRQLKLTQYQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTLVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPYLE-NFDGSRFRGSAQIEGSIIRSPHLMIDILNSITITYDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 DIRLSKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIEANSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

```

```

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

```

```

. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 PQGYFGKDSFNWYSGMYVETRPSIGSSKITITSPFFYGDK-STPEVQKLSFD-GQKIVRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTV--DSLDEIPPO
      : : : : ..... : : : : ..... : : : : .....
gi|114 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      : : : : ..... : : : : ..... : : : : .....
gi|114 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVFFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      : : : : ..... : : : : ..... : : : : .....
gi|114 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

>>gi|40188413|gb|AAR75938.1| Sequence 98 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1042 Z-score: 1221.7 bits: 237.2 E(): 4e-59  
 Smith-Waterman score: 1111; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      : : : : ..... : : : : ..... : : : : .....
gi|114 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . : : : : :
gi|114 VSNEKIYIDKIEFIPVQL
      640      650

```

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY

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Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEEKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VPIIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|128 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 VSNEKIYIDKIEFIPVQL

>>gi|40188390|gb|AAR75915.1| Sequence 28 from patent US (652 aa)
initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.642% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIHWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRSAQIEGSIIRSPHMLDILNSITTYTDA
gi|401 DTRRFRKGVKTELTRDIFTDPIFSLNLTQYEGTFLSIIENSIRKPHLFDYLGIEFHTRL

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRSAQIEGSIIRSPHMLDILNSITTYTDA
gi|401 DTRRFRKGVKTELTRDIFTDPIFSLNLTQYEGTFLSIIENSIRKPHLFDYLGIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKITISPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|401 NTDVAAWPNKQVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEEKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VPIIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL

>>gi|40145949|gb|AAR61461.1| Sequence 28 from patent US (652 aa)
initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.642% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIHWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRSAQIEGSIIRSPHMLDILNSITTYTDA
gi|401 DTRRFRKGVKTELTRDIFTDPIFSLNLTQYEGTFLSIIENSIRKPHLFDYLGIEFHTRL



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>>gi|155684750|gb|ABU27005.1| Sequence 28 from patent US (652 aa)
initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.642% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIW---PSDADPW

Cry1Ac DAFVLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFRRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRSAQGIIEGSIKRSRPHLMDILNSITITDA
gi|155 DTRRRKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 QPGYFGKDSFNWWSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|155 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE

Cry1Ac NNNVPPRQGFHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWHRSVDFNFNTIDAEEKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

540 550 560 570 580 590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630
600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810069|gb|AAE43984.1| Sequence 12 from patent US (652 aa)
initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIW---PSDADPW

Cry1Ac DAFVLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|128 EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNRFRRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRSAQGIIEGSIKRSRPHLMDILNSITITDA
gi|128 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|128 QPGYFGKDSFNWWSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|128 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE

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          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      . . . . .
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDAELITQLPV
          470      480      490      500      510

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . .
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

```

```

          540      550      560      570      580      590
Cry1Ac VTPIHNLNVWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . .
gi|128 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . .
gi|128 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|40145952|gb|AAR61463.1| Sequence 32 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERLETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIVGIFGPSQ---W
      . . . . .
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi|401 KAFMAQVEVLIDKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSDRI
          110      120      130      140      150      160

```

```

          140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAAATIN
      . . . . .
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWYSSSEDVA
          170      180      190      200      210      220

```

```

          200      210      220      230      240      250
Cry1Ac SKRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi|401 EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVFNFRREMTLTVLDLIVLFPFY
          230      240      250      260      270      280

```

```

          260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFRGSAQGIIEGSIIRSPHMLDILNSITITYDA
      . . . . .
gi|401 DIRLYSKGVKTELTRDIFTDPIFILNLTQIEYGPFTLSIENSIRKPHLFDYLGQIEFHTRL
          290      300      310      320      330      340

```

```

          320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASVGVGSGPEFTFPLYGTMGNAAPQQRIVAQGLGGVYRTLS
      . . . . .
gi|401 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
          350      360      370      380      390      400

```

```

          370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPQP
      . . . . .
gi|401 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNHVSQAQSDIDQLPPE
          410      420      430      440      450      460

```

```

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      . . . . .
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDAELITQLPV
          470      480      490      500      510

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . .
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

```

```

          540      550      560      570      580      590
Cry1Ac VTPIHNLNVWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . .
gi|401 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . .
gi|401 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|12810073|gb|AAE43988.1| Sequence 20 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERLETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIVGIFGPSQ---W
      . . . . .
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi|128 KAFMAQVEVLIDKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSDRI
          110      120      130      140      150      160

```

```

          140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAAATIN
      . . . . .
gi|128 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWYSSSEDVA
          170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  EFYHRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQTLTREIYTNPVLE-NFDGSFRGSAQGIIEGSIIRPHLMDILNSITIIYTD
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  DIRLYSKGVKTELTRDIFTDPIFAVNTLWEYGTFLSIEINSIRKPHLFDYLGIEFHTRL
      290      300      310      320      330      340

```

```

      320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYRTLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGV---DSLDEIPPQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac  VPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

```

```

      600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|155684752|gb|ABU27007.1| Sequence 32 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFFGSPQ---W
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSEDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  EFYHRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQTLTREIYTNPV-LENFDGSFRGSAQGIIEGSIIRPHLMDILNSITIIYTD
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  DIRLYSKGVKTELTRDIFTDPIFILNTLQYEGTFLSIEINSIRKPHLFDYLGIEFHTRL
      290      300      310      320      330      340

```

```

      320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYRTLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGV---DSLDEIPPQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : ~ : : :
gi|155  NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . . : : : : ~ : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|155  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac  VPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|155  TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

```

```

      600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|155  VSNEKIYIDKIEFIPVQL
      640      650

```

Regulatory Product Characterization Team

>>gi|155684770|gb|ABU27025.1| Sequence 68 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW
60 70 80 90 100

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230 240 250 260 270 280

260 270 280 290 300 310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQIEGSIKPHLMDILNSITIIYTD
gi|155 DIRLSKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

320 330 340 350 360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 RPYGFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

370 380 390 400 410 420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|155 NTDVAAWPNKGYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQSDIDQLPPE
410 420 430 440 450 460

430 440 450 460 470 480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFTWTHRSVDFNFNTIDAEKITQLPVA
470 480 490 500 510

490 500 510 520 530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRVVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

540 550 560 570 580 590
Cry1Ac VTFPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSSSLGN-IVGVRNF
gi|155 TTNLRLVFNQSNNDPLVIYINKTMNKDDDLTYQTFPLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

600 610 620 630 640 650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40188410|gb|AAR75935.1| Sequence 68 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30 40 50 60 70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW
60 70 80 90 100

80 90 100 110 120 130
Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230 240 250 260 270 280

260 270 280 290 300 310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQIEGSIKPHLMDILNSITIIYTD
gi|401 DIRLSKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

320 330 340 350 360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 RPYGFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

370 380 390 400 410 420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQSDIDQLPPE
410 420 430 440 450 460

```

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEKITQLPV
          470      480      490      500      510

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

```

```

          540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|401 TTNLRLFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|40145934|gb|AAR61453.1| Sequence 12 from patent US (652 aa)  
 initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac DAFVLQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
          110      120      130      140      150      160

```

```

          140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPITYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
          170      180      190      200      210      220

```

```

          200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQYQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
          230      240      250      260      270      280

```

```

          260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLN-NFDGSRFRGSAQIEGSIIRSPHLMIDILNSITITYTDA
gi|401 DIRLSKGVKTBELTRDIFTDPISLNTLQEQYGPFTLSIENSIRKPHLFDYLGQIEFHRTL
          290      300      310      320      330      340

```

```

          320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFFYGDK-STEPVQKLSFD-GQKVYRTIA
          350      360      370      380      390      400

```

```

          370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVTKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
          410      420      430      440      450      460

```

```

          430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEKITQLPV
          470      480      490      500      510

```

```

          490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520      530      540      550      560      570

```

```

          540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|401 TTNLRLFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
          580      590      600      610      620      630

```

```

          600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
          640      650

```

>>gi|40188392|gb|AAR75917.1| Sequence 32 from patent US (652 aa)  
 initn: 1000 init1: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac DAFVLQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
          110      120      130      140      150      160

```

```

          140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPITYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
          170      180      190      200      210      220

```



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>>gi|12810077|gb|AAE43992.1| Sequence 28 from patent US (652 aa)
initn: 999 initl: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.642% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWIGIFGPSQ---W
gi|128 SSTEVLNDSVTKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFINTIWIW---PSDADPW

Cry1Ac DAFVLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|128 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|128 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQTLREIYTNPVLE-NFDGSRGSAQGIIEGSIKPHLMDILNSITTYTDA
gi|128 DTRRFRKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSIENSIRKPHLFDYQLGIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASVGVGSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|128 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|128 NTDVAAPNGKVYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRYGIEVP IHPFSTSTRYRVRVRYAS
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTPIHNLVNWGNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|128 TTNLRLFLVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 VSNEKIYIDKIEFIPVQL

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWIGIFGPSQ---W
gi|155 SSTEVLNDSVTKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFINTIWIW---PSDADPW

>>gi|155684742|gb|ABU26997.1| Sequence 12 from patent US (652 aa)
initn: 999 initl: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWIGIFGPSQ---W
gi|155 SSTEVLNDSVTKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFINTIWIW---PSDADPW

Cry1Ac DAFVLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|155 EFYTRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQTLREIYTNPVLE-NFDGSRGSAQGIIEGSIKPHLMDILNSITTYTDA
gi|155 DIRLSYKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSIENSIRKPHLFDYQLGIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASVGVGSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|155 NTDVAAPNGKVYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE

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      410      420      430      440      450      460
Cry1Ac      430      440      450      460      470      480
NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEKITQLPV
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac VPIIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIIGAESF
      580      590      600      610      620      630

```

```

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|40188386|gb|AAR75911.1| Sequence 20 from patent US (652 aa)  
 initn: 1000 init1: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGFSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
      170      180      190      200      210      220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EFYHRQLKLTQYTDHCVNWYVNLNGLRGSYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGGIEGSIIRPHLMDILNSITITYTDA
gi|401 DIRLYSKGVKTELTRDIFTDPIFAVNTLWEYGPTPLSISIENKIRKPHLFDYLGQIEFHTRL

```

```

      290      300      310      320      330      340
Cry1Ac      320      330      340      350      360
HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYRTLS
gi|401 QPGYFGKDSFNYSWGNVYVETRPSIGSSKITITSPFFYGDK-STEPVQKLSFD-GQKVVYRTIA
      350      360      370      380      390      400

```

```

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVGTVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEKITQLPV
      470      480      490      500      510

```

```

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

```

      540      550      560      570      580      590
Cry1Ac VPIIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIIGAESF
      580      590      600      610      620      630

```

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      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|40145942|gb|AAR61457.1| Sequence 20 from patent US (652 aa)  
 initn: 1000 init1: 432 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59  
 Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGFSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA

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170      180      190      200      210      220
Cry1Ac  200      210      220      230      240      250
CRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRWIRYNQFRRELTLTVLDIVSLFPNY
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280

Cry1Ac  260      270      280      290      300      310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQGIIEGSIKPHLMDILNSITTYTDA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  DIRLYSGVKTELTRDIFTDPIFAVNTLWEYGPTFLSIENSIKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

Cry1Ac  320      330      340      350      360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  QPGYFGKDSFNYSWVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

Cry1Ac  370      380      390      400      410      420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPO
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

Cry1Ac  430      440      450      460      470      480
NNNVPQRQGFVSHRSLHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTWTRSDVFFNTIDAEEKITQLPV
470      480      490      500      510

Cry1Ac  490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

Cry1Ac  540      550      560      570      580      590
VTPHILNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

Cry1Ac  600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  VSNEKIYIDKIEFIPVQL
640      650

>>gi|40188382|gb|AAR75907.1| Sequence 12 from patent US (652 aa)
initn: 999 init1: 431 opt: 1041 Z-score: 1220.5 bits: 237.0 E(): 4.6e-59
Smith-Waterman score: 1110; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIWGFQPSQ---W
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  SSTEVLNDSIVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW

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60      70      80      90      100
Cry1Ac  80      90      100      110      120      130
DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  KAFMAQVEVLIDKKIEEYAKSKALAEQLQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

Cry1Ac  140      150      160      170      180      190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVA
170      180      190      200      210      220

Cry1Ac  200      210      220      230      240      250
CRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRWIRYNQFRRELTLTVLDIVSLFPNY
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  EFYTRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280

Cry1Ac  260      270      280      290      300      310
DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQGIIEGSIKPHLMDILNSITTYTDA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  DIRLYSGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

Cry1Ac  320      330      340      350      360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  QPGYFGKDSFNYSWVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

Cry1Ac  370      380      390      400      410      420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPO
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

Cry1Ac  430      440      450      460      470      480
NNNVPQRQGFVSHRSLHVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTWTRSDVFFNTIDAEEKITQLPV
470      480      490      500      510

Cry1Ac  490      500      510      520      530
VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

Cry1Ac  540      550      560      570      580      590
VTPHILNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

Cry1Ac  600      610      620      630      640      650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :

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gi|401 NTDVAAWPNGKVVYLVGTVKVDVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFPTWTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHLLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|401 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|155684740|gb|ABU26995.1| Sequence 8 from patent US (652 aa)
initn: 998 init1: 430 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.812% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIGWIFGSPQ---W
30 40 50 60 70

gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190

gi|155 RELFSQAESHFRNSMPFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRRELTLTVLDIVSLFPNY
200 210 220 230 240 250

gi|155 EFYRRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLN-NFDGSRFRSAQGIIEGSIIRSHPLMDILNSITITYTDA
260 270 280 290 300 310

gi|155 DIRLYSKGVKTELTRDIFTDPIFSLNLTQEQYGPFTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|155 QPGYFGKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIIPQ
370 380 390 400 410 420

gi|155 NTDVAAWPNGKVVYLVGTVKVDVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFPTWTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHLLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|155 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|155 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810067|gb|AAE43982.1| Sequence 8 from patent US 6 (652 aa)
initn: 998 init1: 430 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.812% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIGWIFGSPQ---W
30 40 50 60 70

gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190

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gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWYSSSEDVA
170 180 190 200 210 220

Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY

gi|128 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQTLTREIYTNPVLNFDGSRFGSAQIEGSIKPHLMDILNSITITYTDA

gi|128 DIRLYSKGVKTELTRDIFDPIFSLNLTQEQYGTFLSIEKIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

gi|128 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGVTV---DSLDEIPPPQ

gi|128 NTDVAAWPNKGVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFHSHLHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|128 TTDEPLEKAYSHQLNYAECFLMQRRTI-----PFFTWTNRSVDFFTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|128 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VPIHLNVNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|128 TTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|128 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810075|gb|AAE43990.1| Sequence 24 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIHWGIFGPSQ---W

gi|128 SSTEVLNDSVTKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEEFARNQAIISRLGLESNLYQIYAESFREWEADPTN-PALREEMRI

gi|128 KAFMAQVEVLIDKKEIEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDR
110 120 130 140 150 160

Cry1Ac 140 150 160 170 180 190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN

gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWYSSSEDVA
170 180 190 200 210 220

Cry1Ac 200 210 220 230 240 250
SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY

gi|128 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300
DSRTYPIRTVSQTLTREIYTNPV----LENFDGSRFGSAQIEGSIKPHLMDILNSITI

gi|128 DIRLYSKGVKTELTRDIFDPIFPTTLQDYGTTF----LSIENSIRKPHLFDYLGQIEFH
290 300 310 320 330 340

Cry1Ac 310 320 330 340 350 360
YTAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVY

gi|128 HTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVY
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410
RTLSS-TLYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGVTV---DSLDE

gi|128 RTIANTDVAAWPNKGVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQ
410 420 430 440 450

Cry1Ac 420 430 440 450 460 470
IPPQNNVPPRQGFHSHLHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSIT

gi|128 LPPETTDEPLEKAYSHQLNYAECFLMQRRTI-----PFFTWTNRSVDFFTIDAEEKIT
460 470 480 490 500 510

Cry1Ac 480 490 500 510 520 530
QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV

gi|128 QLPVVKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIR
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
RYASVTPIHLNVNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG

gi|128 RYASTTNLRLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
VRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ

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      . . . . .
gi|128 AESFVSNEKIYIDKIEFIPVQL
      640      650

>>gi|155684748|gb|ABU27003.1| Sequence 24 from patent US (652 aa)
  initn: 1000 init1: 432 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

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      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . .
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIWIW---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi|155 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . .
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi|155 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFREMRTLIVLDLIVLFPFY
      230      240      250      260      270      280

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      260      270      280      290      300
Cry1Ac DSRTYPIRTVSQLTREIYTNPV----LENFDGSRGSAQIEGSIKIRSPHLMIDILNSITI
      . . . . .
gi|155 DIRLYSKGVKTELTRDIFTDPIFTPTTLQDYGPTF----LSIENSIRKPHLFDYLGQIEF
      290      300      310      320      330      340

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      310      320      330      340      350      360
Cry1Ac YTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVY
      . . . . .
gi|155 HTRLQPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVY
      350      360      370      380      390      400

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      370      380      390      400      410
Cry1Ac RTLSST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTV---DSLDE
      . . . . .
gi|155 RTIANTDVAAPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNNHVSQAQSDIDQ
      410      420      430      440      450

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      420      430      440      450      460      470
Cry1Ac IPPQNNVPPRQGFVSHRSLVSMFRSGFSNSVSIIRAPMFVSWIHRSAEFNIIASDSIT
      . . . . .
gi|155 LPPETDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTWHRSDVDFNTIDAEEKIT
      460      470      480      490      500      510

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      480      490      500      510      520      530
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYVRV

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```

      . . . . .
gi|155 QLPVVKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRI
      520      530      540      550      560      570

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      540      550      560      570      580      590
Cry1Ac RYASVTPIHNLVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSLGN-IVG
      . . . . .
gi|155 RYASTTNLRLVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
      580      590      600      610      620      630

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      600      610      620      630      640      650
Cry1Ac VRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
      . . . . .
gi|155 AESFVSNEKIYIDKIEFIPVQL
      640      650

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>>gi|40145945|gb|AAR61459.1| Sequence 24 from patent US (652 aa)
  initn: 1000 init1: 432 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

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      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . .
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIWIW---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi|401 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . .
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFREMRTLIVLDLIVLFPFY
      230      240      250      260      270      280

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      260      270      280      290      300
Cry1Ac DSRTYPIRTVSQLTREIYTNPV----LENFDGSRGSAQIEGSIKIRSPHLMIDILNSITI
      . . . . .
gi|401 DIRLYSKGVKTELTRDIFTDPIFTPTTLQDYGPTF----LSIENSIRKPHLFDYLGQIEF
      290      300      310      320      330      340

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      310      320      330      340      350      360
Cry1Ac YTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVY
      . . . . .
gi|401 HTRLQPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVY
      350      360      370      380      390      400

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      370      380      390      400      410
Cry1Ac RTLSST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPASAVYRKSQTV---DSLDE

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gi|401 RTIANTDVAAPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQ
410 420 430 440 450

Cry1Ac IPPQNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSIT
420 430 440 450 460 470

gi|401 LPPETTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTWHRSDVFFNTIDAEEKIT
460 470 480 490 500 510

Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
480 490 500 510 520 530

gi|401 QLPVVKAYALSSGASIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRYRVRV
520 530 540 550 560 570

Cry1Ac RYASVTPIHLNVWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG
540 550 560 570 580 590

gi|401 RYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
580 590 600 610 620 630

Cry1Ac VRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
600 610 620 630 640 650

gi|401 AESFVSNKIEYIDKIEFIPVQL
640 650

>>gi|40188388|gb|AAR75913.1| Sequence 24 from patent US (652 aa)
initn: 1000 init1: 432 opt: 1040 Z-score: 1219.3 bits: 236.8 E(): 5.4e-59
Smith-Waterman score: 1109; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQVGFDAATIN
140 150 160 170 180 190

gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
200 210 220 230 240 250

gi|401 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV----LENFDGSRGSAQGIEGSIRSPHLMIDILNSITI
260 270 280 290 300

gi|401 DIRLYSKGVKTELTRDIFTDPIFTPTTLQDYGPTF----LSIENSIRKPHLFDYLGQIEF
290 300 310 320 330 340

Cry1Ac YTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVY
310 320 330 340 350 360

gi|401 HTRLQPGYFGKDSFNYSWGNVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVY
350 360 370 380 390 400

Cry1Ac RTLSS-TLYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDE
370 380 390 400 410

gi|401 RTIANTDVAAPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQ
410 420 430 440 450

Cry1Ac IPPQNNVPPRQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSIT
420 430 440 450 460 470

gi|401 LPPETTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTWHRSDVFFNTIDAEEKIT
460 470 480 490 500 510

Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
480 490 500 510 520 530

gi|401 QLPVVKAYALSSGASIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRYRVRV
520 530 540 550 560 570

Cry1Ac RYASVTPIHLNVWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG
540 550 560 570 580 590

gi|401 RYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
580 590 600 610 620 630

Cry1Ac VRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
600 610 620 630 640 650

gi|401 AESFVSNKIEYIDKIEFIPVQL
640 650

>>gi|12810080|gb|AAE43995.1| Sequence 34 from patent US (652 aa)
initn: 1000 init1: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1107; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQVGFDAATIN
140 150 160 170 180 190



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Cry1Ac AGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|297 EKIIYDKIEFIPVQL
640 650
>>gi|40188384|gb|AAR75909.1| Sequence 16 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1107; 34.812% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVFLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRRELTLTVLDIVSLFPNY
gi|401 EFYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFFPY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQTLTREIYTNPV-LENFDGSFRGSAQGIEGSIIRSPHLMIDILNSITITYDA
gi|401 DIRLYSKGVKTELTRDIFTDPIFLTLTKYGPFTLSIENSIRKPHLFDYLGIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHTRSVDFNTIDEAKITQLPV
470 480 490 500 510

490 500 510 520 530

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATNNSNMFGSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYDKIEFIPVQL
640 650

>>gi|40188393|gb|AAR75918.1| Sequence 34 from patent US (652 aa)
initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1107; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVFLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYQFRRELTLTVLDIVSLFPNY
gi|401 EFYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFFPY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQTLTREIYTNPV-LENFDGSFRGSAQGIEGSIIRSPHLMIDILNSITITYDA
gi|401 DIRLYSKGVKTELTRDIFTDPIFILHTLQYEGPTF---LSIENSIRKPHLFDYLGIEFHTRL
290 300 310 320 330 340

Cry1Ac YTDahrgey-----YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVY
gi|401 HTRLQPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVY
350 360 370 380 390 400

370 380 390 400 410

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Cry1Ac  RTLSST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDE
gi|401  RTIANTDVAAPWNGKVYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQ
      410      420      430      440      450
Cry1Ac  IPPQNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSIT
gi|401  LPPETTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEDIT
      460      470      480      490      500      510
Cry1Ac  QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
gi|401  QLPVVKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRVRI
      520      530      540      550      560      570
Cry1Ac  RYASVTPIHLLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG
gi|401  RYASTTNLRLRFVQNSNDFLVLYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
      580      590      600      610      620      630
Cry1Ac  VRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
gi|401  AESFVSNKIEYIDKIEFIPVQL
      640      650

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>>gi|940200|gb|AAA74198.1| Cry3Bb2 (652 aa)
  initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-650)

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Cry1Ac  VEVLLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIHWGIFGPSQ---W
gi|940  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLDTIW---PSDADPW
      60      70      80      90      100
Cry1Ac  DAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|940  KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANHLHLSVLRDVSFVQRWGFDAATIN
gi|940  RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|940  EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSYDAWVKFNRFREMTLTVLDLIVLFPFY
      230      240      250      260      270      280
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|940  EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSYDAWVKFNRFREMTLTVLDLIVLFPFY
      260      270      280      290      300      310

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Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQIEGSIIRSPHMLDILNSITTYTDA
gi|940  DVRLYSKGVKTELTRDIFSLNTLQEQYGTFLSISIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|940  QPGYSGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400
Cry1Ac  ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN
gi|940  NTDVAAPWNGKVYLGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVGAQDSIDQLPETTD
      410      420      430      440      450      460
Cry1Ac  VPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
gi|940  EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEDITQLPVVKA
      470      480      490      500      510      520
Cry1Ac  NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
gi|940  YALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      530      540      550      560      570
Cry1Ac  IHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFGST
gi|940  LRLRFVQNSNDFLVLYINKTMNKDDDLTYQTFDLATTNSNMGFSGDTNELIIGAESFVSN
      580      590      600      610      620      630
Cry1Ac  AGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|940  EKIIYIDKIEFIPVQL
      640      650

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>>gi|40145954|gb|AAR61464.1| Sequence 34 from patent US (652 aa)
  initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1107; 34.746% identity (66.949% similar) in 590 aa overlap
(55-612:82-650)

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```

Cry1Ac  VEVLLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIHWGIFGPSQ---W
gi|401  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLDTIW---PSDADPW
      60      70      80      90      100
Cry1Ac  DAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401  KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401  EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSYDAWVKFNRFREMTLTVLDLIVLFPFY
      170      180      190      200      210      220
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401  EPHYRQLKLTQQYTDHCVNWNVNLNGLRGSYDAWVKFNRFREMTLTVLDLIVLFPFY
      260      270      280      290      300      310

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Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRFREMTLTLVLDIVLFPFY
230 240 250 260 270 280

260 270 280 290 300
Cry1Ac DSRTYPIRTVSQLTREIYTNPV----LENFDGSGFRGSAQGIIEGSIKPHLMDILNSITI
gi|401 DIRLYSGVKVTELTRDIFTDPIFILHTLQEQYPTF----LSIENSIRKPHLFDYLQGIIEF
290 300 310 320 330 340

310 320 330 340 350 360
Cry1Ac YTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVY
gi|401 HTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVI
350 360 370 380 390 400

370 380 390 400 410
Cry1Ac RTLSST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTIV---DSLDE
gi|401 RTIANTDVAAWPNGKIVLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQ
410 420 430 440 450

420 430 440 450 460 470
Cry1Ac IPPQNNVPPRQGFHSHLHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSIT
gi|401 LPPETDDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEEKIT
460 470 480 490 500 510

480 490 500 510 520 530
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGIEVPIHFPSTSTRYRVRV
gi|401 QLPVVKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRV
520 530 540 550 560 570

540 550 560 570 580 590
Cry1Ac RYASVTPIHNLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG
gi|401 RYASTTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIG
580 590 600 610 620 630

600 610 620 630 640 650
Cry1Ac VRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQAVNALFTSTNQLGLKTNVTDYHIDQ
gi|401 AESFVSNKIEYIDKIEFIPVQL
640 650

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>>gi|40188417|gb|AAR75942.1| Sequence 110 from patent US (652 aa)  
 initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap  
 (55-612:82-650)

30 40 50 60 70

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Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIWIGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPFAGALTSFYQSFLDTIW----PSDADPW
60 70 80 90 100

80 90 100 110 120 130
Cry1Ac DAFVLQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

140 150 160 170 180 190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

200 210 220 230 240 250
Cry1Ac SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRFREMTLTLVLDIVLFPFY
230 240 250 260 270 280

260 270 280 290 300 310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQGIIEGSIKPHLMDILNSITIYTD
gi|401 DVRLYSGVKVTELTRDIFTDPIFSLNLTQEQYPTFSLIENSIRKPHLFDYLQGIIEFHTRL
290 300 310 320 330 340

320 330 340 350 360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLS
gi|401 QPGYSGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVIARTIA
350 360 370 380 390 400

370 380 390 400 410 420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTIVDSLDEIPPQNNN
gi|401 NTDVAAWPNGKIVYFVTKVDFSQYDDQKNETSTQTYDSKRNGHVGAQDSIDQLPPEPTD
410 420 430 440 450 460

430 440 450 460 470 480
Cry1Ac VPPRQGFHSHLHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGN
gi|401 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEEKITQLPVVKA
470 480 490 500 510 520

490 500 510 520 530 540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGIEVPIHFPSTSTRYRVRVRYASVTP
gi|401 YALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
530 540 550 560 570

550 560 570 580 590
Cry1Ac IHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
gi|401 LRLFVQNSNNDFLVIYINKTMNIDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
580 590 600 610 620 630

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600 610 620 630 640 650  
 Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY  
 . . . . .  
 gi|401 EKIIYIDKIEFIPVQL  
 640 650

>>gi|155684744|gb|ABU26999.1| Sequence 16 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1107; 34.812% identity (67.235% similar) in 586 aa overlap  
 (55-612:82-650)

30 40 50 60 70  
 Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W  
 . . . . .  
 gi|155 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW  
 60 70 80 90 100

80 90 100 110 120 130  
 Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI  
 . . . . .  
 gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSDRI  
 110 120 130 140 150 160

140 150 160 170 180 190  
 Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN  
 . . . . .  
 gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWYSSSEDVA  
 170 180 190 200 210 220

200 210 220 230 240 250  
 Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY  
 . . . . .  
 gi|155 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRREMTLTVLDLIVLFFPY  
 230 240 250 260 270 280

260 270 280 290 300 310  
 Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQIEGSIERSPHLMDILNSITIYTDA  
 . . . . .  
 gi|155 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL  
 290 300 310 320 330 340

320 330 340 350 360  
 Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS  
 . . . . .  
 gi|155 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKYVRTIA  
 350 360 370 380 390 400

370 380 390 400 410 420  
 Cry1Ac ST-LYRRP---FNIGINNQQLSVLGDTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ  
 . . . . .  
 gi|155 NTDVAAWPNGKVKVGLTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQSDIDQLPPE  
 410 420 430 440 450 460

430 440 450 460 470 480  
 Cry1Ac NNNVPPRQGFHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA  
 . . . . .  
 gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRVDFNTIDAEEKITQLPV  
 470 480 490 500 510

490 500 510 520 530  
 Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHPFSTSTRYRVRVRYAS  
 . . . . .  
 gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESSNSIAK---FKVTLNSAALLQRYRVRIRYAS  
 520 530 540 550 560 570

540 550 560 570 580 590  
 Cry1Ac VTPIHLLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF  
 . . . . .  
 gi|155 TTNLRLRFVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF  
 580 590 600 610 620 630

600 610 620 630 640 650  
 Cry1Ac SGTAGVIIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNL  
 . . . . .  
 gi|155 VSNEKIYIDKIEFIPVQL  
 640 650

>>gi|114210121|emb|CAL40965.1| unnamed protein product [ (652 aa)  
 initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap  
 (55-612:82-650)

30 40 50 60 70  
 Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W  
 . . . . .  
 gi|114 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLDTIWI---PSDADPW  
 60 70 80 90 100

80 90 100 110 120 130  
 Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI  
 . . . . .  
 gi|114 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSDRI  
 110 120 130 140 150 160

140 150 160 170 180 190  
 Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN  
 . . . . .  
 gi|114 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWYSSSEDVA  
 170 180 190 200 210 220

200 210 220 230 240 250  
 Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY  
 . . . . .  
 gi|114 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRREMTLTVLDLIVLFFPY  
 230 240 250 260 270 280

260 270 280 290 300 310  
 Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIERSPHLMDILNSITIYTDA  
 . . . . .  
 gi|114 DVRLYKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLGQIEFHTRL  
 290 300 310 320 330 340

320 330 340 350 360  
 Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS  
 . . . . .  
 gi|114 QPGYSGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKYVRTIA  
 350 360 370 380 390 400

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370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNN
gi|114 NTDVAAWPNGKIYFGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVGAQDSIDQLPPETTD
410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKG
gi|114 EPLEKAYSHQLNYAECLMQDRRGTI----PFFTWTTHRSVDFNTIDA EKITQLP VVKA
470      480      490      500      510      520

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490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
gi|114 YALSSGASIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
530      540      550      560      570

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550      560      570      580      590
Cry1Ac IHLNVNWGNSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
gi|114 LRLFVQNSNDFIVIIYINKTMNIDDLTYQTFDLATTNSNMGFSGDTNELIIGAESFVSN
580      590      600      610      620      630

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600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|114 EKIIYIDKIEFIPVQL
640      650

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>>gi|77370838|gb|ABA68334.1| Sequence 4 from patent US 6 (652 aa)  
 initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap  
 (55-612:82-650)

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30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

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80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|773 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|773 RELFSQAESHFRNSMPSFAVSKFEVLFVLPYQAANTHLLKDAQVFGEEWYSSSEDVA
170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|773 EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVFNFRPREMTLTVLDLIVLFPFY
230      240      250      260      270      280

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260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIRSPHMLDILNSITIYTD
gi|773 DVRLYSGVKVTELRDIFDTPDFSLNTLQEQYGPFTFLSIENSIRKPHLFDYLOGIEFHFTRL
290      300      310      320      330      340

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320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|773 QPGYSGKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

```

```

370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNN
gi|773 NTDVAAWPNGKIYFGVTKVDFSQYDDQKNETSTQTYDSKRNNGHVGAQDSIDQLPPETTD
410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKG
gi|773 EPLEKAYSHQLNYAECLMQDRRGTI----PFFTWTTHRSVDFNTIDA EKITQLP VVKA
470      480      490      500      510      520

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```

490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
gi|773 YALSSGASIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
530      540      550      560      570

```

>>gi|40145938|gb|AAR61455.1| Sequence 16 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1107; 34.812% identity (67.235% similar) in 586 aa overlap  
 (55-612:82-650)

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600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
gi|773 EKIIYIDKIEFIPVQL
640      650

```

```

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

```

```

80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 EFYHRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQTLTREIYTNPV--LENFDGSFRGSAQGIIEGSIIRSHPLMDILNSITITYTDA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 DIRLYSKGVKTELTRDIFTDPIFLTLTKYGTFLSIEINSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK--STEPVKQLSFD--GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGV---DSLDEIPPPQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 TTNLRLVFNQNSNDFLVIIYINKTMNKDDDLTYQTFDLATTSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 VSNEKIYIDKIEFIPVQL
640      650

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>>gi|155684753|gb|ABU27008.1| Sequence 34 from patent US (652 aa)  
 initn: 1000 initl: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1107; 34.746% identity (66.949% similar) in 590 aa overlap  
 (55-612:82-650)

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30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SSTEVLNDSITVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDR
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 EFYHRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300
Cry1Ac DSRTYPIRTVSQTLTREIYTNPV----LENFDGSFRGSAQGIIEGSIIRSHPLMDILNSITI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DIRLYSKGVKTELTRDIFTDPIFLHTLQIEYGTTF----LSIENSIRKPHLFDYLGQIEFH
290      300      310      320      330      340

310      320      330      340      350      360
Cry1Ac YTDAHRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 HTRLQPGYFGKDSFNWYSGNYVETRPSIGSSKITITSPFYGDK--STEPVKQLSFD--GQKVY
350      360      370      380      390      400

370      380      390      400      410
Cry1Ac RTLSS-TLYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGV---DSLDE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RTIAN-TVAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQ
410      420      430      440      450

420      430      440      450      460      470
Cry1Ac IPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSIT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 LPPETTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEKIT
460      470      480      490      500      510

480      490      500      510      520      530
Cry1Ac QIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QLPVVKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVR
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac RYASVTPPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RYASTTNLRLVFNQNSNDFLVIIYINKTMNKDDDLTYQTFDLATTSNMGFSGDKNELIIG
580      590      600      610      620      630

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        600      610      620      630      640      650
Cry1Ac VRNFGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQ
      . . . . . : : : : :
gi|155 AESFVSNEKIYIDKIEFIPVQL
        640      650

>>gi|155684777|gb|ABU27032.1| Sequence 110 from patent U (652 aa)
  initn: 1000 init1: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap
(55-612:82-650)

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        30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . . : : : : :
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLDTIW---PSDADPW
        60      70      80      90      100

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        80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : :
gi|155 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
        110      120      130      140      150      160

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        140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . . : : : : :
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
        170      180      190      200      210      220

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        200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . . : : : : :
gi|155 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
        230      240      250      260      270      280

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        260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQIEGSIIRSPHLMIDILNSITIIYTD
      . . . . . : : : : :
gi|155 DVRLYSKGVKTELTRDIFTDPIFSLNTLQYEGPTFLSIENSIRKPHLFDYLQGIEFHTRL
        290      300      310      320      330      340

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        320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . . : : : : :
gi|155 QPGYSGKDFSNYWSGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
        350      360      370      380      390      400

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        370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGETVDSLDEIPPPQNNN
      . . . . . : : : : :
gi|155 NTDVAAWPNKGIYFVTKVDFSQYDDQKNETSTQTYDSCRNNNGHGAQDSIDQLPETTD
        410      420      430      440      450      460

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        430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
      . . . . . : : : : :
gi|155 EPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDAELITQLPVVKA
        470      480      490      500      510      520

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        490      500      510      520      530      540
Cry1Ac NFLVNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRVVRVRYASVPT
      . . . . . : : : : :
gi|155 YALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
        530      540      550      560      570

```

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        550      560      570      580      590
Cry1Ac IHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
      . . . . . : : : : :
gi|155 LRLRFVQNSNNDPIVIYINKTMNIDDLTYQTFDLATTNSNMGFSGDTNELIIGAESFVSN
        580      590      600      610      620      630

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        600      610      620      630      640      650
Cry1Ac AGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      . . . . . : : : : :
gi|155 EKIIYIDKIEFIPVQL
        640      650

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>>gi|12810071|gb|AAE43986.1| Sequence 16 from patent US (652 aa)
  initn: 1000 init1: 432 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59
Smith-Waterman score: 1107; 34.812% identity (67.235% similar) in 586 aa overlap
(55-612:82-650)

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        30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . . : : : : :
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIW---PSDADPW
        60      70      80      90      100

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        80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : :
gi|128 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
        110      120      130      140      150      160

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        140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . . . . . : : : : :
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
        170      180      190      200      210      220

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        200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . . : : : : :
gi|128 EPHYRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
        230      240      250      260      270      280

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        260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSGFRGSAQIEGSIIRSPHLMIDILNSITIIYTD
      . . . . . : : : : :
gi|128 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLQGIEFHTRL
        290      300      310      320      330      340

```

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        320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . . : : : : :
gi|128 QPGYFGKDFSNYWSGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
        350      360      370      380      390      400

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      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgtV---DSLDEIPPQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NTDVAAWPNgKvYLVgTKVDFsQYDDQK---NETsTQTYDSKRnNGHVsAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVpPRQgFShRLShVSMFRsGFSnSSVSIIRAPMFsWIHRsAEFNNIiASDSITQIPa
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTDEPLEKAYsHQLNYAEcFLMQDRRGTI----PFFTWThRSVDFfNTIDAEKITQLPv
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNfLfnG-SVIsGpGfTgGDLvRLnSSGnNIQnRGYIEVPIHfPSTsTRyRvRvRYAs
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 VKAYALSSGAsIIEGpGfTgGNLlFLKESsNSIAK---FKVTLnSAALLQRYRvRIRYAs
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VPIHlNvNWGNSSIFsNTVPATATsLDNL--QSSDFGYfESANAFtSSLGN-IVGVRNF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 TTnLrLfvQNSnNDFLVIYInKTMnKDDDLTYQTFDLATtNSnMGfSGDKNELIIgAESf
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVII DRFEfIPVTATLEAEYnLERAQKAVNALfTSTnQLGLKtNVTdYHIDQVSNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 VSNEKIYIDKIEfIPVQL
      640      650

```

>>gi|12810104|gb|AAE44019.1| Sequence 110 from patent US (652 aa)  
 initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGpSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 SSTEVLdNSTVKDAVGTGIsVVGQILGvVGVpFAGALtSFYQsFLDTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIrLEGLSNLYQIYAESfREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNnFEDYVnALNSWkKtPLSLRSKRsqDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLSVLrDVSfVFGQRWGFDAATIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 RELfSQAESHFRNSMPsFAVSKFEVLFLPTyAQAAntHLLLLKDAQVfGEEWGYSSEDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAvRWYNTGLERvWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 EFYHRQLKLTQYQTDHCvNWNvVGLNGLRGStYDAWVKfNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTvSQLTRIEIYNPVLN-NFDGSFRGSAQIEGSIRsPHLMdILNSITiYTDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 DVRLYsKGVKTELTRDIFTDPIfSLNTLQEQYGTpFLSIENsIRKPHLFDYLGQIEFhTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASpVFGSpEFTpFLYGTMGNAAPQQRIVAQLGQGVYRTLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 QPGYSKGSfSNYWSGNyVETRPSIGSSKTIItSPfYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQNNN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NTDVAAWPNgKvYLVgTKVDFsQYDDQKNETsTQTYDSKRnNGHVsAQDSIDQLPPETTD
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac VPPRQgFShRLShVSMFRsGFSnSSVSIIRAPMFsWIHRsAEFNNIiASDSITQIPAVKG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 EPLEKAYsHQLNYAEcFLMQDRRGTI----PFFTWThRSVDFfNTIDAEKITQLPvVKA
      470      480      490      500      510      520

      490      500      510      520      530      540
Cry1Ac NFLfNG-SVIsGpGfTgGDLvRLnSSGnNIQnRGYIEVPIHfPSTsTRyRvRvRYAsVTP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 YALSSGAsIIEGpGfTgGNLlFLKESsNSIAK---FKVTLnSAALLQRYRvRIRYAsTTN
      530      540      550      560      570

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>>gi|40145999|gb|AAR61488.1| Sequence 110 from patent US (652 aa)  
 initn: 1000 initl: 433 opt: 1038 Z-score: 1217.0 bits: 236.3 E(): 7.3e-59  
 Smith-Waterman score: 1113; 34.820% identity (67.067% similar) in 583 aa overlap  
 (55-612:82-650)

```

      550      560      570      580      590
Cry1Ac IHLNvNWGNSSIFsNTVPATATsLDNL--QSSDFGYfESANAFtSSLGN-IVGVRNFSGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 LRLfVQNSnNDFLVIYInKTMnIDDLTYQTFDLATtNSnMGfSGDTNELIIgAESfVSN
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac AGVII DRFEfIPVTATLEAEYnLERAQKAVNALfTSTnQLGLKtNVTdYHIDQVSNLVTY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 EKIIYIDKIEfIPVQL
      640      650

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGpSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SSTEVLdNSTVKDAVGTGIsVVGQILGvVGVpFAGALtSFYQsFLDTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAIrLEGLSNLYQIYAESfREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNnFEDYVnALNSWkKtPLSLRSKRsqDRI
      110      120      130      140      150      160

```



```

580      590      600      610      620      630
600      610      620      630      640      650
Cry1Ac AGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      . . . . .
gi|401 EKIIYIDKIEFIPVQL
      640      650

>>gi|155684765|gb|ABU27020.1| Sequence 58 from patent US (651 aa)
      initn: 1006 initl: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
      Smith-Waterman score: 1106; 34.648% identity (66.895% similar) in 583 aa overlap
      (55-612:82-649)

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```

30      40      50      60      70      80
Cry1Ac VEVLGGERJETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQWDAF
      . . . . .
gi|155 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWPSEDP--WKAF
      60      70      80      90      100

90      100     110     120     130
Cry1Ac LVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQ--
      . . . . .
gi|155 MAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKFHHSRRSRKRSQDRIREL
      110     120     130     140     150     160

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140     150     160     170     180     190
Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQPSQWDAF
      . . . . .
gi|155 FSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSDVAEFY
      170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSR
      . . . . .
gi|155 HRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWKFNFRPREMTLTVLDLIVLFPFYDIR
      230     240     250     260     270     280

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```

260     270     280     290     300     310
Cry1Ac TYPPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIIRSPHLMIDILNSITTYDAHRG
      . . . . .
gi|155 LYSKGVKTELTRDIFTDPIFSLNTLQEGYPTFLSIENSIRKPHLFDYLGIEFHTRLQPG
      290     300     310     320     330     340

320     330     340     350     360
Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-
      . . . . .
gi|155 YFGKDSFNWWSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD
      350     360     370     380     390     400

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370     380     390     400     410     420
Cry1Ac LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQV---DSLDEIIPPQNNN
      . . . . .
gi|155 VAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPETTD
      410     420     430     440     450     460

430     440     450     460     470     480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKG
      . . . . .
gi|155 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWHRSDVDFNTIDAEEKITQLPVVKA

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470      480      490      500      510
490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPTSTSTRYRVRVRYASVTP
      . . . . .
gi|155 YALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      520     530     540     550     560     570

550     560     570     580     590
Cry1Ac IHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
      . . . . .
gi|155 LRLFLVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATNSNMGFSGDKNELIIGAESFVSN
      580     590     600     610     620     630

600     610     620     630     640     650
Cry1Ac AGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      . . . . .
gi|155 EKIIYIDKIEFIPVQL
      640     650

```

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>>gi|12810092|gb|AAE44007.1| Sequence 58 from patent US (651 aa)
      initn: 1006 initl: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
      Smith-Waterman score: 1106; 34.648% identity (66.895% similar) in 583 aa overlap
      (55-612:82-649)

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```

30      40      50      60      70      80
Cry1Ac VEVLGGERJETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQWDAF
      . . . . .
gi|128 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWPSEDP--WKAF
      60      70      80      90      100

90      100     110     120     130
Cry1Ac LVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQ--
      . . . . .
gi|128 MAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKFHHSRRSRKRSQDRIREL
      110     120     130     140     150     160

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140     150     160     170     180     190
Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQPSQWDAF
      . . . . .
gi|128 FSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSDVAEFY
      170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSR
      . . . . .
gi|128 HRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWKFNFRPREMTLTVLDLIVLFPFYDIR
      230     240     250     260     270     280

```

```

260     270     280     290     300     310
Cry1Ac TYPPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIIRSPHLMIDILNSITTYDAHRG
      . . . . .
gi|128 LYSKGVKTELTRDIFTDPIFSLNTLQEGYPTFLSIENSIRKPHLFDYLGIEFHTRLQPG
      290     300     310     320     330     340

320     330     340     350     360
Cry1Ac EY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-
      . . . . .
gi|128 YFGKDSFNWWSGNYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTD

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350      360      370      380      390      400
Cry1Ac LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQNNN
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 VAAWPNGKVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPETTD
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRVDFNTIDAEEKITQLPVVKA
      470      480      490      500      510

      490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 YALSSGASIIIEGPGFTGGNLLFLKESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      520      530      540      550      560      570

      550      560      570      580      590
Cry1Ac IHLNVNWGSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|128 LRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      :   :   :   :   :   :
gi|128 EKIIYDKIEFIPVQL
      640      650

>>gi|40188405|gb|AAR75930.1| Sequence 58 from patent US (651 aa)
  initn: 1006 initl: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.648% identity (66.895% similar) in 583 aa overlap
(55-612:82-649)

      30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGI FGPQWDAF
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSF LNTIWPSEDP--WKAF
      60      70      80      90      100

      90      100      110      120      130
Cry1Ac LVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFREWEA-DPTN PALREEMRIQ--
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 MAQVEVLIDKKIEEYAKSKALAE LQGLQNNFEDYVNALNSWKKFHHSRRSKRSQDRIREL
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQRGWGFPDAATINSRY
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 FSOAESHRFNSMPSFAVSKFEVLF LPTYAQAANTHLLLLKDAQVFGEEWYSSEDVAEYF
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac NDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSR
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 HRQLKLTQYTDHCVNWYVGLNGLR GSTYDAWKFNRFREMTTLVLDLIVLFPFYDIR

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230      240      250      260      270      280
Cry1Ac TYPIRTVSQLTREIYTNPVLE-NFDGSGFRGSAQGI EGSIRSPLMIDILNSITTYDAHRG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 LYSKGVKTELTRDIFTDPIFSLNTLQ EYGPTFLSIENSIRKPHLFDYLGIEFHRLQPG
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac EY-----YWSGHQIMASPVGSGPEFTFP LYGTMGNAAPQQRIVAQLGQGQVYRTLSST-
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 YFGKDSFNYSWGNVYVETRPSIGSSK TITSFPFYGDK-STEPVQKLSFD-GQKYRTIANTD
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQNNN
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 VAAWPNGKVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPETTD
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac VPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 EPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRVDFNTIDAEEKITQLPVVKA
      470      480      490      500      510

      490      500      510      520      530      540
Cry1Ac NFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 YALSSGASIIIEGPGFTGGNLLFLK ESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTN
      520      530      540      550      560      570

      550      560      570      580      590
Cry1Ac IHLNVNWGSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGT
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|401 LRLFVQNSNNDPLVIYINKTMNKDD DLTYQTFDLATTNSNMGFSGDKNELIIGAESFVSN
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac AGVIIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      :   :   :   :   :   :
gi|401 EKIIYDKIEFIPVQL
      640      650

>>gi|155684755|gb|ABU27010.1| Sequence 38 from patent US (652 aa)
  initn: 1000 initl: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.642% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGI FGPQ---W
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSF LNTIW----PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
gi|155 KAFMAQVEVLIDKKIEEYAKSKALAE LQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

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110      120      130      140      150      160
Cry1Ac  140      150      160      170      180      190
Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|155  RELFSQAESHFRNSMPSFAVSKFEVLFLLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155  EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQGIIEGSIIRPHLMDILNSITTYDA
gi|155  DIRLYSKGVKTELTRDIFTDPIFSLRTPPLAYGPTFLSIENSIRKPHLFDYLGIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155  QPGYFGKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|155  NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|155  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATNNSMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155  VSNEKIYIDKIEFIPVQL
640      650

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>>gi|40145957|gb|AAR61466.1| Sequence 38 from patent US (652 aa)  
initn: 1000 initl: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59

Smith-Waterman score: 1106; 34.642% identity (67.065% similar) in 586 aa overlap  
(55-612:82-650)

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30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAG----FVLGLVDIIWIGIFGPSQ---W
gi|401  SSTEVLNDSITVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

80      90      100      110      120      130
Cry1Ac  DAFVLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401  KAFMAQVEVLIDKKIEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDR
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|401  RELFSQAESHFRNSMPSFAVSKFEVLFLLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401  EFYHRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRRFREMRTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFGSAQGIIEGSIIRPHLMDILNSITTYDA
gi|401  DIRLYSKGVKTELTRDIFTDPIFSLRTPPLAYGPTFLSIENSIRKPHLFDYLGIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401  QPGYFGKDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401  NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNIVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATNNSMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401  VSNEKIYIDKIEFIPVQL
640      650

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gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFFYGDK--STEPVQKLSFD--GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTV---DSLDEIPPO
370 380 390 400 410 420

gi|401 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|401 TTNLRFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSQDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40188415|gb|AAR75940.1| Sequence 108 from patent US (652 aa)
initn: 998 init1: 430 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|401 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|401 EPHYRRQKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLLVLDLIVLFFPY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQIEGSIRSPHMDILNSITIYTDA
260 270 280 290 300 310

gi|401 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGSGPEFTFFLYGTMGNAAPQQRIVAQQLQGVYRTLS
320 330 340 350 360

gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFFYGDK--STEPVQKLSFD--GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQTV---DSLDEIPPO
370 380 390 400 410 420

gi|401 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|401 TTNLRFLVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSQDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810102|gb|AAE44017.1| Sequence 108 from patent US (652 aa)
initn: 998 init1: 430 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

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      .....
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      .....
gi|128 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      .....
gi|128 EFYRRQLKLTQQYTDHCVNWNVGNLGRGSTDYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV--LENFDGSFRGSAQGIEGSIRSPHMLDILNSITIYTD
      .....
gi|128 DIRLSYKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVACLGGQVYRTLS
      .....
gi|128 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
      .....
gi|128 NTDVAAWPNQKLVYLVGTVKVDQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDA EKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|128 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN--IVGVRNF
      .....
gi|128 TTNLRLFVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|128 VSNEKIYIDKIEFIPVQL
      640      650

>>gi|12810072|gb|AAE43987.1| Sequence 18 from patent US (652 aa)

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      initn: 1000 init1: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
      Smith-Waterman score: 1106; 34.812% identity (67.065% similar) in 586 aa overlap
      (55-612:82-650)

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIWGFPGSQ---W
      .....
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVVFPAGALTSFYQSFLNTIWI---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN--PALREEMRI
      .....
gi|128 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDR
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      .....
gi|128 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
      .....
gi|128 EFYHRQLKLTQQYTDHCVNWNVGNLGRGSTDYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE--NFDGSFRGSAQGIEGSIRSPHMLDILNSITIYTD
      .....
gi|128 DIRLSYKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVACLGGQVYRTLS
      .....
gi|128 QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
      .....
gi|128 NTDVAAWPNQKLVYLVGTVKVDQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      .....
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDA EKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      .....
gi|128 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN--IVGVRNF
      .....
gi|128 TTNLRLFVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPFIVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      .....
gi|128 VSNEKIYIDKIEFIPVQL
      640      650

      540      550      560      570      580      590

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Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVVYRTIA
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRSLHSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEDITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKGNFLEFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VTPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLRFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40145995|gb|AAR61486.1| Sequence 108 from patent US (652 aa)
initn: 998 init1: 430 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac 80 90 100 110 120 130
DAFLVQIEQLINQRIEFAFNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEIYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQGR
110 120 130 140 150 160

Cry1Ac 140 150 160 170 180 190
Q---FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQRWGFDAATIN
gi|401 RELFQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVA
170 180 190 200 210 220

200 210 220 230 240 250

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EFDYRQLKLTQQYTDHCVNWNVNLNGLRGSSTYDAWVKFNRRFREMRTLVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac 260 270 280 290 300 310
DSRTYPIRTVSQLTREIYTNPV-LENFDGSGFRGSAQIEGSIRSPHMLDILNSITTYTDA
gi|401 DIRLYSKGVKTELTRDIFTDPIFLTLTQKYGPTFLSIENSIRKPHLFDYQLQIEFHTRL
290 300 310 320 330 340

Cry1Ac 320 330 340 350 360
HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVVYRTIA
350 360 370 380 390 400

Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac 430 440 450 460 470 480
NNNVPPRQGFSHRSLHSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEDITQLPV
470 480 490 500 510

Cry1Ac 490 500 510 520 530
VKGNFLEFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VTPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLRFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640 650
SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
640 650

>>gi|40188395|gb|AAR75920.1| Sequence 38 from patent US (652 aa)
initn: 1000 init1: 432 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
Smith-Waterman score: 1106; 34.642% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac 30 40 50 60 70
VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTIWIW---PSDADPW
60 70 80 90 100

80 90 100 110 120 130

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Cry1Ac DAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi | 401 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . .
gi | 401 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi | 401 EFYHRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIKPHLMDILNSITTYTDA
      . . . . .
gi | 401 DIRLYSKGVKTELTRDIFTDPIFSLRTPLAYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . .
gi | 401 QPGYFGKDSFNYSWGNVETRPSIGSSKITISPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . . . . .
gi | 401 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . .
gi | 401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS
      . . . . .
gi | 401 VKAYALSSGASIEEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
      . . . . .
gi | 401 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTDFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . .
gi | 401 VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|155684775|gb|ABU27030.1| Sequence 108 from patent U (652 aa)
      initn: 998 init1: 430 opt: 1037 Z-score: 1215.8 bits: 236.1 E(): 8.4e-59
      Smith-Waterman score: 1106; 34.812% identity (67.065% similar) in 586 aa overlap
      (55-612:82-650)

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIGWIFGPSQ---W
      . . . . .
gi | 155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW----PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi | 155 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . .
gi | 155 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi | 155 EFYHRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQIEGSIKPHLMDILNSITTYTDA
      . . . . .
gi | 155 DIRLYSKGVKTELTRDIFLTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . .
gi | 155 QPYRRQLKLTQQYTDHCVNWNVNLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQIEGSIKPHLMDILNSITTYTDA
      . . . . .
gi | 155 DIRLYSKGVKTELTRDIFLTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . .
gi | 155 QPGYFGKDSFNYSWGNVETRPSIGSSKITISPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . . . . .
gi | 155 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . .
gi | 155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP IHPSTSTRYRVRVRYAS
      . . . . .
gi | 155 VKAYALSSGASIEEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

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      210      220      230      240      250      260
Cry1Ac  TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|161  LKLTQQYTDHCNVNWNVGLNSLRGSTDYDAWKFNFRREMTLTVLDLIVLFPFYDVRVLYS
      240      250      260      270      280      290

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      270      280      290      300      310
Cry1Ac  IRTVSQLTREIYTNPVLN-NFDGSRGSAQGIIEGSIRSPHLMILNSITTYDAHRGEY-
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : : . . . .
gi|161  KGVKTELTRDIFTDPIFTLNALQEYGPFTSSSIENSIRKPHLFDYLRGIEFHTRLRPGYSG
      300      310      320      330      340      350

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      320      330      340      350      360      370
Cry1Ac  -----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  KDSFNWYSGNYVETRPSIGSNDTITSPFYGDK-SIEPIQKLSFD-GQKVYRTIANTDIAA
      360      370      380      390      400      410

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      380      390      400      410      420
Cry1Ac  RP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPNQNNVPPRQG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  FPDGKIYFVGTKVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPPEPTTDEPLEKA
      420      430      440      450      460      470

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      430      440      450      460      470      480
Cry1Ac  FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  YSHQLNYAECFLMQDRRGTI-----PFFTWTHRSDVDFNTIDAEEKITQLPVVKAYALSSG
      480      490      500      510      520

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      490      500      510      520      530      540
Cry1Ac  -SVISGPGFTGGDLVRLNNSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  ASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLRFVQ
      530      540      550      560      570      580

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      550      560      570      580      590      600
Cry1Ac  WGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFGTGTAGVIID
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  NSNNDFLVIYINKTMNIDGLTYQTFDFATSNMGMFGSDTNDFIIGAESFVSNKIIYID
      590      600      610      620      630      640

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      610      620      630      640      650      660
Cry1Ac  RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFEC
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|161  KIEFIPVQ
      650

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>>gi|40145943|gb|AAR61458.1| Sequence 22 from patent US (652 aa)  
 initn: 998 init1: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
 Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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      30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIVGIFGSPQ---W
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFNLNTIW---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSEDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  EFYRRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

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      260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGIIEGSIRSPHLMILNSITTYTDA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLRGIEFHTRL
      290      300      310      320      330      340

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      320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  PQGYFGKDSFNWYSGNYVETRPSIGSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

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      370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGETV---DSLDEIPPG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

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      430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSDVDFNTIDAEEKITQLPV
      470      480      490      500      510

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      490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

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      540      550      560      570      580      590
Cry1Ac  VTPPIHLNVNWNVGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGMFGSKDNELIIGAESF
      580      590      600      610      620      630

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      600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|155684747|gb|ABU27002.1| Sequence 22 from patent US (652 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW

Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFGSAQIEGSIKPHLMDILNSITIIYTD
gi|155 DIRLSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|155 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSVDFNFIDAEEKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRVVRVRYAS
gi|155 VKAYALSSGASIIIEGPGFTGNNLLFLKESNSIAK---FKVTLNSAALLQRVVRIRYAS

540 550 560 570 580 590
Cry1Ac VTFIHLNVNWNSSIFSNVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|155 TTNLRLFLVQNSNNDPLVIYINKTMNKDDDLTYQTFPLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|155 VSNEKIYIDKIEFIPVQL

>>gi|12810074|gb|AAE43989.1| Sequence 22 from patent US (652 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIIV---PSDADPW

Cry1Ac DAFLVQIEQLINQRIEFAFNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|128 KAFMAQVEVLIDKKEIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLKDAQVFGEEWGYSSDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|128 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFGSAQIEGSIKPHLMDILNSITIIYTD
gi|128 DIRLSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|128 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
gi|128 NTDVAAWPNKGYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE







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410      420      430      440      450      460
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|114  TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEEKITQLPVP
      470      480      490      500      510

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490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|114  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

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540      550      560      570      580      590
Cry1Ac  VPIIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|114  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIIGAESF
      580      590      600      610      620      630

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600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|114  VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|29702320|gb|AAO96405.1| Sequence 39 from patent US (653 aa)  
 initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
 Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:83-651)

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30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|297  SSTEVLDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

```

```

80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297  KAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

```

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140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|297  RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVA
      170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|297  EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

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260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFRGSAQGGIEGSIIRPHLMDILNSITITYTDA
gi|297  DIRLYSKGVKTELTRDIFLTLTLLQKYGPTPLSIEINSIRKPHLFDYLGQIEFHTRL

```

```

290      300      310      320      330      340
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYRTLS
gi|297  QPGYFGKDSFNYSWGNVYETRPSIGSSKITITSPFFYGDK-STEPVQKLSFD-GQKIVYRTIA
      350      360      370      380      390      400

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370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV--DSLDEIPPQ
gi|297  NTDVAAWPNKGVYLVGVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

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430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|297  TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSDVDFNTIDAEEKITQLPVP
      470      480      490      500      510

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```

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

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540      550      560      570      580      590
Cry1Ac  VPIIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|297  TTNLRLFVQNSNDFLVIIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIIGAESF
      580      590      600      610      620      630

```

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600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|297  VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|29702311|gb|AAO96396.1| Sequence 16 from patent US (653 aa)  
 initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
 Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:83-651)

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30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|297  SSTEVLDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

```

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80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297  KAFMAQVEVLIDKIEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATIN
gi|297  RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVA

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170      180      190      200      210      220
Cry1Ac  200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFRRELTTLVLDIVSLFPNY
:      .:      .:      .:      .:      .:      .:
gi|297  EFYRRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGIIEGSIKPHLMDILNSITTYTDA
:      .:      .:      .:      .:      .:      .:
gi|297  DIRLYSKGVKTELTRDIFLTDPIFLLTTLQKYGPTFLSIENSIKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
:      .:      .:      .:      .:      .:      .:
gi|297  QPGYFGKDSFNYSWGNVETRPSIGSSKITISPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPO
:      .:      .:      .:      .:      .:      .:
gi|297  NTDVAAWPNKGYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
:      .:      .:      .:      .:      .:      .:
gi|297  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
:      .:      .:      .:      .:      .:      .:
gi|297  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGFESANAFSSLGN-IVGVRNF
:      .:      .:      .:      .:      .:      .:
gi|297  TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
:      .:      .:      .:      .:      .:      .:
gi|297  VSNEKIYIDKIEFIPVQL
640      650

>>gi|77370853|gb|ABA68349.1| Sequence 39 from patent US (653 aa)
initn: 998 init1: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

30      40      50      60      70
Cry1Ac  VEVLGGRIETGYTPIDISLSLTQFLLEFVPGAG----FVLGLVDIIWGFGPSQ---W
:      .:      .:      .:      .:      .:      .:
gi|773  SSTEVLNDSVTKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIWIW---PSDADPW

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60      70      80      90      100
Cry1Ac  80      90      100      110      120      130
Cry1Ac  DAFVLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
:      .:      .:      .:      .:      .:      .:
gi|773  KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN
:      .:      .:      .:      .:      .:      .:
gi|773  RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEWYSSSEDVA
170      180      190      200      210      220

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERLVGPDSDRDWIRYNQFRRELTTLVLDIVSLFPNY
:      .:      .:      .:      .:      .:      .:
gi|773  EFYRRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAWVKFNRFREMTLTVLDLIVLFPFY
230      240      250      260      270      280

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGIIEGSIKPHLMDILNSITTYTDA
:      .:      .:      .:      .:      .:      .:
gi|773  DIRLYSKGVKTELTRDIFLTDPIFLLTTLQKYGPTFLSIENSIKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
:      .:      .:      .:      .:      .:      .:
gi|773  QPGYFGKDSFNYSWGNVETRPSIGSSKITISPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPNAVYRKSQTV---DSLDEIPPO
:      .:      .:      .:      .:      .:      .:
gi|773  NTDVAAWPNKGYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410      420      430      440      450      460

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
:      .:      .:      .:      .:      .:      .:
gi|773  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTNRSVDFNTIDAEEKITQLPV
470      480      490      500      510

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
:      .:      .:      .:      .:      .:      .:
gi|773  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

540      550      560      570      580      590
Cry1Ac  VTIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGFESANAFSSLGN-IVGVRNF
:      .:      .:      .:      .:      .:      .:
gi|773  TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

600      610      620      630      640      650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
:      .:      .:      .:      .:      .:      .:

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gi|114 NTDVAAWPNGKVYLGVTQVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|114 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFFTWTTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|114 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|114 TTNLRLVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|114 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370852|gb|ABA68348.1| Sequence 37 from patent US (653 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIGWIFGPSQ---W
30 40 50 60 70

gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|773 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190

gi|773 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVGEWGYSSDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDRWIRYNQFRRELTTLTVLDIVSLFPNY
200 210 220 230 240 250

gi|773 EFYRRQLKLTQYTDHCNVNWNVGLNGLRGSTYDAWVKFNFRPREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGIEGSIRSPHLMIDILNSITITYTDA
260 270 280 290 300 310

gi|773 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|773 QPGYFGKDSFNYSWGNVYVETRPSIGSSKITITSPFFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIIPQ
370 380 390 400 410 420

gi|773 NTDVAAWPNGKVYLGVTQVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRTI-----PFFTWTTHRSVDFNTIDAELITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370840|gb|ABA68336.1| Sequence 8 from patent US 6 (653 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIGWIFGPSQ---W
30 40 50 60 70

gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWI---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|773 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190





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gi|773 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 VSNEKIYIDKIEFIPVQL
640 650

>>gi|12810101|gb|AAE44016.1| Sequence 100 from patent US (653 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|128 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

gi|128 RELFSQAESHFNMSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|128 EFYRRQLKLTQYQTDHCNVNWNVGLNGLRGSTYDAWVKFNFRREMTLTVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQIEGSIIRSPHLMIDILNSITITYTDA
260 270 280 290 300 310

gi|128 DIRLYSKGVKTELTRDIFLTLTLLKQYGFPTFLSIENSRKPHLFYDLQGIIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|128 QPGYFGKDSFNYSWGNVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINQQQLSVLDGTEFAYGTSSNLPASAVYRKSQTV--DSLDEIPPQ
370 380 390 400 410 420

gi|128 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|128 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|128 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370841|gb|ABA68337.1| Sequence 10 from patent US (653 aa)
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAIISRLGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|773 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

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gi|773 RELFSQAESHFRNSMPFAVSKFEVLFLEPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|773 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRETTLVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGIIEGSIKPHLMDILNSITIIYTD
260 270 280 290 300 310

gi|773 DIRLYSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASVGFSGPEFTPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|773 RPYGFKDSFNYSWGNVETRPSIGSSKITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
370 380 390 400 410 420

gi|773 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLFVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370844|gb|ABA68340.1| Sequence 16 from patent US (653 aa)
initn: 998 init1: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
30 40 50 60 70

gi|773 SSTEVLNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|773 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGDAATIN
140 150 160 170 180 190

gi|773 RELFSQAESHFRNSMPFAVSKFEVLFLEPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|773 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRRFRETTLVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGIIEGSIKPHLMDILNSITIIYTD
260 270 280 290 300 310

gi|773 DIRLYSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASVGFSGPEFTPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|773 QPYGFKDSFNYSWGNVETRPSIGSSKITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
370 380 390 400 410 420

gi|773 NTDVAAWPNKGVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLFVQNSNNDLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFGPSQ---W
600 610 620 630 640 650









```

370          380          390          400          410          420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|401 NTDVAAWPNGKVKVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410          420          430          440          450          460

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430          440          450          460          470          480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDA EKITQLPV
470          480          490          500          510

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```

490          500          510          520          530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520          530          540          550          560          570

```

```

540          550          560          570          580          590
Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580          590          600          610          620          630

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600          610          620          630          640          650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
640          650

```

>>gi|29702319|gb|AA096404.1| Sequence 37 from patent US (653 aa)  
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap  
(55-612:83-651)

```

30          40          50          60          70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|297 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFINTIWI---PSDADPW
60          70          80          90          100

```

```

80          90          100          110          120          130
Cry1Ac DAFVLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
110          120          130          140          150          160

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140          150          160          170          180          190
Cry1Ac Q--FNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|297 RELFSQAESHFRNSMPSFAVSKFEVFLFPTYAQAANTHLLLLKDAQVFGEEGWYSSDVA
170          180          190          200          210          220

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200          210          220          230          240          250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
gi|297 EFYRRQLKLTQQYTDHCVNWYVNLNGLRGSTYDAWVKFNRPREMTLTVLDLIVLFPFY
230          240          250          260          270          280

```

```

260          270          280          290          300          310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGI EGSIRSPLHMDILNSITIIYTD
gi|297 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLOGIEFHTRL
290          300          310          320          330          340

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320          330          340          350          360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|297 QPGYFGKDSFNYSWGNVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350          360          370          380          390          400

```

```

370          380          390          400          410          420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|297 NTDVAAWPNGKVKVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410          420          430          440          450          460

```

```

430          440          450          460          470          480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWTHRSVDFNTIDA EKITQLPV
470          480          490          500          510

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```

490          500          510          520          530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520          530          540          550          560          570

```

>>gi|29702313|gb|AA096398.1| Sequence 20 from patent US (653 aa)  
initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap  
(55-612:83-651)

```

540          550          560          570          580          590
Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|297 TTNLRLVQNSNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580          590          600          610          620          630

```

```

600          610          620          630          640          650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|297 VSNEKIYIDKIEFIPVQL
640          650

```

```

30          40          50          60          70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|297 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFINTIWI---PSDADPW
60          70          80          90          100

```

```

80          90          100          110          120          130
Cry1Ac DAFVLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297 KAFMAQVEVLIDKKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
110          120          130          140          150          160

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140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|297 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

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200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
gi|297 EFYRRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230      240      250      260      270      280

```

```

260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGIIEGSIKPHLMDILNSITITYTDA
gi|297 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGIEFHTRRL
290      300      310      320      330      340

```

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320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLS
gi|297 RPYGFKGDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

```

```

370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|297 NTDVAAWPNGKVKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE
410      420      430      440      450      460

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRAEFNNIIASDSITQIPA
gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSDVFFNTIDAEEKITQLPV
470      480      490      500      510

```

```

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

```

```

540      550      560      570      580      590
Cry1Ac VTIHLNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|297 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

```

```

600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNLGLKTNVTDYHIDQVSNL
gi|297 VSNEKIYIDKIEFIPVQL
640      650

```

>>gi|29702307|gb|AAO96392.1| Sequence 8 from patent US 6 (653 aa)  
 initn: 998 initl: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59  
 Smith-Waterman score: 1105; 34.81% identity (67.06% similar) in 586 aa overlap  
 (55-612:83-651)

```

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|297 SSTEVLNDSITVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFLNTIWI---PSDADPW
60      70      80      90      100

```

```

80      90      100      110      120      130
Cry1Ac DAFVLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110      120      130      140      150      160

```

```

140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|297 RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSSEDVA
170      180      190      200      210      220

```

```

200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
gi|297 EFYRRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
230      240      250      260      270      280

```

```

260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGIIEGSIKPHLMDILNSITITYTDA
gi|297 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLGIEFHTRRL
290      300      310      320      330      340

```

```

320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRTLS
gi|297 PPGYFKGDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

```

```

370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
gi|297 NTDVAAWPNGKVKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE
410      420      430      440      450      460

```

```

430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRAEFNNIIASDSITQIPA
gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSDVFFNTIDAEEKITQLPV
470      480      490      500      510

```

```

490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

```

```

540      550      560      570      580      590
Cry1Ac VTIHLNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|297 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

```

```

600      610      620      630      640      650
Cry1Ac  SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . .
gi|297  VSNEKIYIDKIEFIPVQL
      640      650

>>gi|155684774|gb|ABU27029.1| Sequence 100 from patent U (653 aa)
  initn: 998 init1: 430 opt: 1036 Z-score: 1214.6 bits: 235.9 E(): 9.8e-59
Smith-Waterman score: 1105; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

```

```

30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---W
      . . . . .
gi|155  SSTEVLDNSTVKDAVGTGISVVGQILGVVGVPPFAGALTSFYQSFNLTIW---PSDADPW
      60      70      80      90      100

```

```

80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . .
gi|155  KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRKRSQDR
      110      120      130      140      150      160

```

```

140      150      160      170      180      190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATIN
      . . . . .
gi|155  RELFSQAESHFRNSMPSFAVSKFEVFLFLPTYAQAANTHLLKDAQVFGEEWYSSSEDVA
      170      180      190      200      210      220

```

```

200      210      220      230      240      250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . .
gi|155  EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

```

```

260      270      280      290      300      310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQIEGSIIRSPHLMIDILNSITITYTDA
      . . . . .
gi|155  DIRLSKGVKTELTRDIFTDPIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHRTL
      290      300      310      320      330      340

```

```

320      330      340      350      360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . . . . .
gi|155  QPGYFGKDFSNYWSGNYVETRPSIGSSKITITSPFYGDK--STEPVQKLSFD--GQKVYRTIA
      350      360      370      380      390      400

```

```

370      380      390      400      410      420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSGTV---DSLDEIPPQ
      . . . . .
gi|155  NTDVAAWPNGKYLGVTKVDFSQYDDQK---NETSTQYDSCRNNGHVSQAQSDIDQLPPE
      410      420      430      440      450      460

```

```

430      440      450      460      470      480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . .
gi|155  TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWHRSVDFNFIIDAEKITQLPVA
      470      480      490      500      510

```

```

490      500      510      520      530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . .
gi|155  VKAYALSSGASIEEGPGFTGGNLLFLKESSENSIAK---FKVTLNSAALLQRVYRIRYAS
      520      530      540      550      560      570

```

```

540      550      560      570      580      590
Cry1Ac  VTIPIHLNVNWNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . .
gi|155  TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFLATNNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

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600      610      620      630      640      650
Cry1Ac  SGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . .
gi|155  VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|40146003|gb|AAR61490.1| Sequence 112 from patent US (659 aa)
  initn: 1007 init1: 435 opt: 1036 Z-score: 1214.5 bits: 235.9 E(): 9.9e-59
Smith-Waterman score: 1114; 33.646% identity (65.258% similar) in 639 aa overlap
(5-612:37-658)

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10      20
Cry1Ac  CMQAMDNNPNIN-ECIPYNCL---SNPEVEVLG
      . . . . .
gi|401  RKMNPNRSEYDTIKVTPNSELPTNHNQYPLADNPSTLEELNYKEFLRMTADNSTVELD
      10      20      30      40      50      60

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30      40      50      60      70      80
Cry1Ac  GERIETGY-TPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGIFGPSQ---WDAFL
      . . . . .
gi|401  SSTVKDAVGTGISV---VGQILGVVGVPPFAGALTSFYQSFNLAIW---PSDADPWKAFM
      70      80      90      100      110

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90      100      110      120      130
Cry1Ac  VQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPAALR---EEMRIQF
      . . . . .
gi|401  AQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALDSWKKAPVNLRSRRSQDRIRELF
      120      130      140      150      160      170

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140      150      160      170      180      190
Cry1Ac  NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYN
      . . . . .
gi|401  SQAESHFRNSMPSFAVSKFEVFLFLPTYAQAANTHLLKDAQVFGEEWYSSSEDIAEFYQ
      180      190      200      210      220      230

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200      210      220      230      240      250
Cry1Ac  DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRT
      . . . . .
gi|401  RQLKLTQQYTDHCVNWNVGLNLSLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDVR
      240      250      260      270      280      290

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260      270      280      290      300      310
Cry1Ac  YPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIIRSPHLMIDILNSITITYDAHRGE
      . . . . .
gi|401  YSKGVKTELTRDIFTDPIFLNALQYEGPTFSSIENSIRKPHLFDYLRGIEFHTRLRPGY
      300      310      320      330      340      350

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          320      330      340      350      360      370
Cry1Ac Y-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-L
          ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401 SGKDSFNYSWNGYVETRPSIGSNDTITSPFYGDK-SIEPIQKLSFD-GQKVYRTIANTDI
          360      370      380      390      400      410

          380      390      400      410      420
Cry1Ac YRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPQNNNVPPR
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401 AAFPDKGIYFGVTKVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPETTDEPLE
          420      430      440      450      460      470

          430      440      450      460      470      480
Cry1Ac QGFSHRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF
          ..... : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401 KAYSHQLNYAECFLMQDRRTI----PFFTWTWHRVDFNTIDAEEKITQLPVVKAYALS
          480      490      500      510      520      530

          490      500      510      520      530      540
Cry1Ac NG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNL
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401 SGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLF
          540      550      560      570      580

          550      560      570      580      590      600
Cry1Ac VNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401 VQNSNNDFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSNKIIY
          590      600      610      620      630      640

          610      620      630      640      650      660
Cry1Ac IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
          : . . . . . :
gi|401 IDKIEFIPVQ
          650

>>gi|40259|emb|CAA34983.1| unnamed protein product [Baci (659 aa)
  initn: 1007 initl: 435 opt: 1036 Z-score: 1214.5 bits: 235.9 E(): 9.9e-59
Smith-Waterman score: 1114; 33.646% identity (65.258% similar) in 639 aa overlap
(5-612:37-658)

          10      20
Cry1Ac          CMQAMDNNPNIN-ECIPYNCL----SNPEVEVLG
          . . . . . : . . . . . : . . . . . :
gi|402 RKMNNRNRSEYDTIKVTPNSELPTNHNQYPLADNPNSTLEELNYKEFLRMTADNSTEVLD
          10      20      30      40      50      60

          30      40      50      60      70      80
Cry1Ac GERIETGY-TPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWIGFPGSQ---WDAFL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 SSTVKDAVGTGLSV--VGQLLGVVGVFPFAGALTSFYQSFLNAIW---PSDADPWKAFM
          70      80      90      100      110

          90      100      110      120      130
Cry1Ac VQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALR---EEMRIQF
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 AQVEVLIDKKEIEYAKSKALAEQLQGNFEDYVNALDWSKKAPVNLRSRRSQDRIRELF
          120      130      140      150      160      170

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          140      150      160      170      180      190
Cry1Ac NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWFDAATINSRYN
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 SQAESHFRNSMPFSAVSKFEVLFPLPTAQAANTHLLLLKDAQVFGEEWYSSEDIAEFYQ
          180      190      200      210      220      230

          200      210      220      230      240      250
Cry1Ac DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRT
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 RQLKLTQQYTDHCVNWYVGLNSLRGSTDYDAWVKFNRFRREMTTLVLDLIVLFPFYDVR
          240      250      260      270      280      290

          260      270      280      290      300      310
Cry1Ac YPIRTVSQLTREIYTNPVLE-NFDGSRGSAQIEGSIRSPHLMIDLNSITTYTDAHRGE
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 YSKGVKTELTRDIFITDPIFTLNALQYEGPTFSSIENSIRKPHLFDYLRGIEFHTRLRPGY
          300      310      320      330      340      350

          320      330      340      350      360      370
Cry1Ac Y-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-L
          ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 SGKDSFNYSWNGYVETRPSIGSNDTITSPFYGDK-SIEPIQKLSFD-GQKVYRTIANTDI
          360      370      380      390      400      410

          380      390      400      410      420
Cry1Ac YRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPQNNNVPPR
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 AAFPDKGIYFGVTKVDFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPETTDEPLE
          420      430      440      450      460      470

          430      440      450      460      470      480
Cry1Ac QGFSHRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF
          ..... : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 KAYSHQLNYAECFLMQDRRTI----PFFTWTWHRVDFNTIDAEEKITQLPVVKAYALS
          480      490      500      510      520      530

          490      500      510      520      530      540
Cry1Ac NG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNL
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 SGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLF
          540      550      560      570      580

          550      560      570      580      590      600
Cry1Ac VNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|402 VQNSNNDFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSNKIIY
          590      600      610      620      630      640

          610      620      630      640      650      660
Cry1Ac IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
          : . . . . . :
gi|402 IDKIEFIPVQ
          650

>>gi|155684779|gb|ABU27034.1| Sequence 112 from patent U (659 aa)
  initn: 1007 initl: 435 opt: 1036 Z-score: 1214.5 bits: 235.9 E(): 9.9e-59
Smith-Waterman score: 1114; 33.646% identity (65.258% similar) in 639 aa overlap
(5-612:37-658)

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                10         20
Cry1Ac      CMQAMDNNPNIN-ECIPYNCL----SNPEVEVLG
gi|155      RKMNPNNRSEYDTIKVTPNSELPNTNHNQYPLADNPNSTLEELNLYKEFLRMTADNSTEVL
            10         20         30         40         50         60

                30         40         50         60         70         80
Cry1Ac      GERIETGY-TPIDISLSLTQFLLSSEFVPGAG----FVLGLVDIIWGFPGSQ---WDAFL
gi|155      SSTVKDAVGTGISV---VGQILGVVGVFPFAGALTSFYQSFLNAIW---PSDADPWKAFM
            70         80         90         100        110

                90         100        110        120        130
Cry1Ac      VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALR---EEMRIQF
gi|155      AQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALDSWKKAPVNLRSRRSQDRIRELF
            120        130        140        150        160        170

                140        150        160        170        180        190
Cry1Ac      NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYN
gi|155      SQAESHFRNSMPSFAVSKFEVLFLPTYQAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQ
            180        190        200        210        220        230

                200        210        220        230        240        250
Cry1Ac      DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPPNYDSRT
gi|155      RQLKLTQQYTDHCVNWNVGLNSLRGSTDYDAWVKFNRFRREMTLTVLDLIVLFFPYDVRL
            240        250        260        270        280        290

                260        270        280        290        300        310
Cry1Ac      YPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIRSPHLMIDILNSITTYTDAHRGE
gi|155      YSKGVKTELTRDIFTDPIFTLNALQEYGPFTFSSSIENSIRKPHLFDYLRGIEFHTRLRPGY
            300        310        320        330        340        350

                320        330        340        350        360        370
Cry1Ac      Y-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-L
gi|155      SGKDSFNYSWGNVETRPSIGSNDTITSPFYGDK-SIEPIQKLSFD-GQKVYRTIANTDI
            360        370        380        390        400        410

                380        390        400        410        420
Cry1Ac      YRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNNVPPR
gi|155      AAFPDKGIYFVTKVDVFSQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPPEPTTDEPLE
            420        430        440        450        460        470

                430        440        450        460        470        480
Cry1Ac      QGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF
gi|155      KAYSHQLNYAEFLMQDRRGTI----PFFTWTHRSVDFNTIDAEEKITQLPVVKAYALS
            480        490        500        510        520        530

                490        500        510        520        530        540
Cry1Ac      NG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTSTRYRVRVRYASVTPIHNL
gi|155      SGASIEGPGFTGGNLLFLKESNSIAK--FKVTLNSAALLQRVRYRIRYASTNLRFL

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                540        550        560        570        580
Cry1Ac      VNWGNSSIFSNTVTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVI
gi|155      VQNSNNDFLVIYINKTMNIDGDLTYQTFDFATSNSNMGFSGDTNDFIIGAESFVSNEKIY
            590        600        610        620        630        640

                610        620        630        640        650        660
Cry1Ac      IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
gi|155      IDKIEFIPVQ
            650

>>gi|12810106|gb|AAE44021.1| Sequence 112 from patent US (659 aa)
  initn: 1007 init1: 435 opt: 1036 Z-score: 1214.5 bits: 235.9 E(): 9.9e-59
Smith-Waterman score: 1114; 33.646% identity (65.258% similar) in 639 aa overlap
(5-612:37-658)

                10         20
Cry1Ac      CMQAMDNNPNIN-ECIPYNCL----SNPEVEVLG
gi|128      RKMNPNNRSEYDTIKVTPNSELPNTNHNQYPLADNPNSTLEELNLYKEFLRMTADNSTEVL
            10         20         30         40         50         60

                30         40         50         60         70         80
Cry1Ac      GERIETGY-TPIDISLSLTQFLLSSEFVPGAG----FVLGLVDIIWGFPGSQ---WDAFL
gi|128      SSTVKDAVGTGISV---VGQILGVVGVFPFAGALTSFYQSFLNAIW---PSDADPWKAFM
            70         80         90         100        110

                90         100        110        120        130
Cry1Ac      VQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALR---EEMRIQF
gi|128      AQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALDSWKKAPVNLRSRRSQDRIRELF
            120        130        140        150        160        170

                140        150        160        170        180        190
Cry1Ac      NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYN
gi|128      SQAESHFRNSMPSFAVSKFEVLFLPTYQAANTHLLLLKDAQVFGEEWGYSSEDIAEFYQ
            180        190        200        210        220        230

                200        210        220        230        240        250
Cry1Ac      DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPPNYDSRT
gi|128      RQLKLTQQYTDHCVNWNVGLNSLRGSTDYDAWVKFNRFRREMTLTVLDLIVLFFPYDVRL
            240        250        260        270        280        290

                260        270        280        290        300        310
Cry1Ac      YPIRTVSQLTREIYTNPVLE-NFDGSRGSAQGIIEGSIRSPHLMIDILNSITTYTDAHRGE
gi|128      YSKGVKTELTRDIFTDPIFTLNALQEYGPFTFSSSIENSIRKPHLFDYLRGIEFHTRLRPGY
            300        310        320        330        340        350

                320        330        340        350        360        370
Cry1Ac      Y-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSST-L
gi|128      SGKDSFNYSWGNVETRPSIGSNDTITSPFYGDK-SIEPIQKLSFD-GQKVYRTIANTDI

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360      370      380      390      400      410
Cry1Ac  YRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPR
      : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . :
gi|128  AAFPdGKIYFGVTKVDFsQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPpETTDEPLE
420      430      440      450      460      470
Cry1Ac  QGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|128  KAYSHQLNYAEcFLMQDRRGTI----PFFTWTThRSVDFNTIDAeKITQLPvVKAYALS
480      490      500      510      520      530
Cry1Ac  NG-SVISGPGFTGGDLVRLNssGNNIQNRGYIEVPIHFPSTSTRYRVrVRYASVTPiHLN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|128  SGASIIeGPGFTGGNLLFLKessNSIAK---FKVTLNSAALLQRyRVrIRYASTTnLRLF
540      550      560      570      580
Cry1Ac  VNWGNSSIFsNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNfSGTAGVI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|128  VQNSNNDfLVIIYINKTMNIDGLTYQTFDFATSNMgFSGDTNDFIIgAESFVSNekiY
590      600      610      620      630      640
Cry1Ac  IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      : . . . . . :
gi|128  IDKIEFIPVQ
650

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>>gi|40188419|gb|AAR75944.1| Sequence 112 from patent US (659 aa)  
 initn: 1007 initl: 435 opt: 1036 Z-score: 1214.5 bits: 235.9 E(): 9.9e-59  
 Smith-Waterman score: 1114; 33.646% identity (65.258% similar) in 639 aa overlap  
 (5-612:37-658)

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10      20
Cry1Ac  CMQAMDNPNIN-ECIPYCL----SNPEVEVLG
      : . . . . . :
gi|401  RKMNNRSEYDITIKVTPNSELPTNHNQYPLADNPSTLEELNYKEFLRMTADNSTEVLd
10      20      30      40      50      60
Cry1Ac  GERIETGY-TPIDISLSLTQFLlSEFVPGAG----FVLGLVDIIWGIgFSQ---WDAFL
      : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . :
gi|401  SStVKDAVGTGISV---VGQILGVVGVPFAGALTSFYQsFLNAIw----PSDADPWKAfM
70      80      90      100      110
Cry1Ac  VQIEQLINQRIEEFARNQAIsrLEGLSNLYQIYAESFrEWEADPTNPALR---EEMRIQF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  AQVEVLIDKKIEEYAKSkALAEQLGQNfEDYVNALDSWKKAPVNLRSRRSQDRIRelF
120      130      140      150      160      170
Cry1Ac  NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLrDVSVFGRQWGfDAATINSRYN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  SQAEShFRNSMPSFAVSKFEVLFLPTyAQAAntHLLLLKDAQVfGEEWGYSSEDIaEFYQ
140      150      160      170      180      190
Cry1Ac  NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLrDVSVFGRQWGfDAATINSRYN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  SQAEShFRNSMPSFAVSKFEVLFLPTyAQAAntHLLLLKDAQVfGEEWGYSSEDIaEFYQ

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180      190      200      210      220      230
Cry1Ac  DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRT
      : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . :
gi|401  RQLKLTQQYTDHCVNWNyVGLNSLRGStYDAWVKFNrFRREMTLTVLDLIVLFPFYdVRL
240      250      260      270      280      290
Cry1Ac  YPIRTVSQTLTREIYTNpVLE-NFDGSGFRGSAQGIeGSIRSPHLMDILNSITiYTDahrGE
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  YSKGVKTELTRDIFTDPIfTLNALQeYGPtFSSIENSIRKPHLFDYLRGIEFhTRLRPGY
300      310      320      330      340      350
Cry1Ac  Y-----YWSGHQIMASpVGFSGPEFTfPlyGTMGNAAPQQRiVAQLGQGVYrTLSSt-L
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  SGKDSFNyWSGNyVETRPsiGSNDTITSPfyGDK-SIEPIQKLsFD-GQKVYrTIAntDI
360      370      380      390      400      410
Cry1Ac  YRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPR
      : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . :
gi|401  AAFPdGKIYFGVTKVDFsQYDDQKNETSTQTYDSKRYNGYLGAQDSIDQLPpETTDEPLE
420      430      440      450      460      470
Cry1Ac  QGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  KAYSHQLNYAEcFLMQDRRGTI----PFFTWTThRSVDFNTIDAeKITQLPvVKAYALS
480      490      500      510      520      530
Cry1Ac  NG-SVISGPGFTGGDLVRLNssGNNIQNRGYIEVPIHFPSTSTRYRVrVRYASVTPiHLN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  SGASIIeGPGFTGGNLLFLKessNSIAK---FKVTLNSAALLQRyRVrIRYASTTnLRLF
540      550      560      570      580
Cry1Ac  VNWGNSSIFsNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNfSGTAGVI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|401  VQNSNNDfLVIIYINKTMNIDGLTYQTFDFATSNMgFSGDTNDFIIgAESFVSNekiY
590      600      610      620      630      640
Cry1Ac  IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      : . . . . . :
gi|401  IDKIEFIPVQ
650

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>>gi|114210123|emb|CAL40966.1| unnamed protein product [ (652 aa)  
 initn: 1000 initl: 432 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58  
 Smith-Waterman score: 1104; 34.642% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLlSEFVPGAG----FVLGLVDIIWGIgFSQ---W
      : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . :
gi|114  SStEVLdNSTVKDAVGTGISVVGQILGVVGVPFAGALTSFYQsFLNTIw----PSDADPW

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60      70      80      90      100
Cry1Ac 80      90      100      110      120      130
DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|114 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110     120     130     140     150     160

140     150     160     170     180     190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|114 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|114 EPHYRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTLVLDLIVLFPFY
230     240     250     260     270     280

260     270     280     290     300     310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIRSPHMLDILNSITIYTDA
gi|114 DIRLYSGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIRKPHLFDYLQGIEFHTRL
290     300     310     320     330     340

320     330     340     350     360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|114 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350     360     370     380     390     400

370     380     390     400     410     420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLP SAVYRKSGTV---DSLDEIPPQ
gi|114 NTDVAAWPNKGYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410     420     430     440     450     460

430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|114 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470     480     490     500     510

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|114 VKAYALS SSGAIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRIRYAS
520     530     540     550     560     570

540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|114 TTNLRLFQNSNNDPLVIYINKTMNKDDDLTYNTFDLATNSNMGFSGDKNELIIGAESF
580     590     600     610     620     630

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
.. . . . .

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gi|114 VSNEKIYIDKIEFIPVQL
640     650
>>gi|29702306|gb|AA096391.1| Sequence 6 from patent US 6 (652 aa)
initn: 1000 init1: 432 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.642% identity (67.065% similar) in 586 aa overlap
(55-612:82-650)

30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
gi|297 SSTEVLDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIW---PSDADPW
60      70      80      90      100

80      90      100     110     120     130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|297 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110     120     130     140     150     160

140     150     160     170     180     190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
gi|297 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDEV
170     180     190     200     210     220

200     210     220     230     240     250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|297 EPHYRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFREMTLTLVLDLIVLFPFY
230     240     250     260     270     280

260     270     280     290     300     310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIRSPHMLDILNSITIYTDA
gi|297 DIRLYSGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIENSIRKPHLFDYLQGIEFHTRL
290     300     310     320     330     340

320     330     340     350     360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|297 QPGYFGKDSFNWYSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350     360     370     380     390     400

430     440     450     460     470     480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTTHRSVDFNTIDAEEKITQLPV
470     480     490     500     510

490     500     510     520     530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|297 VKAYALS SSGAIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRIRYAS
520     530     540     550     560     570

540     550     560     570     580     590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFSTSSLGN-IVGVRNF
gi|297 TTNLRLFQNSNNDPLVIYINKTMNKDDDLTYNTFDLATNSNMGFSGDKNELIIGAESF
580     590     600     610     620     630

600     610     620     630     640     650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
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gi|297 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|297 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYNTFDLATTNSNMGFGSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|297 VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|77370839|gb|ABA68335.1| Sequence 6 from patent US 6 (652 aa)  
 initn: 1000 initl: 432 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58  
 Smith-Waterman score: 1104; 34.642% identity (67.065% similar) in 586 aa overlap  
 (55-612:82-650)

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      30      40      50      60      70
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGFPGSQ---W
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTIWI---PSDADPW
      60      70      80      90      100

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      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 KAFMAQVEVLIDDKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAATIN
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLKDAQVFGEEWYSSSEDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 EFYHRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAVVKFNRFRREMTTLVLDLIVLFPFY
      230      240      250      260      270      280

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      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSIKPHLMDILNSITITYTDA
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 DIRLYSKGVKTELTRDIFTDPIFSLNTLQEYGPFTLSIENSIRKPHLFDYQGIIEFHTRL
      290      300      310      320      330      340

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      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYRTLS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 QPGYFGKDSFNWYSGNYVETRPSIGSSKTTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

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      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :

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gi|773 NTDVAAWPNGKVVYLVTKVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRSDVDFNTIDAEEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

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      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 TTNLRLRFVQNSNNDLFLVIYINKTMNKDDDLTYNTFDLATTNSNMGFGSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|773 VSNEKIYIDKIEFIPVQL
      640      650

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>>gi|114210129|emb|CAL40969.1| unnamed protein product [ (653 aa)  
 initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58  
 Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap  
 (55-612:83-651)

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      30      40      50      60      70
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDIIWGFPGSQ---W
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|114 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTIWI---PSDADPW
      60      70      80      90      100

```

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      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|114 KAFMAQVEVLIDDKIEEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAATIN
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|114 RELFSQAESHFRNSMPFAVSKFEVLFPLPTYAQAANTHLLKDAQVFGEEWYSSSEDVA
      170      180      190      200      210      220

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      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|114 EFYRRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAVVKFNRFRREMTTLVLDLIVLFPFY
      230      240      250      260      270      280

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      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFRGSAQGIIEGSIKPHLMDILNSITITYTDA
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :

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gi|114 DIRLSYKGVKTELTRDIFDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLQGIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|114 RPYGFKGDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
370 380 390 400 410 420

gi|114 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|114 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|114 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIHLNWNWGNSSIFSNTV PATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|114 TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|114 VSNEKIYIDKIEFIPVQL
640 650

>>gi|29702309|gb|AA096394.1| Sequence 12 from patent US (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|297 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTI W---PSDADPW
60 70 80 90 100

Cry1Ac DAFVLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|297 KAFMAQVEVLIDKIEEYAKSKALAEQLQGNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

gi|297 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEWGYSSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|297 EFYRRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTTLVLDLIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQGI EGSIRSPHMDILNSITIYTDA
260 270 280 290 300 310

gi|297 DIRLSYKGVKTELTRDIFDPIFLLTTLQKYGPTFLSIENSIRKPHLFDYLQGIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|297 RPYGFKGDSFNYSWGNVYVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
370 380 390 400 410 420

gi|297 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
430 440 450 460 470 480

gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRSVDFNTIDA EKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|297 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIHLNWNWGNSSIFSNTV PATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|297 TTNLRLVFNQSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|297 VSNEKIYIDKIEFIPVQL
640 650

>>gi|114210139|emb|CAL40974.1| unnamed protein product [ (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70



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gi|773 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSISFNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNMGMFGSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 VSNEKIYIDKIEFIPVQL
640 650

>>gi|29702314|gb|AAO96399.1| Sequence 22 from patent US (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|297 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|297 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190

gi|297 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|297 EFYRRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTTLVLDIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFGSAQIEGSIRSPHLMIDILNSITIYTDA
260 270 280 290 300 310

gi|297 DIRLYSKGVKTELTRDIFTDPIFLLTTLQKYGPTFLSIENSIRKPHLFYDLQGIIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
320 330 340 350 360

gi|297 RPYGFGKDFSNFYWSGNYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQGV---DSLDEIPPQ
370 380 390 400 410 420

gi|297 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFHSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
430 440 450 460 470 480

gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWHRVDFVNTIDAEEKITQLPV
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVLSGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRVRYAS
490 500 510 520 530

gi|297 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTPIHNLVNWGNSISFNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
540 550 560 570 580 590

gi|297 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNMGMFGSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|297 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370847|gb|ABA68343.1| Sequence 22 from patent US (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
30 40 50 60 70

gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|773 KAFMAQVEVLIDKKEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
140 150 160 170 180 190

gi|773 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYQAANTHLLKDAQVFGEEWGYSSDVA
170 180 190 200 210 220

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|773 EFYRRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTTLVLDIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRFGSAQIEGSIRSPHLMIDILNSITIYTDA
260 270 280 290 300 310

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gi|773 DIRLSYKGVKTELTRDIFLDTLQKYGPTFLSLIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYR TLS
320 330 340 350 360

gi|773 RPYGFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTV---DSLDEIPPQ
370 380 390 400 410 420

gi|773 NTDVAAWPNGKVVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
430 440 450 460 470 480

gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWT HRSVDFNTIDA EKITQLP V
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|773 VKAYALSSGASIIIEGPGFTGGNLLFLKESSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAF TSSLGN-IVGVRNF
540 550 560 570 580 590

gi|773 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|773 VSNEKIYIDKIEFIPVQL
640 650

>>gi|29702315|gb|AAO96400.1| Sequence 24 from patent US (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
30 40 50 60 70

gi|297 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSLNTIW---PSDADPW
60 70 80 90 100

Cry1Ac DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
80 90 100 110 120 130

gi|297 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
140 150 160 170 180 190

gi|297 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSEDVA
170 180 190 200 210 220

Cry1Ac SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
200 210 220 230 240 250

gi|297 EFYRRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAVVKFNRFRREMTTLVLDIVLFPFY
230 240 250 260 270 280

Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSFRGSAQIEGSIRSPHMDILNSIT IYTD
260 270 280 290 300 310

gi|297 DIRLSYKGVKTELTRDIFLDTLQKYGPTFLSLIENSIRKPHLFDYLGQIEFHTRL
290 300 310 320 330 340

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAQLGGQVYR TLS
320 330 340 350 360

gi|297 RPYGFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350 360 370 380 390 400

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTV---DSLDEIPPQ
370 380 390 400 410 420

gi|297 NTDVAAWPNGKVVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
410 420 430 440 450 460

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
430 440 450 460 470 480

gi|297 TTDEPLEKAYSHQLNYAECFLMQDRRGTI-----PFFTWT HRSVDFNTIDA EKITQLP V
470 480 490 500 510

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
490 500 510 520 530

gi|297 VKAYALSSGASIIIEGPGFTGGNLLFLKESSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAF TSSLGN-IVGVRNF
540 550 560 570 580 590

gi|297 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
600 610 620 630 640 650

gi|297 VSNEKIYIDKIEFIPVQL
640 650

>>gi|77370842|gb|ABA68338.1| Sequence 12 from patent US (653 aa)
initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
30 40 50 60 70

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      :: :: : .... :: ... :
gi|773 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLLNTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|773 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 EFYRRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGIIEGSIKPHLMDILNSITITDA
      : : : . : : : : : : : . : . : . : : : : : : : : : : : : : : : : : : :
gi|773 DIRLYSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|773 RPYGFKDSFNWWSGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|773 NTDVAAPNGKVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      . . . : : : : : : . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|773 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWRSVDFNFNTIDA EKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
      . : . : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|773 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|773 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650

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Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . . : : : : : :
gi|773 VSNEKIYIDKIEFIPVQL
      640      650

>>gi|114210141|emb|CAL40975.1| unnamed protein product [ (653 aa)
      initn: 998 initl: 430 opt: 1035 Z-score: 1213.4 bits: 235.7 E(): 1.1e-58
Smith-Waterman score: 1104; 34.812% identity (67.065% similar) in 586 aa overlap
(55-612:83-651)

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLLNTIW---PSDADPW
      60      70      80      90      100

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
      110      120      130      140      150      160

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|114 RELFSQAESHFRNSMPSFAVSKFEVLFPLTYAQAANTHLLLLKDAQVFGEEGWYSSSDVA
      170      180      190      200      210      220

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
      : : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 EFYRRQLKLTQQYTDHCVNWYNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
      230      240      250      260      270      280

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPV-LENFDGSRGSAQGIIEGSIKPHLMDILNSITITDA
      : : : . : : : : : : : . : . : . : : : : : : : : : : : : : : : : : : :
gi|114 DIRLYSKGVKTELTRDIFLTLQKYGPTFLSIENSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|114 RPYGFKDSFNWWSGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQ
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|114 NTDVAAPNGKVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA
      . . . : : : : : : . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|114 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTWRSVDFNFNTIDA EKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
      . : . : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 VKAYALSSGASIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNWNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|114 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMFGSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650

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Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|114 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTIPIHLNVNWNSSIFSNTVVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|114 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|114 VSNEKIYIDKIEFIPVQL

>>gi|40188383|gb|AAR75908.1| Sequence 14 from patent US (652 aa)
initn: 992 initl: 424 opt: 1034 Z-score: 1212.3 bits: 235.4 E(): 1.3e-58
Smith-Waterman score: 1103; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGI FGP SQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSF LNTI W---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEIEYAKSKALAE LQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLF LPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDIVLFPFY

Cry1Ac DSRTYPIRITVSQLTRREIYTNPVLE-NFDGSRFRSAQGGIEGSI RSPHLMIDILNSITITYTDA
gi|401 DINLYSKGVKTELTRDIFTDPIFSLNTLQEQYPTFLSIENSIRKPHLFDYLOGIEFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQGVYRTLS
gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTI TSPFYGDK-STEPVQKLSFD-GQKVYRTIA

370 380 390 400 410 420

Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGT V---DSLDEIPQP
gi|401 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVS AQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPA
gi|401 TTDEPLEKAYSHQLNVAECFLMQDRRTI-----PFFTWT HRSVDFNTIDA EKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTIPIHLNVNWNSSIFSNTVVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLRFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL

>>gi|40145936|gb|AAR61454.1| Sequence 14 from patent US (652 aa)
initn: 992 initl: 424 opt: 1034 Z-score: 1212.3 bits: 235.4 E(): 1.3e-58
Smith-Waterman score: 1103; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGI FGP SQ---W
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSF LNTI W---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|401 KAFMAQVEVLIDKKEIEYAKSKALAE LQGLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLF LPTYAQAANTHLLLKDAQVFGEEWGYSSSEDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDIVLFPFY

260 270 280 290 300 310

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSIIRSPHLMIDLNSITTYTDA

gi|401 DINLYSKGVKTELTRDIFTDPIFSLNLTQEQYGPFTFLSIENSIIRKPHLFDYLQGI EFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

gi|401 QPGYFGKDSFNWYSGNYVETRPSIGSSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ

gi|401 NTDVAAWPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRVDFNTIDA EKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|401 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|401 VSNEKIYIDKIEFIPVQL

>>gi|155684743|gb|ABU26998.1| Sequence 14 from patent US (652 aa)
initn: 992 init1: 424 opt: 1034 Z-score: 1212.3 bits: 235.4 E(): 1.3e-58
Smith-Waterman score: 1103; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIHWGIFGSPQ---W

gi|155 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIIV---PSDADPW

Cry1Ac DAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI

gi|155 KAFMAQVEVLIDKKIEYAKSKALAEQLQGLQNNFEDYVNALNSWKKTPLSRKRSDQRI

Cry1Ac

Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATIN

gi|155 RBLFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLKDAQVFGEEWYSSDVA

Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY

gi|155 EPYHRQLKLTQQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFREMTLTVLDIVLFPFY

Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSRFRGSAQGIIEGSIIRSPHLMIDLNSITTYTDA

gi|155 DINLYSKGVKTELTRDIFTDPIFSLNLTQEQYGPFTFLSIENSIIRKPHLFDYLQGI EFHTRL

Cry1Ac HRGEY-----YWSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

gi|155 QPGYFGKDSFNWYSGNYVETRPSIGSSKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

Cry1Ac ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ

gi|155 NTDVAAWPNGKVLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE

Cry1Ac NNNVPPRQGFSHRSLHVSVMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPA

gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRTI----PFFTWTHRVDFNTIDA EKITQLPV

Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS

gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS

Cry1Ac VTPIHNLVNWGNSSIFSNTPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF

gi|155 TTNLRLFVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF

Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL

gi|155 VSNEKIYIDKIEFIPVQL

>>gi|12810070|gb|AAE43985.1| Sequence 14 from patent US (652 aa)
initn: 992 init1: 424 opt: 1034 Z-score: 1212.3 bits: 235.4 E(): 1.3e-58
Smith-Waterman score: 1103; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

Cry1Ac







```

          30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
          60      70      80      90      100

```

```

          80      90      100      110      120      130
Cry1Ac  DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
          110     120     130     140     150     160

```

```

          140     150     160     170     180     190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
          170     180     190     200     210     220

```

```

          200     210     220     230     240     250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
          230     240     250     260     270     280

```

```

          260     270     280     290     300     310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQIEGSIKPHLMDILNSITTYTDA
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  DIVLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTPLFSIENSIRKPHLFDYLGQIEFHTRL
          290     300     310     320     330     340

```

```

          320     330     340     350     360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
          350     360     370     380     390     400

```

```

          370     380     390     400     410     420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
          410     420     430     440     450     460

```

```

          430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  TTDEPLEKAYSHQLNYAECFLMQRDRGTI----PFFTWTTHRSVDFNNTIDAEEKITQLPVP
          470     480     490     500     510

```

```

          490     500     510     520     530
Cry1Ac  VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYAS
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
          520     530     540     550     560     570

```

```

          540     550     560     570     580     590
Cry1Ac  VPIHLNWNWGNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  TTNLRLFLVQNSNNDPLVIYINKTMNKDDDLTYQTFDLATTSNMGFSGDKNELIIGAESF
          580     590     600     610     620     630

```

```

          600     610     620     630     640     650
Cry1Ac  SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
          ..  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|401  VSNEKIYIDKIEFIPVQL
          640     650

```

>>gi|12810084|gb|AAE43999.1| Sequence 42 from patent US (652 aa)  
 initn: 990 initl: 422 opt: 1032 Z-score: 1209.9 bits: 235.0 E(): 1.8e-58  
 Smith-Waterman score: 1101; 34.642% identity (66.894% similar) in 586 aa overlap  
 (55-612:82-650)

```

          30      40      50      60      70
Cry1Ac  VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGIFGPSQ---W
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFLNTIWIW---PSDADPW
          60      70      80      90      100

```

```

          80      90      100     110     120     130
Cry1Ac  DAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  KAFMAQVEVLIDKKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
          110     120     130     140     150     160

```

```

          140     150     160     170     180     190
Cry1Ac  Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  RELFSQAESHFRNSMPSFAVSKFEVLFPLPTYAQAANTHLLLLKDAQVFGEEWGYSSDVA
          170     180     190     200     210     220

```

```

          200     210     220     230     240     250
Cry1Ac  SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTLTVLDIVSLFPNY
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFY
          230     240     250     260     270     280

```

```

          260     270     280     290     300     310
Cry1Ac  DSRTYPIRTVSQLTREIYTNPVLNFDGSGFRGSAQIEGSIKPHLMDILNSITTYTDA
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  DIVLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTPLFSIENSIRKPHLFDYLGQIEFHTRL
          290     300     310     320     330     340

```

```

          320     330     340     350     360
Cry1Ac  HRGEY-----YWSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  QPGYFGKDSFNYSWGNVYVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
          350     360     370     380     390     400

```

```

          370     380     390     400     410     420
Cry1Ac  ST-LYRRP---FNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  NTDVAAWPNKGVYLVGTVKDFVDFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
          410     420     430     440     450     460

```

```

          430     440     450     460     470     480
Cry1Ac  NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
          ::  ::  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|128  TTDEPLEKAYSHQLNYAECFLMQRDRGTI----PFFTWTTHRSVDFNNTIDAEEKITQLPVP
          470     480     490     500     510

```



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```

                260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIKRSRPHLMDILNSITIIYTD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DIVLSKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSLENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

                320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAVQLGGVYR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

                370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NTDVAAWPNKGVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410      420      430      440      450      460

                430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEDITQLPV
470      480      490      500      510

                490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VKAYALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

                540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

                600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VSNEKIYIDKIEFIPVQL
640      650

>>gi|40145924|gb|AAR61448.1| Sequence 2 from patent US 6 (652 aa)
  initn: 992 initl: 432 opt: 1031 Z-score: 1208.7 bits: 234.8 E(): 2.1e-58
Smith-Waterman score: 1100; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

                30      40      50      60      70
Cry1Ac VEVLGGIERIETGYPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFPGSQ---W
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SSTEVLNDSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFINTIWIW---PSDADPW
60      70      80      90      100

                80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEA-DPTNPALEEMRI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKFHHSRRSRKRSQDRI
110      120      130      140      150      160

```

```

                140      150      160      170      180      190
Cry1Ac Q--FNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSSDVA
170      180      190      200      210      220

                200      210      220      230      240      250
Cry1Ac SRYNLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 EPHYRQLKLTQQYTDHCVNWNVYVGLNGLRGSTYDAVVKFNRFRREMTLTVLDIVLFPFNY
230      240      250      260      270      280

                260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQIEGSIKRSRPHLMDILNSITIIYTD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 DIRLSKGVKTELTRDIFTDPIFSLNLTQEQYGTFLSLENSIRKPHLFDYLGQIEFHTRL
290      300      310      320      330      340

                320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFFLYGTMGNAAPQQRIVAVQLGGVYR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKTIITSPFYGDK-STEPVQKLSFD-GQKVYRTIA
350      360      370      380      390      400

                370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTV---DSLDEIPPQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 NTDVAAWPNKGVYLVGTVKDFSQYDDQK---NETSTQTYDSKRNNHVSQAQDSIDQLPPE
410      420      430      440      450      460

                430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEDITQLPV
470      480      490      500      510

                490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

                490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKSSNSIAK---FKVTLNSAALLQRYRVRIRYAS
520      530      540      550      560      570

                540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580      590      600      610      620      630

                600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 VSNEKIYIDKIEFIPVQL
640      650

>>gi|155684737|gb|ABU26992.1| Sequence 2 from patent US (652 aa)
  initn: 992 initl: 432 opt: 1031 Z-score: 1208.7 bits: 234.8 E(): 2.1e-58
Smith-Waterman score: 1100; 34.642% identity (66.894% similar) in 586 aa overlap
(55-612:82-650)

```



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```

      470      480      490      500      510
Cry1Ac 490 500 510 520 530
VKG NLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|128 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

```

```

      540      550      560      570      580      590
Cry1Ac VPIHLNVNWGSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|128 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

```

```

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|128 VSNEKIYIDKIEFIPVQL
640 650

```

>>gi|40188377|gb|AAR75902.1| Sequence 2 from patent US 6 (652 aa)  
 initn: 992 init1: 432 opt: 1031 Z-score: 1208.7 bits: 234.8 E(): 2.1e-58  
 Smith-Waterman score: 1100; 34.642% identity (66.894% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|401 SSTEVLDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW---PSDADPW
60 70 80 90 100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRI
gi|401 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKFHHSRRSKRSQDRI
110 120 130 140 150 160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|401 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLKDAQVFGEEWGYSSPEDVA
170 180 190 200 210 220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|401 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLVLDLIVLFPFY
230 240 250 260 270 280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTYPIRTVSQLTREIYTNPVLE-NFDGSFRGSAQGGIEGSIKPHLMDILNSITTYTDA
gi|401 DIRLYSKGVKTELTRDIFTDPIFSLNLTQYEGPTFLSIENSIRKPHLFDYLGIEFHTRL
290 300 310 320 330 340

```

```

      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS
gi|401 QPGYFGKDSFNYSWGNVETRPSIGSSKITITSPFYGDK-STEPVQKLSFD-GQKVYRTIA

```

```

      350      360      370      380      390      400
Cry1Ac 370 380 390 400 410 420
ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQ
gi|401 NTDVAAWPNKGKYLGVTKVDFSQYDDQK---NETSTQTYDSKRNGHVSQAQDSIDQLPPE
410 420 430 440 450 460

```

```

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPA
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTHRVDFNTIDAEEKITQLPV
470 480 490 500 510

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      490      500      510      520      530
Cry1Ac VKG NLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
gi|401 VKAYALSSGASIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
520 530 540 550 560 570

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      540      550      560      570      580      590
Cry1Ac VPIHLNVNWGSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
580 590 600 610 620 630

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      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|401 VSNEKIYIDKIEFIPVQL
640 650

```

>>gi|155684739|gb|ABU26994.1| Sequence 6 from patent US (652 aa)  
 initn: 988 init1: 420 opt: 1030 Z-score: 1207.5 bits: 234.6 E(): 2.4e-58  
 Smith-Waterman score: 1099; 34.642% identity (66.724% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGIFGPSQ---W
gi|155 SSTEVLDNSTVKDAVGTGISVVGQILGVVGVFPFAGALTSFYQSFNLTIW---PSDADPW
60 70 80 90 100

```

```

      80      90      100      110      120      130
Cry1Ac DAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
gi|155 KAFMAQVEVLIDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSQDRI
110 120 130 140 150 160

```

```

      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATIN
gi|155 RELFSQAESHFRNSMPFAVSKFEVLFPLTYAQAANTHLLLKDAQVFGEEWGYSSPEDVA
170 180 190 200 210 220

```

```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNY
gi|155 EPHYRQLKLTQQYTDHCVNWNVGLNGLRGSTYDAWVKFNRFRREMTLVLDLIVLFPFY

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Smith-Waterman score: 1091; 34.300% identity (66.894% similar) in 586 aa overlap (55-612:82-650)

Sequence alignment for Cry1Ac vs gi|401. Includes residue numbers 30-70, 80-130, 140-190, 200-250, 260-310, 320-360, 370-420, 430-480, 490-540, 540-590.

Sequence alignment for gi|401 vs Cry1Ac. Includes residue numbers 580-630, 600-650.

>>gi|40188396|gb|AAR75921.1| Sequence 40 from patent US (652 aa)
initn: 980 initl: 412 opt: 1022 Z-score: 1198.1 bits: 232.8 E(): 8.2e-58
Smith-Waterman score: 1091; 34.300% identity (66.894% similar) in 586 aa overlap (55-612:82-650)

Sequence alignment for Cry1Ac vs gi|401. Includes residue numbers 30-70, 80-130, 140-190, 200-250, 260-310, 320-360, 370-420, 430-480, 490-540, 540-590.

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... : ..... : ... :... :... : : .....
gi|401 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      : : : : ..... : : : : ..... : : : : .....
gi|401 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      : : : : ..... : : : : ..... : : : : .....
gi|401 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . : : : : :
gi|401 VSNEKIYIDKIEFIPVQL
      640      650

```

>>gi|12810083|gb|AAE43998.1| Sequence 40 from patent US (652 aa)  
 initn: 980 init1: 412 opt: 1022 Z-score: 1198.1 bits: 232.8 E(): 8.2e-58  
 Smith-Waterman score: 1091; 34.300% identity (66.894% similar) in 586 aa overlap  
 (55-612:82-650)

```

      30      40      50      60      70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDIIWGFGPSQ---W
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 SSTEVLNDNSTVKDAVGTGISVVGQILGVVGVFPAGALTSFYQSFLNTIWI---PSDADPW
      60      70      80      90      100

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```

      80      90      100      110      120      130
Cry1Ac DAFVLQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTN-PALREEMRI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 KAFMAQVEVLIDDKIEEYAKSKALAEQLQNNFEDYVNALNSWKKTPLSLRSKRSDQRI
      110      120      130      140      150      160

```

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      140      150      160      170      180      190
Cry1Ac Q--FNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATIN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 RELFSQAESHFRNSMPSFAVSKFEVLFLPTYAQAANTHLLLLKDAQVFGEEWGYSSQDVA
      170      180      190      200      210      220

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```

      200      210      220      230      240      250
Cry1Ac SRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVLSLFPNY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 EPHYRQLKLTQOQYTDHCNVNWNVGLNGLRGSTYDAWVKFNRFRREMTLTLVLDLIVLFPFF
      230      240      250      260      270      280

```

```

      260      270      280      290      300      310
Cry1Ac DSRTPYPIRTVSQLTREIYTNPVLNFDGSRFRGSAQIEGSIIRSPHLMIDILNSITITYTDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NILLYSKGVKTELTRDIFTDPIFSLNTLQEQYGTFLSIEANSIRKPHLFDYLGQIEFHTRL
      290      300      310      320      330      340

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      320      330      340      350      360
Cry1Ac HRGEY-----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLS

```

```

. : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi|128 PQGYFGKDSFNWWSGNYVETRPSIGSSKITITSPFFYGDK-STEPVQKLSFD-GQKVVRTIA
      350      360      370      380      390      400

      370      380      390      400      410      420
Cry1Ac ST-LYRRP---FNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTV--DSLDEIPPO
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128 NTDVAAWPNKGVYLVGTVKVDVFSQYDDQK---NETSTQTYDSKRNNGHVSAQDSIDQLPPE
      410      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac NNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIIPA
      : : : : ..... : : : : ..... : : : : .....
gi|128 TTDEPLEKAYSHQLNYAECFLMQDRRGTI----PFFTWTNRSVDFNTIDAEKITQLPV
      470      480      490      500      510

      490      500      510      520      530
Cry1Ac VKGNFLFNG-SVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS
      : : : : ..... : : : : ..... : : : : .....
gi|128 VKAYALSSGASIIIEGPGFTGGNLLFLKESNSIAK---FKVTLNSAALLQRYRVRIRYAS
      520      530      540      550      560      570

```

>>gi|112088023|gb|ABI06945.1| Sequence 6 from patent US (653 aa)  
 initn: 1612 init1: 888 opt: 972 Z-score: 1139.1 bits: 221.9 E(): 1.6e-54  
 Smith-Waterman score: 1639; 45.763% identity (70.108% similar) in 649 aa overlap  
 (4-628:25-653)

```

      540      550      560      570      580      590
Cry1Ac VTIPIHLNVNWNSSIFSNTVPATATSLDNL--QSSDFGYFESANAFTSSLGN-IVGVRNF
      : : : : ..... : : : : ..... : : : : .....
gi|128 TTNLRLFVQNSNNDFLVIYINKTMNKDDDLTYQTFDLATTNSNMGFSGDKNELIIGAESF
      580      590      600      610      620      630

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
      . . : : : : :
gi|128 VSNEKIYIDKIEFIPVQL
      640      650

```

```

      10      20      30
Cry1Ac CMQAMDNPNINCEIPYCNLSNPEVEVLGGERIETGYTP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 ENENEIINALSIPAVSNHSAQMDLSLDARIEDSLCIAEGNNINP---LVSASTVQGT---
      10      20      30      40      50

```

```

      40      50      60      70      80      90
Cry1Ac IDISLSLTQFLLSEFVPG-AGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEFARN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 INIAGRILGVLVGPPAGQLASFPYFLVGLWPS-GRDPWEIIFLEYVEQLIRQVQVTESTRN
      60      70      80      90      100      110

```

```

      100      110      120      130      140      150
Cry1Ac QAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 TAIARLEGLGRGYSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEE
      120      130      140      150      160      170

```

```

      160      170      180      190      200      210
Cry1Ac VPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTG

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gi|112 VPLLVMVYAQAANLHLLLRDASLFGSEWGMASDDVNQYYQEQIRYTEEYSNHCVQWYNTG
      180   190   200   210   220   230
      220   230   240   250   260   270
Cry1Ac LERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTPVRTVSQLTREIYTNPVLE
      . . . . .
gi|112 LNNLRGTNAESWLRYNQFRRLDTLGVLDLVALFPSPYDTRTPINTSAQLTREIYTDPIGR
      240   250   260   270   280   290
      280   290   300   310   320
Cry1Ac -NFDGSGFRG-----SAQGIEGSI-RSPHLMILNSITTYTDAHRGEYYWSGHQIMA
      . . . . .
gi|112 TNAPSGFASTNWFNNAPSFSAEAAIFRPPHLLDFPEQLTIYSASSR----WSSTQHMN
      300   310   320   330   340
      330   340   350   360   370   380
Cry1Ac SPVGFSGPEFTF-PLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNIGINNQQLS
      . . . . .
gi|112 YWVGH---RLNFRPIGGTLNTSTQGLTNNTSINPVTLHYVSSRDVYRTESNAGTNILFTT
      350   360   370   380   390   400
      390   400   410   420   430
Cry1Ac VLDGTEFAYGTSSNLPASVYRKSQVDSLDEIPP-----QNNVPPRQGFSHRLSHVS
      . . . . .
gi|112 PVNGVPWARFNFTL--RIFMKEAPLPTVNRIRELGFNYLIQKLNHYQKQQNDQIMNHIV
      410   420   430   440   450   460
      440   450   460   470   480   490
Cry1Ac M---FRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGP
      . . . . .
gi|112 IDISYRLIIGNT---LRAPVYSWTHRSADRNTTIGPNRITQIPAVKGRFLFNGSVISGP
      470   480   490   500   510   520
      500   510   520   530   540   550
Cry1Ac GFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIF
      . . . . .
gi|112 GFTGGDVRLNRNNGNIQNRGYIEVPIQFTSTSTRYRVRVRYASVTSIELNVNWNSSIF
      530   540   550   560   570   580
      560   570   580   590   600   610
Cry1Ac SNTVPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFGTAGVIIDRFEFIPVTAT
      . . . . .
gi|112 TNTLPATAASLDNLQSGDFGYVEINNAFTSATGNIVGARNFSANAEEVIIDRFEFIPVTAT
      590   600   610   620   630   640
      620   630   640   650   660   670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      . . . . .
gi|112 FEVEYDLERAQKA
      650

```

>>gi|33765713|gb|AAQ52364.1| Sequence 6 from patent US 6 (653 aa)  
 initn: 1612 initl: 888 opt: 972 Z-score: 1139.1 bits: 221.9 E(): 1.6e-54  
 Smith-Waterman score: 1639; 45.763% identity (70.108% similar) in 649 aa overlap  
 (4-628:25-653)

```

      10   20   30
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGRIETGYTP

```

```

gi|337 ENENEIINALSIPAVSNHSAQMDLSLDARIEDSLCIAEGNNINP---LVSASTVQTG---
      10   20   30   40   50
      40   50   60   70   80   90
Cry1Ac IDISLSLTQFLLSEFVPG-AGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINRIEEFARN
      . . . . .
gi|337 INIAGRILGVLGVPPAGQLASFYSFLVGLWPS-GRDPWEIFLEYVEQLIRQVVTENTRN
      60   70   80   90   100   110
      100   110   120   130   140   150
Cry1Ac QAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQ
      . . . . .
gi|337 TAIARLEGLGRGYRSYQQALETWLDNRNDARSRSIILERYVALELDITTAIPLFRIRNEE
      120   130   140   150   160   170
      160   170   180   190   200   210
Cry1Ac VPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTG
      . . . . .
gi|337 VPLLMVYAQAANLHLLLRDASLFGSEWGMASDDVNQYYQEQIRYTEEYSNHCVQWYNTG
      180   190   200   210   220   230
      220   230   240   250   260   270
Cry1Ac LERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTPVRTVSQLTREIYTNPVLE
      . . . . .
gi|337 LNNLRGTNAESWLRYNQFRRLDTLGVLDLVALFPSPYDTRTPINTSAQLTREIYTDPIGR
      240   250   260   270   280   290
      280   290   300   310   320
Cry1Ac -NFDGSGFRG-----SAQGIEGSI-RSPHLMILNSITTYTDAHRGEYYWSGHQIMA
      . . . . .
gi|337 TNAPSGFASTNWFNNAPSFSAEAAIFRPPHLLDFPEQLTIYSASSR----WSSTQHMN
      300   310   320   330   340
      330   340   350   360   370   380
Cry1Ac SPVGFSGPEFTF-PLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRPFNIGINNQQLS
      . . . . .
gi|337 YWVGH---RLNFRPIGGTLNTSTQGLTNNTSINPVTLHYVSSRDVYRTESNAGTNILFTT
      350   360   370   380   390   400
      390   400   410   420   430
Cry1Ac VLDGTEFAYGTSSNLPASVYRKSQVDSLDEIPP-----QNNVPPRQGFSHRLSHVS
      . . . . .
gi|337 PVNGVPWARFNFTL--RIFMKEAPLPTVNRIRELGFNYLIQKLNHYQKQQNDQIMNHIV
      410   420   430   440   450   460
      440   450   460   470   480   490
Cry1Ac M---FRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGP
      . . . . .
gi|337 IDISYRLIIGNT---LRAPVYSWTHRSADRNTTIGPNRITQIPAVKGRFLFNGSVISGP
      470   480   490   500   510   520
      500   510   520   530   540   550
Cry1Ac GFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIF
      . . . . .
gi|337 GFTGGDVRLNRNNGNIQNRGYIEVPIQFTSTSTRYRVRVRYASVTSIELNVNWNSSIF
      530   540   550   560   570   580
      560   570   580   590   600   610
Cry1Ac SNTVPATATSLDNLQSSDFGYFESANAFSTSLGNIVGVRNFGTAGVIIDRFEFIPVTAT
      . . . . .
gi|337 TNTLPATAASLDNLQSGDFGYVEINNAFTSATGNIVGARNFSANAEEVIIDRFEFIPVTAT
      590   600   610   620   630   640
      620   630   640   650   660   670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      . . . . .
gi|337 FEVEYDLERAQKA
      650
      500   510   520   530   540   550
Cry1Ac GFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIF
      . . . . .
gi|337 GFTGGDVRLNRNNGNIQNRGYIEVPIQFTSTSTRYRVRVRYASVTSIELNVNWNSSIF
      530   540   550   560   570   580
      560   570   580   590   600   610

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Cry1Ac SNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTAT
gi|337 TNTLPATAASLDNLQSGDFGYVEINNAFTSATGNIVGARNFSANAEVIIIDRFEFIPVTAT

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELSEK
gi|337 FEVEYDLERAQKA

>>gi|118628709|emb|CAL85377.1| unnamed protein product [ (669 aa)
initn: 833 initl: 555 opt: 968 Z-score: 1134.2 bits: 221.0 E(): 2.9e-54
Smith-Waterman score: 1002; 33.642% identity (63.272% similar) in 648 aa overlap
(5-614:52-663)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPE-VEVLGGERI
gi|118 ASRHVNESDNNRQRNLSNTIFSNLSSNYPLASNPNT----PFQNMNYKEYLNITEGGII

Cry1Ac ETGY--TPIDISLSLTQFLLSEFVPGA-GFVLGLV-DIIWGIFGSPQWDAFLVQIEQLIN
gi|118 NPTLAGSAIVVAQNVSKTILKKGSTILGKILGSLVDILWPTNTEEIWLELIDEVEELIN

Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAI
gi|118 QKIEQQVIIDAETALESVKLNVDLYLNAFEWEKRPTEYSELVYKRFRTDAYNYARTSI

Cry1Ac PLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDA--ATINSRYNDLTRLIGN
gi|118 PFFRVKTYEVSLLSVYAQAANISLLSRDAQIYGLWGFDEHDKATFDSERK-LFR--AE

Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQ
gi|118 YIDHCTKYKVGDLRLKSSYGSWVWYNYRREMTLMILDITIAFPFYDIEEYPIEVSTQ

Cry1Ac LTREIYTNPVLENFDGSRG-SAQGIEGS-IRSPHLMIDLNSITTYTDAHR---GEY---
gi|118 LAREVYTDPIITSFVESDHGSPSFSFMESNAIRKPHLVLDYLDNLYIYTSRFRFSNEFPQPD

Cry1Ac --YWSGHQIMASPVGFSG-PEF-TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRP
gi|118 LNYWAAHKVKYK---YSGDPTLHETPIYGNASNYESTGNYSPFR-GNSIYQTLSA-----P

380 390 400 410 420

Cry1Ac FNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSG----TVDSLDEIPPQNNNVPRQG
gi|118 SALLTPNYIYGLIEQVEF-YGNKGN----VYVRGGNKYPLSVDSANQLPPDVE--PITEN

Cry1Ac FSHRLSHVSMF--RSGFSNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPAVKG--NF
gi|118 YNHVLCHATAVPVKGGT-----VPIFSWTHRSADYNTIYPDKITQLPAVKSTPSP

Cry1Ac LFNG-SVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTSTRYRVRVRYASVTPIH
gi|118 EVEGLKVQEGPGFTGGDLVVAKSSNQTIIVR---LKVTVDSPGTQ-KYRIRLKYAATSNFY

Cry1Ac LNV---NWGNSSIFNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR--NFS
gi|118 LGAYAGSNGGNGIPGISTVPKTMNIEDPLSYTSFAYIDLPSYTFQKDEV-IRFTINLY

Cry1Ac GTAGVII-DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
gi|118 ESGGAVYADKVEFIPVDADYDEGV

>>gi|118628711|emb|CAL85378.1| unnamed protein product [ (704 aa)
initn: 833 initl: 555 opt: 968 Z-score: 1133.9 bits: 221.1 E(): 3.1e-54
Smith-Waterman score: 1002; 33.642% identity (63.272% similar) in 648 aa overlap
(5-614:83-694)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPE-VEVLGGERI
gi|118 ASRHVNESDNNRQRNLSNTIFSNLSSNYPLASNPNT----PFQNMNYKEYLNITEGGII

Cry1Ac ETGY--TPIDISLSLTQFLLSEFVPGA-GFVLGLV-DIIWGIFGSPQWDAFLVQIEQLIN
gi|118 NPTLAGSAIVVAQNVSKTILKKGSTILGKILGSLVDILWPTNTEEIWLELIDEVEELIN

Cry1Ac QRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAI
gi|118 QKIEQQVIIDAETALESVKLNVDLYLNAFEWEKRPTEYSELVYKRFRTDAYNYARTSI

Cry1Ac PLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDA--ATINSRYNDLTRLIGN
gi|118 PFFRVKTYEVSLLSVYAQAANISLLSRDAQIYGLWGFDEHDKATFDSERK-LFR--AE

210 220 230 240 250 260

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Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 YIDHCTKYKVKGLDRKLGSSYGSWVYNNRNRREMTLMILDITAAFPYYDIEEYPIEVSTQ
290 300 310 320 330 340

270 280 290 300 310
Cry1Ac LTREIYTNPLENFDGSGFRG-SAQGIEGS-IRSPHLMIDLNSITTYTDAHR---GEY---
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 LAREVYVTDPIITSFVESDHGSPSFSFMESNAIRKPHLVDYLDNLIYTSRFRTFSSNEFPQPD
350 360 370 380 390 400

320 330 340 350 360 370
Cry1Ac --YWSGHQIMASPVGFSG-PEF-TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 LNYWAAHKVKYK---YSGDPTLHETPIYGNASNYESTGNYSFR-GNSIYQTLSA-----P
410 420 430 440 450

380 390 400 410 420
Cry1Ac FNIGINNQLSVLDGTEFAYGTSSNLPsAVYRKSG----TVDSLDEIPPQNNVPPRQG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 SAILTPNYIYGYIEQVEF-YGNKGN---VYYRGGNKYPLSVDSANQLPPDVE--PITEN
460 470 480 490 500

430 440 450 460 470 480
Cry1Ac FSHRLSHVSMF--RSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG--NF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 YNHVLCCHATAVPKDGGT-----VPIFSWTHRSADYNTIYDPDKITQLPAVKSTPSP
510 520 530 540 550 560

490 500 510 520 530 540
Cry1Ac LFNQ-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 EVEGLKVGQGGPGFTGGDLVVAKSSNQTVR---LKVTVDSPTGQ-KYRIRLKYAATSIFY
570 580 590 600 610

550 560 570 580 590
Cry1Ac LNV---NWNSSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR---NFS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 LGAYAGSNGGNGIPGISTVPKTMNIEDPLSYTSFAYIDLPPDSTYFSQKDEV-IRFTINIY
620 630 640 650 660 670

600 610 620 630 640 650
Cry1Ac GTAGVII-DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|118 ESGGAVYADKVEFIPVDADYDEGVKDEL
680 690 700

```

>>gi|42682721|gb|AAS28784.1| Sequence 25 from patent US (643 aa)  
 inits: 1062 inits: 655 opt: 954 Z-score: 1118.0 bits: 218.0 E(): 2.4e-53  
 Smith-Waterman score: 1172; 38.047% identity (66.162% similar) in 594 aa overlap  
 (55-617:72-643)

```

30 40 50 60 70 80
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWIGIFGP---SQWDAFL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 AEGNNIDPFVSASTVQTGINIAGRILGVLGVPFAGQIASFYSLVGEIWRGRDPWEIFL
50 60 70 80 90 100

90 100 110 120 130 140

```

```

Cry1Ac VQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 EHVEQLIRQVQVTESTRDALARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTQYIAL
110 120 130 140 150 160

150 160 170 180 190 200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 ELDFLNLAMPFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQV
170 180 190 200 210 220

210 220 230 240 250 260
Cry1Ac RLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 EKTREYSDYCARWYNTGLNLRGTNAESWLRYNQFRDLTLGVLDLVALFPSYDTRVYPM
230 240 250 260 270 280

270 280 290 300 310
Cry1Ac RTVSQLTREIYTNPLE-NFDGSGFRG-----SAQGIEGS-IRSPHLMIDLNSITTY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 NTSACLREIYTDPIGRTNAPSGFASTNWFNNSNAPSFAIEAAVIRPPHLLDFPEQLTIF
290 300 310 320 330 340

320 330 340 350 360
Cry1Ac TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ-QRIVAQL-GQGVY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 SVLSRWSNTQYMYVWVGHRLSRTI--RGSLSLST---STHGNTNTSINPVTIQLFTSRDVI
350 360 370 380 390

370 380 390 400 410
Cry1Ac RTLS----STLYRRPFIINQQLSVLDGTEFAYGTSSNLPsAVYRKSGT--VDSLDEI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 RTESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYITGYTGVTQLDFTEL
400 410 420 430 440 450

420 430 440 450 460 470
Cry1Ac PPQNNVPPRQGFHSRLSHVSMFERSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 PPETTERPNYESYSHRLSNIRLI-SG-----NTRAPVYSWTHRSADRNTNTISSDSITQ
460 470 480 490 500

480 490 500 510 520 530
Cry1Ac IPAVKGNFLFNQ-SVISGPGFTGGDLVRLNSSGNIIQNRGYIEVPIHFPSTSTRYRVRV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 IPLVKSFNLSGTSVVSQGGFTGGDLIRTNVNGS-VLSMG-----LNFNNTSLQRYRVRV
510 520 530 540 550

540 550 560 570 580 590
Cry1Ac RYASVTPIHNLVNWGNSSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 RYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRAEFVPGISASGSQTAGISL
560 570 580 590 600 610

600 610 620 630 640 650
Cry1Ac -NFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|426 SNNAGRQTFHFDPKIEFIPITATLE
620 630 640

```

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>>gi|15110443|gb|AAE68107.1| Sequence 25 from patent US (643 aa)
initn: 1062 initl: 655 opt: 954 Z-score: 1118.0 bits: 218.0 E(): 2.4e-53
Smith-Waterman score: 1172; 38.047% identity (66.162% similar) in 594 aa overlap
(55-617:72-643)

30 40 50 60 70 80
Cry1Ac VEVLGGRIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIFGP--SQWDAFL
gi|151 AEGNNIDPFVSASTVQTGINIAGRILGVLGVPPFAGQIASFYSLVGLVPRGRDPWEIFL

90 100 110 120 130 140
Cry1Ac VQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|151 EHVQLIRQQVTENTRDALARLQGLGNSFRAYQQSLEDWLENRDDARTRSVLYTYIAL

150 160 170 180 190 200
Cry1Ac NSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRQWGFDAATINSRYNDLT
gi|151 ELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQV

210 220 230 240 250 260
Cry1Ac RLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI
gi|151 EKTREYSYCARWYNTGLNNLRGTNAESWLRYNQFRRLDTLGLVLDLVALFPPSYDTRVYPM

270 280 290 300 310
Cry1Ac RTVSQLTREIYTNPVLN-NFDGSRG-----SAQGIEGS-IRSPHLMIDLNSITIIY
gi|151 NTSAQLTREIYTDPIGRTNAPSGFASTNWFNNAPSFAIEAAVIRPPHLLDFPEQLTIF

320 330 340 350 360
Cry1Ac TDAHR---GEY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQ-QRIVAQL-GQGQVY
gi|151 SVLSRWSNTQYMNWVGHRLSRTI--RGSLSLST---STHGNTNTSINPVTLQFTSRDVY

370 380 390 400 410
Cry1Ac RTLS----STLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQT--VDSLDEI
gi|151 RTESFAGINILLTTPVN-GVPWARFNWRNPLNSLRG--SLLYTIGYTGVTQLPDSSETEL

420 430 440 450 460 470
Cry1Ac PPQNNVPPRQGFSHRLSHVSMFRSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQ
gi|151 PPETTERPNYESHRLSNIRLI-SG-----NLTLPVYSWTHRSADRTNTISSDSITQ

480 490 500 510 520 530
Cry1Ac IPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTST-RYRVRV
gi|151 IPLVKSFNLNSGTSVSVSGPGFTGGDIIRTNVNGS-VLSMG-----LNFNNTSLQRVVRV

540 550 560 570 580 590
Cry1Ac RYASVTPIHLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFSSSLGNIVGVR-
gi|151 RYAASQTMVLRVTVGGSTTFDQGFPTMSANESLTSQSFRFAEFVPGVISASGQTAGISI
560 570 580 590 600 610
600 610 620 630 640 650
Cry1Ac -NFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQV
gi|151 SNNAGRQTFHFDKIEFIPITATLE
620 630 640

>>gi|13619539|emb|CAC36454.1| unnamed protein product [s (625 aa)
initn: 1077 initl: 720 opt: 951 Z-score: 1114.6 bits: 217.3 E(): 3.6e-53
Smith-Waterman score: 1093; 35.669% identity (64.490% similar) in 628 aa overlap
(22-619:18-623)

10 20 30 40 50 60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|136 MADYLQMTDEDYTDYSINPSLSISGRDAVQTALTVVGRILGALGVFPFSGQI--VSF
10 20 30 40 50

70 80 90 100 110 120
Cry1Ac VLGLVDIIWGIFGSPQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFRE
gi|136 YQFLNLTLPVNDTALWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNVYQRSLQN
60 70 80 90 100 110

130 140 150 160 170 180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
gi|136 WLADRNDTKNLSVVAQFIALDLDLDFVNAIPLFAVNGQVPLLSVYAQAVNLHLLLLKDas
120 130 140 150 160 170

190 200 210 220 230 240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRREL
gi|136 LFGEGWGFTQGEISTYYDRQLELTAKYNTNYCETWYNTGLDRLRGTNTESWLRYHQFRREM
180 190 200 210 220 230

250 260 270 280 290
Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFD--GSFR--GSA----QG
gi|136 TLVLDVVALFPYYDVRLYPTGNSNPQLTREYVTDPIVFNPPANVGLCRRWGNPNYPTFSE
240 250 260 270 280 290

300 310 320 330 340
Cry1Ac IEGS-IRSPHLMIDLNSITIIYTDH--RGEY--YWSGHQIMASPVGFSGPEFTFPLYGTM
gi|136 LENAFIRPPHLDRLNLSLTSSNRPVSSNFMDYWSGHTLRRSRYLNDASVQED--SYGLI
300 310 320 330 340 350

350 360 370 380 390 400
Cry1Ac GNAAPQQRIVAQLG-QGVYRTLSSTLYRRPFNIGINN-QQLSVLDGTEFAYGTSSNLPSA
gi|136 TTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRASVFPVGGFLN-GTTS--PAN
360 370 380 390 400

```

      410      420      430      440      450      460
Cry1Ac VYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA---PMFSWI
      . . . . .
gi|136 GGCRD-LYDTNDELPPDEST----GSSTHRLSHVTF--SFQTNQAGSIANAGSVPTYVWT
      410      420      430      440      450

```

```

      470      480      490      500      510
Cry1Ac HRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIE
      . . . . .
gi|136 RRDVDLNNITIPNRITQLPLVKASAPVSGTTVLKGPFTGGGILRRTTNGT----FGTLR
      460      470      480      490      500      510

```

```

      520      530      540      550      560      570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDF-----
      . . . . .
gi|136 VTVNSPLTQ-QYRLRVRFASTGNFSIRVLRGGVSIQDVRGSTMNRGQELTYESFFTFREF
      520      530      540      550      560      570

```

```

      580      590      600      610      620      630
Cry1Ac ---GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVN
      . . . . .
gi|136 TTTGPFNPPFTTQAEILTVNAEGVSTGGEYYIDRIEIVPVNPAREAEED
      580      590      600      610      620

```

```

      640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQ

```

>>gi|6064164|emb|CAB58497.1| unnamed protein product [un (625 aa)  
 initn: 1077 initl: 720 opt: 951 Z-score: 1114.6 bits: 217.3 E(): 3.6e-53  
 Smith-Waterman score: 1093; 35.669% identity (64.490% similar) in 628 aa overlap  
 (22-619:18-623)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      . . . . .
gi|606 MADYLQMTDEYDTSYINPSSLISGRDAVQALTAVVGRILGALGVVPSGQI--VSF
      10      20      30      40      50

```

```

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi|606 YQFLNLTLPVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNVYQRSLQN
      60      70      80      90      100     110

```

```

      130     140     150     160     170     180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
      . . . . .
gi|606 WLADRNDTKNLSVVRQAQFIALLDLDFVNAIPLFAVNGQVPLLSVYAQAVNLHLLKLDAS
      120     130     140     150     160     170

```

```

      190     200     210     220     230     240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . . .
gi|606 LFGEGWGFQGEISTYYDRQLELTAKYTYNCEYTWYNTGLDRLRGNTESWLRYHQFRREM
      180     190     200     210     220     230

```

```

      250     260     270     280     290
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFD---GSFR--GSA----QG
      . . . . .

```

```

gi|606 TLVVLDVVALFPYDVRVLYPTGSNPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSE
      240     250     260     270     280     290

```

```

      300     310     320     330     340
Cry1Ac IEGS-IRSPHMLDILNSITITYTDAH--RGEY--YWSGHQIMASPVGFSGPEPTFFPLYGTM
      . . . . .
gi|606 LENA FIRPPHFLDRLNLSLTISSNRFVSSNFMDYWSGHTLRRSYLNDQSAVQED--SYGLI
      300     310     320     330     340     350

```

```

      350     360     370     380     390     400
Cry1Ac GNAAPQQRIVAQLG-QGVYRTLSSTLYRRPFNIGINN-QQLSVLDGTEFAYGTSSNLPSA
      . . . . .
gi|606 TTT---RATINPGVDGNTRIESTAVDFRSALIGIYGVNRASVFPVGGFLN-GTTS--PAN
      360     370     380     390     400

```

```

      410     420     430     440     450     460
Cry1Ac VYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA---PMFSWI
      . . . . .
gi|606 GGCRD-LYDTNDELPPDEST----GSSTHRLSHVTF--SFQTNQAGSIANAGSVPTYVWT
      410     420     430     440     450

```

```

      470     480     490     500     510
Cry1Ac HRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIE
      . . . . .
gi|606 RRDVDLNNITIPNRITQLPLVKASAPVSGTTVLKGPFTGGGILRRTTNGT----FGTLR
      460     470     480     490     500     510

```

```

      520     530     540     550     560     570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDF-----
      . . . . .
gi|606 VTVNSPLTQ-QYRLRVRFASTGNFSIRVLRGGVSIQDVRGSTMNRGQELTYESFFTFREF
      520     530     540     550     560     570

```

```

      580     590     600     610     620     630
Cry1Ac ---GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVN
      . . . . .
gi|606 TTTGPFNPPFTTQAEILTVNAEGVSTGGEYYIDRIEIVPVNPAREAEED
      580     590     600     610     620

```

```

      640     650     660     670     680     690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQ

```

>>gi|27268360|gb|AAN89301.1| Sequence 9 from patent US 6 (625 aa)  
 initn: 1077 initl: 720 opt: 951 Z-score: 1114.6 bits: 217.3 E(): 3.6e-53  
 Smith-Waterman score: 1093; 35.669% identity (64.490% similar) in 628 aa overlap  
 (22-619:18-623)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGF
      . . . . .
gi|272 MADYLQMTDEYDTSYINPSSLISGRDAVQALTAVVGRILGALGVVPSGQI--VSF
      10      20      30      40      50

```

```

      70      80      90      100     110     120
Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
      . . . . .
gi|272 YQFLNLTLPVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNVYQRSLQN
      60      70      80      90      100     110

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                250      260      270      280      290
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVPLENFD---GSFR--GSA----QG
      . . . . . : : : : . : : : : : : : : : : : : : : .
gi|594 TLVVLDDVVALFPYYDVRLYPTGSPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSE
      240      250      260      270      280      290

                300      310      320      330      340
Cry1Ac IEGS-IRSPHLMIDLNSITIYTDH--RGEY--YWSGHQIMASPVGFSGPEFTFPLYGTM
      . . . : : : : : : : . . . : : : . : . . . : : .
gi|594 LENAFIRPPHLDRLNLSLTISSNRFVSSNFMDYWSGHTLRRSYLNDQSAVQED--SYGLI
      300      310      320      330      340      350

                350      360      370      380      390      400
Cry1Ac GNAAPQQRIVAQLG-QGVYRTLSSSTLYRRPFNIGINN-QQLSVLDGTEFAYGTSSNLPSA
      . . : : : : : : : : : : : : : : : : : : : : : : .
gi|594 TTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRSFVPGGLFN-GTTS--PAN
      360      370      380      390      400

                410      420      430      440      450      460
Cry1Ac VYRKSQTVDSLDEIPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRA---PMFSWI
      . . : : : : : . . : : : : : : : : : : : : : : .
gi|594 GGCRD-LYDTNDELPPDEST---GSSTHRLSHVTFF-SFQTNQAGSIANAGSVPTYVWT
      410      420      430      440      450

                470      480      490      500      510
Cry1Ac HRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIE
      . . . . . : : : : . . . : : : : : : : : : : : .
gi|594 RRDVDLNNITPNRITQLPLVKASAPVSGTTLVKGPGFTGGGILRRTTNGT---FGTLR
      460      470      480      490      500      510

                520      530      540      550      560      570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDF-----
      : . . : : : : : : : : : : : : : : : : : : : : .
gi|594 VTVNSPLTQ-QYRLRVRFASTGNF SIRVLRGGVSIQDVRLGSTMNRGQELTYESFFTRF
      520      530      540      550      560      570

                580      590      600      610      620      630
Cry1Ac ---GYFESANAFTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVN
      : . . : : : . : : : : : : : : : : : : : : : .
gi|594 TTTGPFNPPFTTQAQEILTVNAEGVSTGGEYYIDRIEIVPNPAREAEED
      580      590      600      610      620

                640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ

```

>>gi|6064162|emb|CAB58496.1| unnamed protein product [Ba (625 aa)  
 initn: 1076 initl: 719 opt: 950 Z-score: 1113.4 bits: 217.1 E(): 4.2e-53  
 Smith-Waterman score: 1092; 35.669% identity (64.490% similar) in 628 aa overlap  
 (22-619:18-623)

```

                10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINICIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
      . . . . . : : : : . . . . . : : : : . . . . .
gi|606 MADYLQMTDEDYTDSYINPSLSISGRDAVQ TALTVVGRILGALGVPPFSGQI--VSF
      10      20      30      40      50

                70      80      90      100      110      120
Cry1Ac VLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIEEFARNQAI SRLBGLSNLYQIYAESFRE

```

```

      . . . . . : : : : . : : : : : : : : : : : : : : .
gi|606 YQFLNLTLPVNDTAIWEAFMRQVEELVNQQITFARNQALARLQGLGDSFNVYQRSLQN
      60      70      80      90      100      110

                130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
      : : : . . : : : : : : : : : : : : : : : : : : .
gi|606 WLADRNDTRNLSVVRQAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNLHLLKLDAS
      120      130      140      150      160      170

                190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
      . . . : : : . . . : . : : : : : : : : : : : : .
gi|606 LFGEGWGFQGEIISTYDRQLELTAKYNTNYCETWYNTGLDRLRGTNTESWLRVYHQFRREM
      180      190      200      210      220      230

                250      260      270      280      290
Cry1Ac TLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVPLENFD---GSFR--GSA----QG
      . . . . . : : : : . : : : : : : : : : : : : : : .
gi|606 TLVVLDDVVALFPYYDVRLYPTGSPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSE
      240      250      260      270      280      290

                300      310      320      330      340
Cry1Ac IEGS-IRSPHLMIDLNSITIYTDH--RGEY--YWSGHQIMASPVGFSGPEFTFPLYGTM
      . . . : : : : : : : . . . : : : . : . . . : : .
gi|606 LENAFIRPPHLDRLNLSLTISSNRFVSSNFMDYWSGHTLRRSYLNDQSAVQED--SYGLI
      300      310      320      330      340      350

                350      360      370      380      390      400
Cry1Ac GNAAPQQRIVAQLG-QGVYRTLSSSTLYRRPFNIGINN-QQLSVLDGTEFAYGTSSNLPSA
      . . : : : : : : : : : : : : : : : : : : : : : .
gi|606 TTT---RATINPGVDGTNRIESTAVDFRSALIGIYGVNRSFVPGGLFN-GTTS--PAN
      360      370      380      390      400

                410      420      430      440      450      460
Cry1Ac VYRKSQTVDSLDEIPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRA---PMFSWI
      . . : : : : : . . : : : : : : : : : : : : : : .
gi|606 GGCRD-LYDTNDELPPDEST---GSSTHRLSHVTFF-SFQTNQAGSIANAGSVPTYVWT
      410      420      430      440      450

                470      480      490      500      510
Cry1Ac HRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIE
      . . . . . : : : : . . . : : : : : : : : : : .
gi|606 RRDVDLNNITPNRITQLPLVKASAPVSGTTLVKGPGFTGGGILRRTTNGT---FGTLR
      460      470      480      490      500      510

                520      530      540      550      560      570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDF-----
      : . . : : : : : : : : : : : : : : : : : : : .
gi|606 VTVNSPLTQ-QYRLRVRFASTGNF SIRVLRGGVSIQDVRLGSTMNRGQELTYESFFTRF
      520      530      540      550      560      570

                580      590      600      610      620      630
Cry1Ac ---GYFESANAFTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVN
      : . . : : : . : : : : : : : : : : : : : : : .
gi|606 TTTGPFNPPFTTQAQEILTVNAEGVSTGGEYYIDRIEIVPNPAREAEED
      580      590      600      610      620

                640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ

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Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ
>>gi|27268359|gb|AAN89300.1| Sequence 7 from patent US 6 (625 aa)
initn: 1076 init1: 719 opt: 950 Z-score: 1113.4 bits: 217.1 E(): 4.2e-53
Smith-Waterman score: 1092; 35.669% identity (64.490% similar) in 628 aa overlap
(22-619:18-623)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
gi|272 MADYLQMTDEDYTDSYINPSLSISGRDAVQALTAVVGRILGALGVPPFSGQI--VSF

Cry1Ac VLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFRE
gi|272 YQFLNLTLPVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSFNVYQRSLNQ

Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
gi|272 WLADRNDTRNLSVVRAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNLHLLKLDAS

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
gi|272 LFGEGWGFTQGEISTYYDRQLELTAKYTNYCETWYNTGLDRLRGNTESWLRYHQFRREM

Cry1Ac TLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD--GSFR--GSA----QG
gi|272 TLVLDVVALFPYDVRLYPTGNSNPQLTREYVTDPIVFNPPANVGLCRRWGTPNYTFSE

Cry1Ac IEGS-IRSPHLMIDLNSITTYTDAH--RGEY--YWSGHQIMASPVGFGPEFTFPPLYGTM
gi|272 LENAFIRPPHFLDRLNSLTISSNRFVSSNFMDYWSGHTLRRSYLNSDAVQED--SYGLI

Cry1Ac GNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAYGTSSNLPSA
gi|272 TTT---RATINPGVDGNTNRIESTAVDFRSALIGIYGVNRFVPPGGLFN-GTTS--PAN

Cry1Ac VYRKSGETVSDLEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRA---PMFSWI
gi|272 GRCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANAGSVPTVYWT

Cry1Ac HRSAEFNNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNSSGNNIQNRGYIE
gi|272 RRDVDLNNITPNRITQLPLVKASAPVSGTTVLKPGFTGGGILRRRTNGT---FGTLR

460 470 480 490 500 510
520 530 540 550 560 570
Cry1Ac VPIHFPSTSTRYRVRVRYASVTP IHLNVNWGNSSIFSNVTPATATSLDNLQSSDF-----
gi|272 VIVNSPLTQ-QYRLRVRFASTGNFSIRVLRGGVSIQDVRGSGTMMNRQELTYESFFTRF
580 590 600 610 620 630
Cry1Ac ---GYFESANAFSTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVN
gi|272 TTTGPFNPFFTFTQAQEILTVAEGVSTGGEYYIDRIEIVPVNPREAEED
580 590 600 610 620
640 650 660 670 680 690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ

>>gi|25897918|emb|CAD58211.1| unnamed protein product [s (673 aa)
initn: 1103 init1: 719 opt: 950 Z-score: 1113.0 bits: 217.1 E(): 4.5e-53
Smith-Waterman score: 1119; 35.950% identity (64.678% similar) in 637 aa overlap
(22-628:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|258 LASDPNAALQNMNYKDYLMQMTDEDYTDSYINPSLSISGRDAVQALTAVVGRILGALGVPP
30 40 50 60 70 80

Cry1Ac SEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLY
gi|258 SQGI--VSFYQFLNLTLPVNDTAIWEAFMRQVEELVNQQITEFARNQALARLQGLGDSF
90 100 110 120 130 140

Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANL
gi|258 NVYQRSLNWLADRNDTLNLSVVRAQFIALDLDFVNAIPLFAVNGQQVPLLSVYAQAVNL
150 160 170 180 190 200

Cry1Ac HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
gi|258 HLLLLKDALFEGEGWGFTQGEISTYYDRQLELTAKYTNYCETWYNTGLDRLRGNTESWL
210 220 230 240 250 260

Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFD--GSFR--G
gi|258 RYHQFRREMTLVLDVVALFPYDVRLYPTGNSNPQLTREYVTDPIVFNPPANVGLCRRWG
270 280 290 300 310 320

Cry1Ac SA----QGIEGS-IRSPHLMIDLNSITTYTDAH--RGEY--YWSGHQIMASPVGFGPE
gi|258 TNPYNTFSELENAFIRPPHFLDRLNSLTISSNRFVSSNFMDYWSGHTLRRSYLNSDAVQ
330 340 350 360 370 380

340 350 360 370 380 390

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Cry1Ac FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY

gi|258 ED--SYGLITTT---RATINPGVDGTNRISTAVDFRSALIGIYGVNRRASFPVGGFLFN-390 400 410 420 430

Cry1Ac 400 410 420 430 440 450 GTSSNLPASAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRA

gi|258 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA 440 450 460 470 480 490

Cry1Ac 460 470 480 490 500 510 ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFN--VISGPGFTGGDLVRLNSSGN

gi|258 GSVPTYVWTRRDVDLNNITIPNRITQLPLVKASAPVSGTTVLKGPFGTGGILRRITNGT 500 510 520 530 540 550

Cry1Ac 520 530 540 550 560 570 NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTPATATSLDNLQ

gi|258 ---FGTLRVTVNSPLTQ-QYRLRVRFASSTGNF SIRVLRGGVSIIGDVLGSTMNRGQELT 560 570 580 590 600

Cry1Ac 580 590 600 610 620 SSDF-----GYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFIPVTATLEAEYN

gi|258 YESFFTREFTTTGPFPNPPFTTQAQEILTVNAEGVSTGGEYYIDRIEIVPNPAREAEED 610 620 630 640 650 660

Cry1Ac 630 640 650 660 670 680 LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKR

gi|258 LEAAKKA 670

>>gi|25897916|emb|CAD58210.1| unnamed protein product [B (673 aa)
initn: 1103 initl: 719 opt: 950 Z-score: 1113.0 bits: 217.1 E(): 4.5e-53
Smith-Waterman score: 1119; 35.950% identity (64.678% similar) in 637 aa overlap
(22-628:59-673)

Cry1Ac 10 20 30 40 50 CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL

gi|258 LASDPNAAALQNMNYKDYLMQTDDEYDTSYINPSSLISGRDAVQATALTVVGRILGALGVFPF 30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110 SEFVPGAGFVGLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIARLEGLSNLY

gi|258 SGQI--VSFYQLLNTLWPNVNDTAIWEAFMRQVEELVNQQTIEFARNQALARLQGLGDSF 90 100 110 120 130 140

Cry1Ac 120 130 140 150 160 170 QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL

gi|258 NVYQRSLOQNLADRNDTRNLSVVRQAQFIALDLDFVNAIPLFAVNGQVPLLSVYVQAANL 150 160 170 180 190 200

180 190 200 210 220 230

Cry1Ac HLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI

gi|258 HLLLLKDALFEGEGWGFTQGEISTYYDRQLELTAKYTNVCEWYNTGLDRLRGRTNTESWL 210 220 230 240 250 260

Cry1Ac 240 250 260 270 280 RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTPVLENFD---GSFR--G

gi|258 RYHQFRREMTLVVLDVVALFPYDVRLYPTGSNPQLTREYVTDPIVFNPPANVGLCRRWG 270 280 290 300 310 320

Cry1Ac 290 300 310 320 330 SA----QGIEGS-IRSPHLMIDLNSITIIYTDH--RGEY--YWSGHQIMASPVGFSGPE

gi|258 TNPYNTFSELENAFIRPPHLFDRLNSLTISSNRFVSSNFMVMDYWSGHTLRRSYLNDLSAVQ 330 340 350 360 370 380

Cry1Ac 340 350 360 370 380 390 FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY

gi|258 ED--SYGLITTT---RATINPGVDGTNRISTAVDFRSALIGIYGVNRRASFPVGGFLFN-390 400 410 420 430

Cry1Ac 400 410 420 430 440 450 GTSSNLPASAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRA

gi|258 GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA 440 450 460 470 480 490

Cry1Ac 460 470 480 490 500 510 ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFN--VISGPGFTGGDLVRLNSSGN

gi|258 GSVPTYVWTRRDVDLNNITIPNRITQLPLVKASAPVSGTTVLKGPFGTGGILRRITNGT 500 510 520 530 540 550

Cry1Ac 520 530 540 550 560 570 NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTPATATSLDNLQ

gi|258 ---FGTLRVTVNSPLTQ-QYRLRVRFASSTGNF SIRVLRGGVSIIGDVLGSTMNRGQELT 560 570 580 590 600

Cry1Ac 580 590 600 610 620 SSDF-----GYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEFIPVTATLEAEYN

gi|258 YESFFTREFTTTGPFPNPPFTTQAQEILTVNAEGVSTGGEYYIDRIEIVPNPAREAEED 610 620 630 640 650 660

Cry1Ac 630 640 650 660 670 680 LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKR

gi|258 LEAAKKA 670

>>gi|25897920|emb|CAD58212.1| unnamed protein product [s (673 aa)
initn: 1102 initl: 718 opt: 949 Z-score: 1111.8 bits: 216.9 E(): 5.2e-53
Smith-Waterman score: 1118; 35.950% identity (64.678% similar) in 637 aa overlap
(22-628:59-673)

10 20 30 40 50

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Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
              :: . . . . .
gi | 258  LASDPNAALQNMNYKDYLMQMTDEDYTDYSINPSLSISGRDAVQALTAVVGRILGALGVFP
              30          40          50          60          70          80

              60          70          80          90          100         110
Cry1Ac  SEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLY
              . . . . .
gi | 258  SGQI--VSFYQFLNLTLPVNDTAWFAFMRQVEELVNQQITFEFARNQALARLQGLGDSF
              90          100         110         120         130         140

              120         130         140         150         160         170
Cry1Ac  QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANL
              . . . . .
gi | 258  NVYQRSLOQNLADRNDTFNLSVVRQFIALDLDVFNALPLFAVNGQQVPLLSVYAQAVNL
              150         160         170         180         190         200

              180         190         200         210         220         230
Cry1Ac  HLSVLRDVSFVGRQWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
              . . . . .
gi | 258  HLLLLKDALSLFGEGWFTQGEISTYDRQLELTAKYTYNCTWYNTGLDRLRGTNTESWL
              210         220         230         240         250         260

              240         250         260         270         280
Cry1Ac  RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLNF--GSFR--G
              . . . . .
gi | 258  RYHQFRREMTLVVLDVVALFPYDVRLYPTGSGNPQLTREVYTDPIVFNPPANVGLCRRWG
              270         280         290         300         310         320

              290         300         310         320         330
Cry1Ac  SA----QGIEGS-IRSPHMDILNSITIIYTDH--RGEY--YWSGHQIMASPVGFSGPE
              . . . . .
gi | 258  TNPYNTFSELENAFIRPPHLFDRLNSLTISSNRFVSSNFMVWSGHTLRRSYLNDNSAVQ
              330         340         350         360         370         380

              340         350         360         370         380         390
Cry1Ac  FTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGTEFAY
              . . . . .
gi | 258  ED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGYGVNRSFVPGGLFN-
              390         400         410         420         430

              400         410         420         430         440         450
Cry1Ac  GTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
              . . . . .
gi | 258  GTTS--PANGGCRD-LYDTNDELPPDEST---GSSTHRLSHVTF--SFQTNQAGSIANA
              440         450         460         470         480         490

              460         470         480         490         500         510
Cry1Ac  ---PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLNLSGN
              . . . . .
gi | 258  GSVPTYVWTRRDVDLNNNTITPNRITQLPLVKASAPVSGTTVLKPGFTGGGILRRRTTNGT
              500         510         520         530         540         550

              520         530         540         550         560         570
Cry1Ac  NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQ
              . . . . .
gi | 258  ----FGTLRVRTNSPLTQ-QYRLRVRFASTGNFSIRVLRGGVSGIDVRLGSTMNRGQELT
              560         570         580         590         600

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              580         590         600         610         620
Cry1Ac  SSDLF-----GYFESANAFSSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYN
              . . . . .
gi | 258  YESFFTREFTTTTPFPNPPFTTQAQEILTVNAEGVSTGGEYIIDRIEIVPNPAREAEED
              610         620         630         640         650         660

              630         640         650         660         670         680
Cry1Ac  LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKR
              . . . . .
gi | 258  LEAAKKA
              670

>>gi|59750902|gb|AAW99266.1| Sequence 2 from patent US 6 (140 aa)
  initn: 933 initl: 933 opt: 933 Z-score: 1103.1 bits: 213.0 E(): 1.6e-52
Smith-Waterman score: 933; 99.286% identity (99.286% similar) in 140 aa overlap
(5-144:1-140)

              10         20         30         40         50         60
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF
              . . . . .
gi | 597  MDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGF
              10         20         30         40         50

              70         80         90         100        110        120
Cry1Ac  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
              . . . . .
gi | 597  VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
              60         70         80         90         100        110

              130        140        150        160        170        180
Cry1Ac  WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVS
              . . . . .
gi | 597  WEADPTNPALREEMRIQFNDMNSA
              120        130        140

>>gi|71792190|emb|CAJ21124.1| unnamed protein product [B (681 aa)
  initn: 963 initl: 398 opt: 936 Z-score: 1096.4 bits: 214.1 E(): 3.8e-52
Smith-Waterman score: 1046; 35.222% identity (62.940% similar) in 653 aa overlap
(20-636:57-678)

              10         20         30         40
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
              . . . . .
gi | 717  YPLASEQNGVLQNMNYKEYLQTYDGYTGSGLINPNLSINTRDVLQGTITVGRVLG---F
              30         40         50         60         70         80

              50         60         70         80         90         100
Cry1Ac  LLSEFVPGAG---FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLE
              . . . . .
gi | 717  LG---VPFAGQLVTFYFTLLNQLWPTNNAVWEAFMAQVEELIDQRISDQVVRNALDDLT
              90         100        110        120        130        140

              110        120        130        140        150        160
Cry1Ac  GLSNLYQIYAESFREWEADPTNPALREEMRIQ-FNDMNSALTTAIPLFAV---QNYQVP
              . . . . .
gi | 717  GLHDYNEYLAALAEWLDRP-NGA-RANLAFQRFENLHTAFVTRMPFSGTGPQSGQRDAVA
              150        160        170        180        190

              170        180        190        200        210

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Cry1Ac  LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYN---DLTRLIGNYTDHAVRWYNT
gi|717  LLTVYAQAANLHLLKDAEIIYGARWGLQQSQINLYFNAQQDRTRI---YTNHCVATYNR
200      210      220      230      240      250

220      230      240      250      260      270
Cry1Ac  GLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVL
gi|717  GLEDLKGTNTESWYNYHQFRREMTLMAMDVLFPPYINVRQYPNGANPQLTREIYTDPPV
260      270      280      290      300      310

280      290      300      310      320
Cry1Ac  ENF---DGSFR--GSA----QGIEGS-IRSPHLMIDLNSITIIYDHAHRGEY-----YW
gi|717  FNPPANQGLCRRWGNNPYMTFSGLENAFIRPPHLFDRLNSLTI--NSHRFPISSNFMDYW
320      330      340      350      360      370

330      340      350      360      370      380
Cry1Ac  SGHQIMASPVGFSGEFPTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGIN
gi|717  AGHTLRRSYMNSAVQ----EDSYGAIPTRVITINPGVNGTNIHIESTAVDFRSLGVGIY
380      390      400      410      420

390      400      410      420      430
Cry1Ac  N-QQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSM
gi|717  GVHRASFVPGGLFN-GTIS--PANAGCRN-LHDTRDVLPLEENNGSP----SHRLSHVTF
430      440      450      460      470      480

440      450      460      470      480      490
Cry1Ac  --FRSGFNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPG
gi|717  LSFQTNQAGSLANGGSVPLYVWARQDIDFNNTITANRITQLPLVKAFELIAGTITIVKPG
490      500      510      520      530      540

500      510      520      530      540      550
Cry1Ac  FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFS
gi|717  FTGGDILRRTSTGT----LGTIRVNVNSPLTQ-RYRVRFRYASTVDFDFVSRGGTTVNN
550      560      570      580      590

560      570      580      590      600      610
Cry1Ac  NTVPATATSLDNLQSDFF--GYFESANAFSSLGNI-VGVRNFSGTAGVIIDRFEFIPVT
gi|717  FRFPRTMSRGQESRYESYVTSFTTPTFTQSQDFIRTSIQQLSNGEVYLDRIEIIIPVN
600      610      620      630      640      650

620      630      640      650      660      670
Cry1Ac  ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYTLSEDFCLDEKRELS
gi|717  PAREAEEDLEAAKKAVALFTRTRDG
660      670      680

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>>gi|25897926|emb|CAD58215.1| unnamed protein product [s (673 aa)
  in1n: 1020 in1l: 699 opt: 933 Z-score: 1092.9 bits: 213.4 E(): 5.9e-52
Smith-Waterman score: 1078; 35.101% identity (64.431% similar) in 641 aa overlap
(22-628:59-673)

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10 20 30 40 50

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Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|258  LASDPNAALQNMNYKYDLQMTDEDYDTSYINPSLSISGREALQALT-----LLGRILG
30      40      50      60      70      80

60      70      80      90      100
Cry1Ac  SEFVPGAGFVLG----LVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGL
gi|258  ALGVPPSGQILSFYQFLLNLTLPVNDTAWAFAFMRQVEELVNQQITTEFARNQALARLQGL
90      100     110     120     130     140

110     120     130     140     150     160
Cry1Ac  SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|258  GESFNVYQRSLSQNLADRNDRNLSSLRAQFIALDDLDFVNAIPLFAVNGQQVPLLSVYVQ
150     160     170     180     190     200

170     180     190     200     210     220
Cry1Ac  AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|258  ALNHLHLLKESLFGEGWGFQGEISTYERQLELTAKYTNVYCTWYNTGLERLRGTNT
210     220     230     240     250     260

230     240     250     260     270     280
Cry1Ac  RDWIRYNQFRRELTTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLNFDGGSF---
gi|258  ESFLRYHQFRREMTLVVLDVVALFPYDVRVLYPTGSNPQLTREYVTDPIVFNPPANLGLC
270     280     290     300     310     320

290     300     310     320     330
Cry1Ac  -----RGSAQIEGS-IRSPHLMIDLNSITIIYTD---AHRGEYWSGHQIMASPVGF
gi|258  RRWGTNPYNTFSELENAFIRPPHLFRLNLSLTISSNRFVSSNFMEYFSGHTRLSYLN
330     340     350     360     370     380

340     350     360     370     380     390
Cry1Ac  SGPEFTFPLYGTMGNAAPQQRIVAQLG-QGVYRTLSTLYRRPFNIGINN-QQLSVLDGT
gi|258  SAVQED--SYGLITTT---RATINPGVDGTNRIESTAVDFRSALIGYVNRASFVPG
390     400     410     420     430

400     410     420     430     440     450
Cry1Ac  EFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFNSSVS
gi|258  LFN-GTTS--PANGGCRD-LYDINDLPPDEST---GSSTHRLSHLTFP-SFQTNQAGS
440     450     460     470     480

460     470     480     490     500
Cry1Ac  IIRA---PMFWSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLN
gi|258  IANAGSVPTVTRDVLNNTITPNRITQLPLVKASAPVSGTTLKPGPFTGGGILRRT
490     500     510     520     530     540

510     520     530     540     550     560
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPATATSL
gi|258  TNGT----FGTLRVTVNSPLTQ-QYRLRLRFASSTGNFSIRVLRGGVSGIDVRLGSTMNRG
550     560     570     580     590     600

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570          580          590          600          610
Cry1Ac  DNLQSSDF-----GYFESANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  QELTYESFFTRFRTTTGPFNPPFTFTQAQEILTVNAEGVSTGGEYYIDRIEIVPVNPARE
      610          620          630          640          650          660

620          630          640          650          660          670
Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  AEEDLEAAKKA
      670

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>>gi|40145997|gb|AAR61487.1| Sequence 109 from patent US (649 aa)  
 initn: 654 init1: 397 opt: 911 Z-score: 1067.2 bits: 208.6 E(): 1.6e-50  
 Smith-Waterman score: 979; 32.062% identity (66.205% similar) in 577 aa overlap  
 (60-612:89-648)

```

30          40          50          60          70          80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLIN
      . . . . . : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|401  TTKDAIQKGISIIIGDLLGVVGFPPYGGALVSYFYNLLNTIWP--GEDPLKAFMQQVEALID
      60          70          80          90          100         110

```

```

90          100         110         120         130         140
Cry1Ac  QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADP-TNPALREEMRIQ--FNDMNSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  QKIADYAKDKATAELQGLKNVFKDYVSALDSWDKTPPLTLRDGRSQGRIRELFSQAESHFR
      120         130         140         150         160         170

```

```

150         160         170         180         190         200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  RSMPSFAVSGYEVFLPPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHFKQKDLTIE
      180         190         200         210         220         230

```

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210         220         230         240         250         260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVQSQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  YTNHCAKWYKAGLDKLRGSTYE EWVKFNRYRREMTLTVLDLITLFLYDVRTYTKGVKTE
      240         250         260         270         280         290

```

```

270         280         290         300         310
Cry1Ac  LTREIYTNPVL--ENFDGSRFRGSAQGIIEGSIIRSPHLMIDILNSITIYTDahrgey-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  LTRDVLTDPIVAVNNMNG-YGTTFSNIENYIRKPHLFDYLHAIQPHSRLQPGYFGTDSFN
      300         310         320         330         340         350

```

```

320         330         340         350         360         370
Cry1Ac  YWSGHQIMA-SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRFPN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  YWSGNYVTRSSIG-SDEIIRSPFFYGNKSTLDVQN--LEFNGEKVFRAVANGNLAVWPVG
      360         370         380         390         400         410

```

```

380         390         400         410         420
Cry1Ac  IGINNQQLSVLDGTEFA-YGTSSN-LPSAVY---RKSgtv--DSLDEIPQNNNVPPRQG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  TG-GTKIHSgvTKVQFSQYNDKDEVRTQTYSKRNvGGIVFDSIDQLPPIITTTDESLEKA
      420         430         440         450         460         470

```

```

430          440          450          460          470          480
Cry1Ac  FSHRLSHVSMFRSGFNSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  YSHQLNIVYRCF---LLQGGRGII--PVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNS
      480          490          500          510          520

```

```

490          500          510          520          530          540
Cry1Ac  -SVISGPGFTGGDLVR-LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  TSVVAGPGFTGGDIKKTNGSGLTL----YV-TPAPDLTYSKTYKIRIRYASTSQVRFGI
      530          540          550          560          570          580

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```

550          560          570          580          590          600
Cry1Ac  NwGNSSIFsNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIvGVRNFSGTAG--VIID
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|401  DLGSYTHSISYFDKTMdKGNtLTyNSFNlSSVSRPIEISGgNKIGVSVGGIGSGDEVYID
      590          600          610          620          630          640

```

```

610          620          630          640          650          660
Cry1Ac  RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401  KIEFIPMD

```

>>gi|155684776|gb|ABU27031.1| Sequence 109 from patent U (649 aa)  
 initn: 654 init1: 397 opt: 911 Z-score: 1067.2 bits: 208.6 E(): 1.6e-50  
 Smith-Waterman score: 979; 32.062% identity (66.205% similar) in 577 aa overlap  
 (60-612:89-648)

```

30          40          50          60          70          80
Cry1Ac  GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  TTKDAIQKGISIIIGDLLGVVGFPPYGGALVSYFYNLLNTIWP--GEDPLKAFMQQVEALID
      60          70          80          90          100         110

```

```

90          100         110         120         130         140
Cry1Ac  QRIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADP-TNPALREEMRIQ--FNDMNSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  QKIADYAKDKATAELQGLKNVFKDYVSALDSWDKTPPLTLRDGRSQGRIRELFSQAESHFR
      120         130         140         150         160         170

```

```

150         160         170         180         190         200
Cry1Ac  TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  RSMPSFAVSGYEVFLPPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHFKQKDLTIE
      180         190         200         210         220         230

```

```

210         220         230         240         250         260
Cry1Ac  YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVQSQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  YTNHCAKWYKAGLDKLRGSTYE EWVKFNRYRREMTLTVLDLITLFLYDVRTYTKGVKTE
      240         250         260         270         280         290

```

```

270         280         290         300         310
Cry1Ac  LTREIYTNPVL--ENFDGSRFRGSAQGIIEGSIIRSPHLMIDILNSITIYTDahrgey-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155  LTRDVLTDPIVAVNNMNG-YGTTFSNIENYIRKPHLFDYLHAIQPHSRLQPGYFGTDSFN
      300         310         320         330         340         350

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320      330      340      350      360      370
Cry1Ac YWSGHQIMA-SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS--TLYRRFPN
gi|155 YWSGNVYSTRSSIG-SDEIIRSPFYGNKSTLDVQN--LEFNGEKVFRAVANGNLAVWPVG
360      370      380      390      400      410

```

```

380      390      400      410      420
Cry1Ac IGINNQQLSVLDGTEFA-YGTSSN-LPSAVY---RKSQTV--DSLDEIPPQNNVPPRQG
gi|155 TG-GTKIHSQVTKVQFSQYNDRKDEVRTQTYDSKRNKRVGGIVFDSIDQLPPITDESLEKA
420      430      440      450      460      470

```

```

430      440      450      460      470      480
Cry1Ac FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG
gi|155 YSHQLNRYVRCF---LLQGGRII--PVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNS
480      490      500      510      520

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```

490      500      510      520      530      540
Cry1Ac -SVISGPGFTGGDLVR-LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV
gi|155 TSVVAGPGFTGGDIKCTNGSGLTL---YV-TPAPDLTYSKYIRIRYASTSQVRFGI
530      540      550      560      570      580

```

```

550      560      570      580      590      600
Cry1Ac NWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG--VIID
gi|155 DLGSYTHSISYFDKTMKGNLTLYNSFNLSVSRPIEISGGNKIGVSVGGIGSGDEVYID
590      600      610      620      630      640

```

```

610      620      630      640      650      660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
gi|155 KIEFIPMD

```

>>gi|40188416|gb|AAR75941.1| Sequence 109 from patent US (649 aa)  
 initn: 654 initl: 397 opt: 911 Z-score: 1067.2 bits: 208.6 E(): 1.6e-50  
 Smith-Waterman score: 979; 32.062% identity (66.205% similar) in 577 aa overlap  
 (60-612:89-648)

```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|401 TTKDAIQKGISIIIGDLLGVVGFPPYGGALVSYFTNLLNTIWP--GEDPLKAFMQQVEALID
60      70      80      90      100     110

```

```

90      100     110     120     130     140
Cry1Ac QRIIEFARNQAI SRLEGLSNLYQIYAESFREWEADP-TNPALREEMRIQ--FNDMNSALT
gi|401 QKIADYAKDKATAELQGLKNVFKDYVSALDSWDKTPLTLRDRGRSQRIRLFSQAESHFR
120     130     140     150     160     170

```

```

150     160     170     180     190     200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|401 RSMPSFAVSGYEVFLPPTYAQAANTHLLLLKDAQIYGTDWGYSTDDLNEFHTKQKDLTIE
180     190     200     210     220     230

```

```

210     220     230     240     250     260
Cry1Ac YTDHAVRWYNTGLERWVGPDSDRWIRYQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQ
gi|401 YTNHCAKWKYKAGLDKLRGSTEYEEWVKFNRYRREMTLTVLDLITLFLYDVRTYTKGVKTE
240     250     260     270     280     290

```

```

270     280     290     300     310
Cry1Ac LTREIYTNPVL--ENFDGSRFRGSAQIEGSIRSPHMLDILNSITTYTDAHRGEY-----
gi|401 LTRDVLTDPIVAVNNMNG-YGTFNSNIENYIRKPHLFDYLHAIQFHSRLQPGYGFDTDFSN
300     310     320     330     340     350

```

```

320     330     340     350     360     370
Cry1Ac YWSGHQIMA-SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS--TLYRRFPN
gi|401 YWSGNVYSTRSSIG-SDEIIRSPFYGNKSTLDVQN--LEFNGEKVFRAVANGNLAVWPVG
360     370     380     390     400     410

```

```

380     390     400     410     420
Cry1Ac IGINNQQLSVLDGTEFA-YGTSSN-LPSAVY---RKSQTV--DSLDEIPPQNNVPPRQG
gi|401 TG-GTKIHSQVTKVQFSQYNDRKDEVRTQTYDSKRNKRVGGIVFDSIDQLPPITDESLEKA
420     430     440     450     460     470

```

```

430     440     450     460     470     480
Cry1Ac FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG
gi|401 YSHQLNRYVRCF---LLQGGRII--PVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNS
480     490     500     510     520

```

```

490     500     510     520     530     540
Cry1Ac -SVISGPGFTGGDLVR-LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV
gi|401 TSVVAGPGFTGGDIKCTNGSGLTL---YV-TPAPDLTYSKYIRIRYASTSQVRFGI
530     540     550     560     570     580

```

```

550     560     570     580     590     600
Cry1Ac NWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG--VIID
gi|401 DLGSYTHSISYFDKTMKGNLTLYNSFNLSVSRPIEISGGNKIGVSVGGIGSGDEVYID
590     600     610     620     630     640

```

```

610     620     630     640     650     660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
gi|401 KIEFIPMD

```

>>gi|12810103|gb|AAE44018.1| Sequence 109 from patent US (649 aa)  
 initn: 654 initl: 397 opt: 911 Z-score: 1067.2 bits: 208.6 E(): 1.6e-50  
 Smith-Waterman score: 979; 32.062% identity (66.205% similar) in 577 aa overlap  
 (60-612:89-648)

```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|128 TTKDAIQKGISIIIGDLLGVVGFPPYGGALVSYFTNLLNTIWP--GEDPLKAFMQQVEALID
60      70      80      90      100     110

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90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADP--TNPALREEMRIQ--FNDMNSALT
gi|128 QKIADYAKDKATAELQGLKNVFKDYVSALDSWDKTPPLTLRDGRSQGRIRELFSQAESHFR
120      130      140      150      160      170

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|128 RSMPSFAVSGYEVFLPTYAQAANTHLLKDAQIYGTDWGYSTDDLNEFHFKQKDLTIE
180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|128 YTNHCAKWKYKAGLDKLRGSTYEWWKFNRYRREMTLTVLDLITLFLPLYDVRTYTKGVKTE
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSFRGSAQIEGSI RSPHLM DILNSIT IYTD AHRGEY-----
gi|128 LTRDVL TDP IVAVNNMNG-YGTF TFSNIENYIRKPHLFDYLHAIQFHSRLQPGYFGTDSFN
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac YWSGHQIMA-SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS--TLYRRPFN
gi|128 YWSGNYVSTRSSIG-SDEIIRSPFYGNKSTLDVQN--LEFNGEKVFRAVANGNLAVWPVG
360      370      380      390      400      410

380      390      400      410      420
Cry1Ac IGINNQQLSVLDGTEFA-YGTSSN-LPSAVY---RKS GTV--DSLDEIPPQNNVPPRQG
gi|128 TG-GTKIHS GVTKVQFSQYNDRKDEVRTQTYDSKRN VGGIVFDSIDQLPPIITDESLEKA
420      430      440      450      460      470

430      440      450      460      470      480
Cry1Ac FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG
gi|128 YSHQLN YVRCF---LLQGGRGII--PVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNS
480      490      500      510      520

490      500      510      520      530      540
Cry1Ac -SVISGPGFTGGDLVR-LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV
gi|128 TSVVAGPGFTGGDIKCTNGSGLTL----YV-TPAPDLTYSKTYKIRIRYASTSQVRFGI
530      540      550      560      570      580

550      560      570      580      590      600
Cry1Ac NWNSSIFSNTV PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG--VIID
gi|128 DLGSYTHSISYFDKTM DKGNTLTYSNLFNLSSVSRPIEISGGNKIGVSVGGIGSGDEVYID
590      600      610      620      630      640

610      620      630      640      650      660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFEC
gi|128 KIEFIPMD

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>>gi|40288|emb|CAA42469.1| CryIIID [Bacillus thuringiens (649 aa)
initn: 654 initl: 397 opt: 911 Z-score: 1067.2 bits: 208.6 E(): 1.6e-50
Smith-Waterman score: 979; 32.062% identity (66.205% similar) in 577 aa overlap
(60-612:89-648)

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```

30      40      50      60      70      80
Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLIN
gi|402 TTKDAIQKGISIIIGDLLGVVGFYGGALVSFYTNLLNTIWP--GEDPLKAFMQQVEALID
60      70      80      90      100      110

90      100      110      120      130      140
Cry1Ac QRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADP--TNPALREEMRIQ--FNDMNSALT
gi|402 QKIADYAKDKATAELQGLKNVFKDYVSALDSWDKTPPLTLRDGRSQGRIRELFSQAESHFR
120      130      140      150      160      170

150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
gi|402 RSMPSFAVSGYEVFLPTYAQAANTHLLKDAQIYGTDWGYSTDDLNEFHFKQKDLTIE
180      190      200      210      220      230

210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQ
gi|402 YTNHCAKWKYKAGLDKLRGSTYEWWKFNRYRREMTLTVLDLITLFLPLYDVRTYTKGVKTE
240      250      260      270      280      290

270      280      290      300      310
Cry1Ac LTREIYTNPVL--ENFDGSFRGSAQIEGSI RSPHLM DILNSIT IYTD AHRGEY-----
gi|402 LTRDVL TDP IVAVNNMNG-YGTF TFSNIENYIRKPHLFDYLHAIQFHSRLQPGYFGTDSFN
300      310      320      330      340      350

320      330      340      350      360      370
Cry1Ac YWSGHQIMA-SPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSS--TLYRRPFN
gi|402 YWSGNYVSTRSSIG-SDEIIRSPFYGNKSTLDVQN--LEFNGEKVFRAVANGNLAVWPVG
360      370      380      390      400      410

380      390      400      410      420
Cry1Ac IGINNQQLSVLDGTEFA-YGTSSN-LPSAVY---RKS GTV--DSLDEIPPQNNVPPRQG
gi|402 TG-GTKIHS GVTKVQFSQYNDRKDEVRTQTYDSKRN VGGIVFDSIDQLPPIITDESLEKA
420      430      440      450      460      470

430      440      450      460      470      480
Cry1Ac FSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG
gi|402 YSHQLN YVRCF---LLQGGRGII--PVFTWTHKSVDFYNTLDSEKITQIPFVKAFILVNS
480      490      500      510      520

490      500      510      520      530      540
Cry1Ac -SVISGPGFTGGDLVR-LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV
gi|402 TSVVAGPGFTGGDIKCTNGSGLTL----YV-TPAPDLTYSKTYKIRIRYASTSQVRFGI
530      540      550      560      570      580

550      560      570      580      590      600
Cry1Ac NWNSSIFSNTV PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG--VIID
gi|402 DLGSYTHSISYFDKTM DKGNTLTYSNLFNLSSVSRPIEISGGNKIGVSVGGIGSGDEVYID
590      600      610      620      630      640

610      620      630      640      650      660
Cry1Ac RFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFEC
gi|402 KIEFIPMD

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550      560      570      580      590      600
Cry1Ac  NWNSSIFSNTV PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG--VIID
gi|402  DLGSYTHSISYFDK TMDKGNLTLYNSFNLSSVSRPIETISGGNKIGVSVGGIGSGDEVYID
      590      600      610      620      630      640

```

```

610      620      630      640      650      660
Cry1Ac  RPEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFC
gi|402  KIEFIPMD

```

>>gi|79014092|gb|ABB51652.1| crystal protein Cry26Aa [Ba (1164 aa)  
 initn: 2021 initl: 640 opt: 905 Z-score: 1056.3 bits: 207.4 E(): 6.4e-50  
 Smith-Waterman score: 2188; 36.279% identity (63.215% similar) in 1188 aa overlap  
 (40-1181:68-1163)

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10      20      30      40      50      60
Cry1Ac  NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVDII
gi|790  FCADDFLQSYGEFNMDFGESEFFIDASGAINAAIGVTGTVLGFVGFAGALTTFYQKL
      40      50      60      70      80      90

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70      80      90      100     110     120
Cry1Ac  WGIFGPS----QWDAFLVQIEQLINQRIEIEFARNQAIISRLLEGLSNLYQIYAESFREWEAD
gi|790  FGFLFPNNNTKQWEEFMKQVEALIDEKISDAVRNKAISELQGLVNNITLYTEALEEWLEN
      100     110     120     130     140     150

```

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130     140     150     160     170     180
Cry1Ac  PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
gi|790  KENPAVRDRVLQRWRILDGFFEQQMPSFAVKGFVLLLVVYTAQANLHLLSLRDAYIYGA
      160     170     180     190     200     210

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190     200     210     220     230     240
Cry1Ac  RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWRIRYNQFRRELTTLV
gi|790  EWGLTPTNIDQNHTRLLRHSAEYTDHCVNWYNTGLKQLENSDAKSWFYQYRFRREMTLSV
      220     230     240     250     260     270

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250     260     270     280     290
Cry1Ac  LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE----NFDGSFRGSA---QGIEGS-IR
gi|790  LDVIALFPAYDVKMYPIPTNFQLTREVYTDVIGKIGRNDSDHWYSANAPSFNSLESTLIR
      280     290     300     310     320     330

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300     310     320     330     340     350
Cry1Ac  SPHLM DILNSITIIY--TDAHRGEY----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAP
gi|790  TPHVV DVIK KLIKIFATVDYGIYGRSGKWVGH-IITSATSANTTETRN--YGTIVNHDS
      340     350     360     370     380     390

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360     370     380     390     400
Cry1Ac  QQRIV AQLGQGVYRTLSS TLYRRPFNIGINNQLSVLDGTEF--AYGTSSNLPSAVYRKS
gi|790  VE--L NFGKN IYK TGS LFPQGVPPYQIGYVTP IYF ITRAVNFFT VSGSKTSVEKYYSKDD
      400     410     420     430     440     450

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410      420      430      440      450
Cry1Ac  ----GT----VDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFS
gi|790  RYYSEGLPEEQGVFSTEQLP PNSIAEPEHIAYSRHLCHVTFTI--SVSNGNKYSKDLPLFS
      460      470      480      490      500      510

```

```

460      470      480      490      500      510
Cry1Ac  WIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYI
gi|790  WTHSSVDFPNYVYPTKITQLPATKG---YNVSIVKEPFGIGGDIGK----NNGQILGKY
      520      530      540      550      560

```

```

520      530      540      550      560      570
Cry1Ac  EVPIHFPSTSTRYRVRVRYASVTPHILNVNWNSSIFSNTV PATATSLDNLQSSDFGY--
gi|790  KVNVE--DVSQKYRFRVRVYATETEGELGKIDGRVTNLYQYKKTAPGDPPTYKAFDYL
      570      580      590      600      610      620

```

```

580      590      600      610      620      630
Cry1Ac  FESANAFTSSLGNI-VGVRN-FSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFT
gi|790  FSTPVKFNNASSTIELFLQNKTSGT--FYLAGIEIIPVKSNYEEELTLEAKKAVSSSLFT
      630      640      650      660      670

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640      650      660      670      680      690
Cry1Ac  STNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNF
gi|790  DARN-ALKTDVTDYQIDQAANLVEICISGDLYAKEKIVLLRAVKFAKQLSQSNLSDPEF
      680      690      700      710      720      730

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700      710      720      730      740      750
Cry1Ac  KDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFFDECYPTYLYQKIDESKLFKAFTRY
gi|790  NNVNR--ENSWTASTSVAIIEGDPLYKGRAVQLSSARDENFPPTYLYQKIDESTLKPYPTRY
      740      750      760      770      780      790

```

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760      770      780      790      800
Cry1Ac  QLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPN-----
gi|790  QLRGFVEGSENLDVYLIRYGAHVRMNVPY--NLEIIDTSSPVNCPCEEVDGLSHRSCNVF
      800      810      820      830      840      850

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810      820      830      840      850      860
Cry1Ac  -RCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTDLNEDLGVWVIFKIKTKQDGH
gi|790  DRCKQSI SVAPDANTG---PDQIDGDPHAFSFDHIDTGTVDSTENLGIWVAFKISELDGSA
      860      870      880      890      900      910

```

```

870      880      890      900      910      920
Cry1Ac  RLG NLFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD
gi|790  IFGNLELIEVGPLSGEALAQVQRKEEKWKQVLAKKRETTAKLYAAAKQAIDQLFADSQNT
      920      930      940      950      960      970

```

```

930      940      950      960      970      980
Cry1Ac  QLQADTNIAIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVI
gi|790  KLRFDTEFSNILSAEHLVYKIQDIYNNELSAIPGLNYDLFMELENRIQNAITLYDARNIL

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120      130      140      150      160
Cry1Ac  750      760      770      780      790      800
ESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGE
gi|742  ESKLKPYTRYLVRGVFVSSKDVVELVVSRYGEEIDAIMNVPADLNLYLPSTFD----CEG
170      180      190      200      210      220

```

```

810      820      830      840      850
Cry1Ac  PNR-----AP-HLEWNPDLDCSCR--DGEK---CAHSHHFSLDIDVGTDLNEDLVGVV
gi|742  SNRCETSAVPANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDTNENIGVWV
230      240      250      260      270      280

```

```

860      870      880      890      900      910
Cry1Ac  IFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKWRDKREKLEWETNIVYKEAKES
gi|742  MFKISSPDGYASLDNLEVEEGAI DGEALSRVKHMEKKWNDQMEAKRLETQQAIDVAKQA
290      300      310      320      330      340

```

```

920      930      940      950      960      970
Cry1Ac  VDALFVNSQYDQLQADNTNIAMIHAADKRVHSIREAYLPESVIPGVNAAIFELEGRIFT
gi|742  IDALFTNVQDEALQFDTTLAQIQYAEYLVQSIPIVYVNDWLSDPVGMNYDIYVELDARVAQ
350      360      370      380      390      400

```

```

980      990      1000     1010     1020     1030
Cry1Ac  AFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQSVLVPVEWAEVVSQEVRCVCPGR
gi|742  ARYVYDTRNIKNGDFTQGVMGWHVTGNADVQ-QIDGVSVLVLCNWSAGVCEK---CPSP
410      420      430      440      450

```

```

1040     1050     1060     1070     1080     1090
Cry1Ac  GYLRTVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTCDNYTVNQEEYGG
gi|742  THQVMIVGASTPPYQC
460      470

```

>>gi|4583416|gb|AAD25075.1|AF122897\_1 Cry26Aa1 protein [ (1163 aa)  
 initn: 1759 initl: 640 opt: 896 Z-score: 1045.7 bits: 205.5 E(): 2.5e-49  
 Smith-Waterman score: 1996; 34.612% identity (61.218% similar) in 1199 aa overlap  
 (40-1181:68-1162)

```

10      20      30      40      50      60
Cry1Ac  NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF-VPGAGFVLGLVDII
gi|458  FCADDFLQSYGEFNMDFGESEFFIDASGAINAAIGVTGTVLGFLGVPFAGALTTFFYQKL
40      50      60      70      80      90

```

```

70      80      90      100     110     120
Cry1Ac  WGIFGPS----QWDAFLVQIEQLINQRIEIEFARNQAI SRLEGLSNLYQIYAESFREWEAD
gi|458  FGFLFPNNTKQWEEFMKQVEALIDEKISDAVRNKAISELQGLVNNITLYTEALBEWLEN
100     110     120     130     140     150

```

```

130     140     150     160     170     180
Cry1Ac  PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
gi|458  KENPAVRDRVLQRWRILDGFFEQMPSFAVKGFVLLLVVYVYTAQANLHLLSLRDAYIYGA

```

```

160      170      180      190      200      210
Cry1Ac  190      200      210      220      230      240
RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV
gi|458  EWGLTPTNIDQNHTRLLRHSAEYTDHCVNWNWYNTGLKQLENSDAKSWFQYNNFRREMRLSV
220     230     240     250     260     270

```

```

250     260     270     280     290
Cry1Ac  LDIVSLFPNYSRITYPIRTVSQLTREIYTNPVLE---NFDGSGFRGSA---QGIEGS-IR
gi|458  LDVIALFPAYDKMYPPIPTNFQLTREVYTDVIGKIGRNDSDHWYSANAPSFNLESTLIR
280     290     300     310     320     330

```

```

300     310     320     330     340     350
Cry1Ac  SPHLMIDILNSITYI--TDAHRGEY---YWSGHQIMASPVGFGPEFTFPPLYGTMGNAAP
gi|458  TPHVVDYIKKLIKIFYATVDYIYGRSGKWVGH-IITSATSANTTETRN--YGTIVNHDS
340     350     360     370     380     390

```

```

360     370     380     390     400
Cry1Ac  QQRIVAQQLGGVYRTLSSTLYRRPFNIGINNQLSVLDGTEF--AYGTSSNLPSSAVYRKS
gi|458  VE--LNFEGKNYKYGSLPQGVPPYQIGYVTPYFIFITRAVNFPTVSGSKTSVEKYYSKKD
400     410     420     430     440     450

```

```

410     420     430     440     450
Cry1Ac  -----GT-----VDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSVSIIRAPMFS
gi|458  RYSEGLPEEQGVFSTEQLPNNSIAEPEHIAVSHRSLCHVTFI--SVSNKYSKDLPLFS
460     470     480     490     500     510

```

```

460     470     480     490     500     510
Cry1Ac  WIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYI
gi|458  WTHSSVDFPNYVYPTKITQLPATKG---YNSIVKEPGFIFGGDIGK----NNGQILGKY
520     530     540     550     560

```

```

520     530     540     550     560     570
Cry1Ac  EVDIHFPTSTSTRYRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGY--
gi|458  KVNVE--DVSQYRFRVRYATEETEGELGKIDGRVTNLYQYKTKAPGDPPTYKAFDYLS
570     580     590     600     610     620

```

```

580     590     600     610     620     630
Cry1Ac  FESANAFTSSLGNI-VGVRN-FSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFT
gi|458  FSTPVKFNNASSTIELFLQNKTSQT--FYLAGEIIPVKSNEYEELTLEAKKAVSSSLFT
630     640     650     660     670

```

```

640     650     660     670     680     690
Cry1Ac  STNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRSLDERNLLQDSNF
gi|458  DARN-ALKIDVTDYQIDQANLVEICISGDLYAKEKIVLLRAVKFAKQLSQSNLLSDPEF
680     690     700     710     720     730

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700     710     720     730     740     750
Cry1Ac  KDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRY

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gi|458 NNVNR--ENSWTASTVVAIEGDPLYKGRAVQLSSARDENFPTYLYQKIDESTLKPYTRY
740 750 760 770 780 790

Cry1Ac QLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLWPLSAQSPIGKCGEPN-----
760 770 780 790 800

gi|458 QLRGFVEGSENLDVYLIRYGAHVVMNVPY--NLEIIDTSSPVNCEVDGLSHRSCNVF
800 810 820 830 840 850

Cry1Ac -RCAPHLEWNPDLDCSCRDGEKCAHSHHFLDIDVGCITDLNEDLGVWVIFKIKIQDGH
810 820 830 840 850 860

gi|458 DRCKQISIVAPDANTG---PDQIDGDPHAFSFHIDTGTVDSTENLGIWVAFKISELDGSA
860 870 880 890 900 910

Cry1Ac RLGNFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD
870 880 890 900 910 920

gi|458 IFGNLELIEVGPLSGEALAQVQRKEEKWKQ-----VLAKKRETTAQTVCSEAS
920 930 940 950

Cry1Ac QLQADTNIAAMIHAADK---RVHSIREAYLPELSVI-----PG--VNAAIFEELEGRIFT
930 940 950 960 970

gi|458 QLTNSSQLIKIRNYDLIQNFRIFSLRNTLSIKFKIYITITNYPYSLRNLVDLMELENRIQN
960 970 980 990 1000 1010

Cry1Ac AFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVEEQNNQRSVLVPEWEAEVSEQEVRVCPGR
980 990 1000 1010 1020 1030

gi|458 A-SLYMTSNILQNGGFKSDVTSWETTANAQVQ-QIDGASVLVLSNWNASVAQSVNVQNDH
1020 1030 1040 1050 1060 1070

Cry1Ac GYILRVTAKEGYEGCVTIHEIENNTDELKFSNCVVEEIIYPNNTVTCDNYTVNQEEYGG
1040 1050 1060 1070 1080 1090

gi|458 GYVLRVTAKEGIGNGYVITILDCAHIDTLTFSAC----RSDSTSSNELTA-----
1080 1090 1100 1110 1120

Cry1Ac AYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRYRDTPLPVGYVTKLEY
1100 1110 1120 1130 1140 1150

gi|458 -----YVTKTLEI
1130

Cry1Ac FPETDKVVIEIGETEGTFIVDSVELLLMEE
1160 1170 1180

gi|458 FPDTEQIRIEIGETEGMFYVESVELIRMEN
1140 1150 1160

>>gi|162767638|emb|CAP58822.1| unnamed protein product [ (404 aa)
initn: 658 initl: 243 opt: 890 Z-score: 1045.5 bits: 203.9 E(): 2.6e-49
Smith-Waterman score: 890; 42.217% identity (67.689% similar) in 424 aa overlap
(229-624:1-404)

Cry1Ac DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRT
200 210 220 230 240 250

gi|162 DWITYNRLRRDLTLTLVLDIAAFFPNYDNR
10 20 30

Cry1Ac YPIRTVSQLTREIYTNPLENFDGSRGSAQG-----IEGS-IRSPHMLDILNSITTYTD
260 270 280 290 300 310

gi|162 YPIQPVGQLTREVVYTDPLI-NFNPQLQSVAQLPTFNVMESSAIRNPHLFDILNNTIFTD
40 50 60 70 80

Cry1Ac AHR-GE-YYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSLT
320 330 340 350 360 370

gi|162 WFSVGRNFYWGHRVISSLIG--GGNITSPIYGREANQEPFRSFT--FNGPVFRTLNSPT
90 100 110 120 130 140

Cry1Ac YR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVSDLSDEIPPNQNNVPPR
380 390 400 410 420

gi|162 LRLQLQPWPAPPFN--LRGVEGVEFS--TPTN--SFTYRGRGTVDLSLTELPPEDNSVPPR
150 160 170 180 190

Cry1Ac QGFSHRLSHVSMF-RSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL
430 440 450 460 470 480

gi|162 EGYSHRLCHATFVQRSGTFFLTGGV---FSWTHRSATLNTIDPERINQIPLVKGFRV
200 210 220 230 240 250

Cry1Ac FNG-SVISGPGTGGDLVRLNSSGNINQNRGYIEVP IHPSTSTRYRVRVRYASVTPIHL
490 500 510 520 530 540

gi|162 WGGTSVITGPGTGGDILRRNTFGDFVS---LQVNINSPIQ-RYRLRFYASSRDARV
260 270 280 290 300 310

Cry1Ac NVNWGNSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIVGVRN--
550 560 570 580 590

gi|162 IVLTGAASTGVGQVSVNMPLQKTMEIGENLTSRTFRYTDFSNPFSTRANPDIIGISEQP
320 330 340 350 360 370

Cry1Ac -F---SGTAG-VIIDRFEPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
600 610 620 630 640 650

gi|162 LFGAGSISSGELYIDKIEIILADATFEAESDLER
380 390 400

Cry1Ac DQVSNLVTVLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG
660 670 680 690 700 710

>>gi|162767642|emb|CAP58824.1| unnamed protein product [ (404 aa)
initn: 658 initl: 243 opt: 890 Z-score: 1045.5 bits: 203.9 E(): 2.6e-49
Smith-Waterman score: 890; 42.217% identity (67.689% similar) in 424 aa overlap
(229-624:1-404)

Cry1Ac DLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRT
200 210 220 230 240 250

gi|162 DWITYNRLRRDLTLTLVLDIAAFFPNYDNR
10 20 30

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260      270      280      290      300      310
Cry1Ac YPIRTVSQLTREIYTNPVLENFDGSRGSAQG----IEGS-IRSPHLMIDLNSITIYTD
      . . . . .
gi|162 YPIQPVGQLTREYVTDPLI-NFNPQLQSVLPTFNVMESSAIRNPHLFDILNLTIFTD
      40      50      60      70      80

      320      330      340      350      360      370
Cry1Ac AHR-GE-YWVSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL
      . . . . .
gi|162 WFSVGRNFYWGHRVIVSSLIG--GGNITSPIYGREANQEPFRSFT--FNGPVFRTLSNPT
      90      100      110      120      130      140

      380      390      400      410      420
Cry1Ac YR---RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPR
      . . . . .
gi|162 LRLQLQPPWAPPFN--LRGVEGVFES--TPTN--SFTYRGRGTVDLSLTELPPEDNSVPPR
      150      160      170      180      190

      430      440      450      460      470      480
Cry1Ac QGFSHRLSHVSMF-RSGFSNNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL
      . . . . .
gi|162 EGYSHRLCHATFVQRSGTFFLTGVV---FSWTHRSATLNTIDPERINQIPLVKGRV
      200      210      220      230      240      250

      490      500      510      520      530      540
Cry1Ac FNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHL
      . . . . .
gi|162 WGGTSVITGPGFTGGDILRRNTFGDFVS----LQVINSPIITQ-RYRLRFYASSRDARV
      260      270      280      290      300      310

      550      560      570      580      590
Cry1Ac NVNWNSSSI----FSNTVPATATSL--DNLQSSDFGYFESANAFTSSLG-NIVGVRN--
      . . . . .
gi|162 IVLTGAASTGVGGQVSVNMPLQKTMEIGENLTSRTFRYTDSPNPFSPANPDIIGISEQP
      320      330      340      350      360      370

      600      610      620      630      640      650
Cry1Ac -F---SGTAG-VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
      . . . . .
gi|162 LFGAGSISGELYIDKIEIILADATFEAESDLR
      380      390      400

      660      670      680      690      700      710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG

>>gi|110734453|gb|ABG88860.1| Cry1-like Bt toxin 1 [Baci (143 aa)
initn: 520 initl: 520 opt: 884 Z-score: 1045.1 bits: 202.3 E(): 2.7e-49
Smith-Waterman score: 884; 92.308% identity (95.804% similar) in 143 aa overlap
(1043-1181:1-143)

      1020      1030      1040      1050      1060      1070
Cry1Ac LVVPEWEAEVSVQEVRCVGRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFSNCVEEII
      . . . . .
gi|110      EGYGEGCVTIHEIENNTDELKFSNCVEEIV
      10      20      30

      1080      1090      1100      1110      1120
Cry1Ac YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNP
      . . . . .

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gi|110 YPNNTVTCNDYATQEEYEGTYTSRNRGYDEAYGNNPSPADYASVYEEKSYTDRRREN
      40      50      60      70      80      90

      1130      1140      1150      1160      1170      1180
Cry1Ac CEFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi|110 CEFNRGYRDTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLME
      100      110      120      130      140

>>gi|12810098|gb|AAE44013.1| Sequence 70 from patent US (493 aa)
initn: 870 initl: 432 opt: 889 Z-score: 1043.0 bits: 203.7 E(): 3.5e-49
Smith-Waterman score: 958; 34.800% identity (67.200% similar) in 500 aa overlap
(131-612:5-491)

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
      . . . . .
gi|128      SKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVL
      10      20      30

      170      180      190      200      210      220
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
      . . . . .
gi|128 FLPTYAQAANTHLLKDAQVFGESSEDVAEFYHRQLKLTQQYTDHCVNWNVGLN
      40      50      60      70      80      90

      230      240      250      260      270
Cry1Ac RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-N
      . . . . .
gi|128 GLRGSTYDAWVKFNRRFRREMTLTVLIDLIVLPPFYDIRLYSKGVKTELTRDIFSLN
      100      110      120      130      140      150

      280      290      300      310      320      330
Cry1Ac FDGSRGSAQGIIEGSIIRSPHLMIDLNSITIYDHAHRGEY-----YWSGHQIMASPVGFS
      . . . . .
gi|128 TLQEYGTFLSIEHSIRKPHLFDYLGQIEFHTRLPQGYFGKDSFNYSWGNVETRPSIGS
      160      170      180      190      200      210

      340      350      360      370      380
Cry1Ac GPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRP---FNIGINNQLSVLDG
      . . . . .
gi|128 SKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTDVAAWPNKGYLGVTKVDFSQYDD
      220      230      240      250      260      270

      390      400      410      420      430      440
Cry1Ac TEFAYGTSSNLPSAVYRKSQVTV---DSLDEIPPQNNVPPRQGFSHRLSHVSMRSGFSN
      . . . . .
gi|128 QK---NETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAEACFLMQDRR
      280      290      300      310      320

      450      460      470      480      490      500
Cry1Ac SSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRL
      . . . . .
gi|128 GTI-----PFFTWTWHRSDVFNITDAEKITQLPVPVKAYALSSGASIIIEGPGFTGGNLLFL
      330      340      350      360      370      380

      510      520      530      540      550      560
Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNTVPATATS
      . . . . .

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gi|128 KESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLRFVQNSNNDFLVIYINKTMNK
390 400 410 420 430 440

Cry1Ac LDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNL
570 580 590 600 610 620

gi|128 DDDLTQTDFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL
450 460 470 480 490

Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL
630 640 650 660 670 680

>>gi|40188411|gb|AAR75936.1| Sequence 70 from patent US (493 aa)
initn: 870 init1: 432 opt: 889 Z-score: 1043.0 bits: 203.7 E(): 3.5e-49
Smith-Waterman score: 958; 34.800% identity (67.200% similar) in 500 aa overlap
(131-612:5-491)

Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
110 120 130 140 150 160

gi|401 SKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVL
10 20 30

Cry1Ac LLSVVYQAAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
170 180 190 200 210 220

gi|401 FLPTYAQAANTHLLKDAQVFGGEWGYSSDEVAEFYHRQLKLTQQYTDHCVNWNVYVGLN
40 50 60 70 80 90

Cry1Ac RVWGPDSRDWIRYQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-N
230 240 250 260 270

gi|401 GLRGSTYDAWVKFNFRREMTLTVLDLIVLFFPYDIRLYSKGVKTELTRDIFTDPIFSLN
100 110 120 130 140 150

Cry1Ac FDGSFRGSAQGIIEGSIRSPHLMIDILNSITIIYTDHRGEY-----YWSGHQIMASPVGFS
280 290 300 310 320 330

gi|401 TLQEYGPFTFLSIENSIRKPHLFDYLGIEFHTRLQPGYFGKDSFNYSNGVYVETRPSIGS
160 170 180 190 200 210

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRP---FNIGINNQQLSVLDG
340 350 360 370 380

gi|401 SKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTDVAAWPNGKVLVGVTKVDFSQYDD
220 230 240 250 260 270

Cry1Ac TEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSN
390 400 410 420 430 440

gi|401 QK---NETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR
280 290 300 310 320

Cry1Ac SSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRL
450 460 470 480 490 500

gi|401 GTI-----PFFTWTWRSVDFNFNTIDAEEKITQLPVVKAYALSSGASIIIEGPGFTGGNLLFL
330 340 350 360 370 380

Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNWNWGNSSIFSNTVPATATS
510 520 530 540 550 560

gi|401 KESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLRFVQNSNNDFLVIYINKTMNK
390 400 410 420 430 440

Cry1Ac LDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNL
570 580 590 600 610 620

gi|401 DDDLTQTDFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL
450 460 470 480 490

Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL
630 640 650 660 670 680

>>gi|155684771|gb|ABU27026.1| Sequence 70 from patent US (493 aa)
initn: 870 init1: 432 opt: 889 Z-score: 1043.0 bits: 203.7 E(): 3.5e-49
Smith-Waterman score: 958; 34.800% identity (67.200% similar) in 500 aa overlap
(131-612:5-491)

Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
110 120 130 140 150 160

gi|155 SKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVL
10 20 30

Cry1Ac LLSVVYQAAANLHLSVLRDVSVFGQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
170 180 190 200 210 220

gi|155 FLPTYAQAANTHLLKDAQVFGGEWGYSSDEVAEFYHRQLKLTQQYTDHCVNWNVYVGLN
40 50 60 70 80 90

Cry1Ac RVWGPDSRDWIRYQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-N
230 240 250 260 270

gi|155 GLRGSTYDAWVKFNFRREMTLTVLDLIVLFFPYDIRLYSKGVKTELTRDIFTDPIFSLN
100 110 120 130 140 150

Cry1Ac FDGSFRGSAQGIIEGSIRSPHLMIDILNSITIIYTDHRGEY-----YWSGHQIMASPVGFS
280 290 300 310 320 330

gi|155 TLQEYGPFTFLSIENSIRKPHLFDYLGIEFHTRLQPGYFGKDSFNYSNGVYVETRPSIGS
160 170 180 190 200 210

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSST-LYRRP---FNIGINNQQLSVLDG
340 350 360 370 380

gi|155 SKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTDVAAWPNGKVLVGVTKVDFSQYDD
220 230 240 250 260 270

Cry1Ac TEFAYGTSSNLPSAVYRKSGTV---DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSN
390 400 410 420 430 440

gi|155 QK---NETSTQTYDSKRNNGHVSAQDSIDQLPPETTDEPLEKAYSHQLNYAECFLMQDRR
280 290 300 310 320

Cry1Ac SSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRL
450 460 470 480 490 500

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gi|155 GTI-----PFFTWTTHRSVDFPNTIDAEEKITQLPVVKAYALSSGASIEGPGFTGGNLLFL
330      340      350      360      370      380
      510      520      530      540      550      560
Cry1Ac NSSGNNIQNRGYIEVPIHFHSTSTRYRVRVRYASVTPHILNWNWGNSSIFSNTVPATATS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLRFVQNSNNDFLVIYINKTMNK
390      400      410      420      430      440
      570      580      590      600      610      620
Cry1Ac LDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNL
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DDDLTQYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL
450      460      470      480      490
      630      640      650      660      670      680
Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL

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>>gi|40145987|gb|AAR61482.1| Sequence 70 from patent US (493 aa)  
 initn: 870 init1: 432 opt: 889 Z-score: 1043.0 bits: 203.7 E(): 3.5e-49  
 Smith-Waterman score: 958; 34.800% identity (67.200% similar) in 500 aa overlap  
 (131-612:5-491)

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      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SKRSQDRIRELFSQAESHFRNSMPSFAVSKFEVL
      10      20      30
      170      180      190      200      210      220
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 FLPTYAQAANTHLLKDAQVFGEEWGYSSSEDAEYFHRQLKLTQQYTDHCVNWNVYVGLN
40      50      60      70      80      90
      230      240      250      260      270
Cry1Ac RVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLE-N
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 GLRGSTYDAWVKFNRFRREMTLTVLDLIVLFPFYDIRLYSKGVKTELTRDIFTDPIFSLN
100      110      120      130      140      150
      280      290      300      310      320      330
Cry1Ac FDGSFRGSAQGLEGSIRSPHLMILNSITITYDAHRGEY-----YWSGHQIMASPVGFS
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 TLQEYGPFFLSIENSIRKPHLFDYLQGIIEFHTRLQPGYFGKDSFNWYSGNVVETRPSIGS
160      170      180      190      200      210
      340      350      360      370      380
Cry1Ac GPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLSST-LYRRP---FNIGINNQQLSVLDG
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 SKTITSPFYGDK-STEPVQKLSFD-GQKVYRTIANTDVAAWPNGKVVYLGVTKVDVDFSQYDD
220      230      240      250      260      270
      390      400      410      420      430      440
Cry1Ac TEFAYGTSSNLPSAVYRKSQTV---DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSN
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 QK---NETSTQYTDKSRNNGHVSQAQDSIDQLPPEPTTDEPLEKAYSHQLNLYAEFCFLMQRDR
280      290      300      310      320

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      450      460      470      480      490      500
Cry1Ac SSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRL
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 GTI-----PFFTWTTHRSVDFPNTIDAEEKITQLPVVKAYALSSGASIEGPGFTGGNLLFL
330      340      350      360      370      380
      510      520      530      540      550      560
Cry1Ac NSSGNNIQNRGYIEVPIHFHSTSTRYRVRVRYASVTPHILNWNWGNSSIFSNTVPATATS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 KESSNSIAK---FKVTLNSAALLQRYRVRIRYASTTNLRLRFVQNSNNDFLVIYINKTMNK
390      400      410      420      430      440
      570      580      590      600      610      620
Cry1Ac LDNL--QSSDFGYFESANAFTSSLGN-IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNL
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|401 DDDLTQYQTFDLATTNSNMGFSGDKNELIIGAESFVSNEKIYIDKIEFIPVQL
450      460      470      480      490
      630      640      650      660      670      680
Cry1Ac ERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRL

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>>gi|162767637|emb|CAP58821.1| unnamed protein product [ (224 aa)  
 initn: 880 init1: 880 opt: 880 Z-score: 1037.5 bits: 201.6 E(): 7.2e-49  
 Smith-Waterman score: 880; 59.070% identity (80.465% similar) in 215 aa overlap  
 (5-219:1-215)

```

      10      20      30      40      50      60
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLESEFVPGAGF
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 MAEENNQICIPYNCLSNPEEVLDDGERISTGNSSIDISLSLVQPLVFNFPVGGGF
      10      20      30      40      50
      70      80      90      100      110      120
Cry1Ac VLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFRE
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 LVGLIDFVWIGVGPSQWDAFLVQIEQLINERIAEFARNAAIANLEGLGNFNFIYVEAFKE
60      70      80      90      100      110
      130      140      150      160      170      180
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 WEEDPNNPETRTVRIDRFRILDGLLERDIPSPFRISGFVPLLSVYVQAANLHLLAILRDSV
120      130      140      150      160      170
      190      200      210      220      230      240
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRREL
.: : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 IFGERWGLTTINWENYRNLIRHIDEYADHCANTYNRGLNLPKSTYQ
180      190      200      210      220
      250      260      270      280      290      300
Cry1Ac TLTVLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLENFDFGSRGSAQGLEGSIRSPHL

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>>gi|62548293|gb|AAH86793.1| Cry1A toxin [Bacillus thuri (132 aa)  
 initn: 875 init1: 875 opt: 875 Z-score: 1035.0 bits: 200.3 E(): 9.9e-49  
 Smith-Waterman score: 875; 99.242% identity (100.000% similar) in 132 aa overlap  
 (95-226:1-132)

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      70      80      90      100      110      120

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Cry1Ac  VDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD
          .....
gi|625   FARNQAISRLEGLSNLYQIYAESFREWEAD
          10      20      30

```

```

          130      140      150      160      170      180
Cry1Ac  PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
          .....
gi|625   PTNPALREEMRIQFNDMNSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
          40      50      60      70      80      90

```

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          190      200      210      220      230      240
Cry1Ac  RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV
          .....
gi|625   RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
          100     110     120     130

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          250      260      270      280      290      300
Cry1Ac  LDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDFGSRGSAQIEGSIIRSPHLMIDL

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>>gi|162767641|emb|CAP58823.1| unnamed protein product [ (346 aa)
  initn: 877 initl: 877 opt: 877 Z-score: 1031.2 bits: 201.0 E(): 1.6e-48
Smith-Waterman score: 877; 60.000% identity (80.952% similar) in 210 aa overlap
(10-219:128-337)

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```

          10      20      30
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTP
          .....
gi|162   KSTASLPVARRSSRSLGNVSNNGGRIRCEENNQNQCIPYNCLSNPEEVLDDGERISTGNSS
          100     110     120     130     140     150

```

```

          40      50      60      70      80      90
Cry1Ac  IDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQ
          .....
gi|162   IDISLSLVQFLVSNFVPGGFLVGLIDFVWGVGPSQWDAFLVQIEQLINERIAEFARNA
          160     170     180     190     200     210

```

```

          100     110     120     130     140     150
Cry1Ac  AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
          .....
gi|162   AIANLEGLGNFNFIYVEAFKEWEEDPNPNPETRTRVDRFRILDGLLERDIPSRISGFV
          220     230     240     250     260     270

```

```

          160     170     180     190     200     210
Cry1Ac  PLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
          .....
gi|162   PLLSVYVQAANLHLAALRDSVIFGERWGLTTINVNENYRIRHIDEYADHCANTYNRGL
          280     290     300     310     320     330

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          220     230     240     250     260     270
Cry1Ac  ERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLN
          .....
gi|162   NNLPKSTYQ
          340

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>>gi|25277384|emb|CAD57543.1| unnamed protein product [B (1210 aa)
  initn: 1962 initl: 807 opt: 883 Z-score: 1030.1 bits: 202.6 E(): 1.9e-48
Smith-Waterman score: 2605; 40.200% identity (67.389% similar) in 1199 aa overlap
(22-1179:59-1207)

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          10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
          .....
gi|252   FANEPTNALQNMDYKDYLLKMSAGNASEYPGSPPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

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          60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          .....
gi|252   VPFVGPVIVSLYTLQIDILWPSGQKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
          90      100     110     120     130     140

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```

          120     130     140     150     160     170
Cry1Ac  YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
          .....
gi|252   YQLYLTALEEWKENPNNGSRALRDVRNRFEILDLSFTQYMPSFRVTNFVFPFLTVYQAA
          150     160     170     180     190     200

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          180     190     200     210     220     230
Cry1Ac  LHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
          .....
gi|252   LHLLLLKDISIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSKQW
          210     220     230     240     250     260

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          240     250     260     270     280
Cry1Ac  IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFD--GSRGSS
          .....
gi|252   VDYNQFRREMTLVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDK
          270     280     290     300     310     320

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          290     300     310     320     330
Cry1Ac  AQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWGHQIMASPVGFSGPEFT
          .....
gi|252   APSFGVIESSVIRPPHFVFDYITGLTVYITQSRSSISSARYIRHWAGHQISYHRI-FSD-NII
          330     340     350     360     370     380

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          340     350     360     370     380
Cry1Ac  FPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQLSVLDG
          .....
gi|252   KQMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVFPGYTYIF-FGMPEVEFFMVNQ
          390     400     410     420     430     440

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```

          390     400     410     420     430     440
Cry1Ac  TEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSV
          .....
gi|252   LNNTRKTLKYNPVSKDIIAGTRDSELELPPETSQPNYESYSHRCHITSIPA--TGSTT
          450     460     470     480     490

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          450     460     470     480     490     500
Cry1Ac  SIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF-----NGSVISGPGFTGGDL
          .....
gi|252   GLV--PVFSWTHRSADLINAVHSDKITQIPVVKVSDLAPSIITGPNNTVVSGPGFTGGGI
          500     510     520     530     540     550

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          510     520     530     540     550     560
Cry1Ac  VRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPAT
          .....
gi|252   IKVIRNGVIIS---HMRVKI--SDINKEYSMRIRYASANNTEFYINPSEENVKSHA-QKT

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560      570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGY-----FESANAFTSSLGNIVGVNRNFGTAVGIIDRFEFIPVTAT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 MNRGEALTYNKFNYATLPPIKFTTTEPFIT-LGAIFEAEDFLGIEAYI-DRIEFIPVDET
      620      630      640      650      660
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 YEAEQDLLEAAKAVNALFTNTKD-GLRPGVTDYEVNQANLVECLSDDLYPNEKRLLFDA
      670      680      690      700      710      720
Cry1Ac VKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 VREAKRLSEARNLLQDPDFQEI--GENGWTAETGIEVIEGDALFKGRYLRLPGAREIDT
      730      740      750      760      770      780
Cry1Ac ECPYTYLYQKIDESKLKAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLSWLPLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 ETYPYTYLYQKVEEGVLPYTRYRLRGFVGSQGLEIFTIRHQTNRIVKNVPD--DLLP--
      790      800      810      820      830      840
Cry1Ac AQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSLDIDVGTDLNEDLGVWV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 DVSPVNSDGSINRCSEQKYVNSRLEVENRSGE----AHEFSIPIDTGEIDYNENAGIYW
      850      860      870      880      890
Cry1Ac IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKES
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 GFKITDPEGYATLGNLELVEEGPLSGDALERLQREEQWKIQMTRRREETDRRYMASKQA
      900      910      920      930      940      950
Cry1Ac VDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNAIIFELEGRIFT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 VDRLYADYDQQLNPDVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFTLTDRLQQ
      960      970      980      990      1000      1010
Cry1Ac AFSLYDARNVIKNGDFNGLSCWNKGVHDVVEEQNNQRSVLVVPWEAEVVSQEVRCVCPGR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 AWSLYDQRNAPNGDFRNGLSNWNATPGVEVQ-QINHTSVLVIPNWDEQVSQFTVQPNQ
      1020      1030      1040      1050      1060      1070
Cry1Ac GYILRVTAAYKEGYGECVCTIHEIENNTDELKFSNVCVEE--IYPNNTVTCNDYTVNQEEY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|252 RYVLRVTARKEGVNGYVSIIRDGGNQTETLTFASDYDTNGMYNTQVSNNTNGYNTNNA-Y
      1080      1090      1100      1110      1120      1130
Cry1Ac GGAYTSRNRNGYNEAPSVPADYASVYEEKSYTDGRENCEFNRRGYRDTPLPVGIVTKEL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

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gi|252 NTQASSTN-GYN-ANNM---YNT---QASNTNGYNTNSV-----YNDQT---GYITKTV
      1140      1150      1160      1170
Cry1Ac EYFPETDKVWIEIGETEGTFIVDSVELLMEE
      1160      1170      1180
gi|252 TFIPYTDQMWIEMSETEGTFYIESVELIVDVE
      1180      1190      1200      1210
>>gi|115828939|gb|ABJ38778.1| Sequence 4 from patent US (1210 aa)
      initn: 1962 init1: 807 opt: 883 Z-score: 1030.1 bits: 202.6 E(): 1.9e-48
      Smith-Waterman score: 2605; 40.200% identity (67.389% similar) in 1199 aa overlap
      (22-1179:59-1207)
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      10      20      30      40      50
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA--IDIVGKLLSGLG
      30      40      50      60      70      80
Cry1Ac SEFV-PGAGFVLGLVDIIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
      60      70      80      90      100      110
gi|115 VPFVGLIVSLYTLQIDILWPSGQKSQWEIFMEQVVELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140
Cry1Ac YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
      120      130      140      150      160      170
gi|115 YQLYLTALEEKENPNRSRALRDVNRFEILDLSLFTQYMPSPFRVTNFEVPLFTVYTAQAN
      150      160      170      180      190      200
Cry1Ac LHLVLRDVSFVQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
      180      190      200      210      220      230
gi|115 LHLLLLKDAIFGPEWGWSTTTINNYDRQMKLTAEYSDHCWKWYETGLAKLKGTSAKQW
      210      220      230      240      250      260
Cry1Ac IRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGS
      240      250      260      270      280
gi|115 VDYNQFRREMTTLTVLDVVALFPNYDTRTYPMETKAQLTREIVYTDPLGAVNVSSIGSWYDK
      270      280      290      300      310      320
Cry1Ac AQG---IEGS-IRSPHMLDILNSITIYTDH-----RGEYYSWGHQIMASPVGFSGPEFT
      290      300      310      320      330
gi|115 APSFGVIESSVIRPPHVPDYITGLTVYTSQRSISSARYIRHWAGHQISYHRI-FSD-NII
      330      340      350      360      370      380
Cry1Ac FPLYGTMGNAAPQRIVAQGLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDG
      340      350      360      370      380
gi|115 KQMYGTNQNLSHSTSF-DFTNYDIYKTLKSDAVLLDIVFPGYTYIF-FGMPEVEFFMVNQ
      390      400      410      420      430      440
Cry1Ac TEFAYGTSNNLPSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSV
      390      400      410      420      430      440

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gi|115 LNNTRKTLKYNVSKDIIAGTRDSELELPPETSDQPNYESYSHRLCHITSIPA--TGSTT
      450      460      470      480      490
Cry1Ac SIIRAPMFSWIHRSAEFNNI IASDSITQIPAVKGNFLF-----NGSVISGPGFTGGDL
      450      460      470      480      490      500
gi|115 GLV--PVFSWTHRSADLINAVHSDKITQIPVVKVSDLAPSITGGPNNTVWVSGPGFTGGGI
      500      510      520      530      540      550
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVRYASVTPIHLNVNWNSSIFSNTVPAT
      510      520      530      540      550      560
gi|115 IKVIRNGVIIS--HMRVKI--SDINKEYSMRIRYASANNTFEYINPSEENVKSHA-QKT
      560      570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGY-----FESANAFTSSLGNIVGVRNFSGTAGVIIDRFEPVPTAT
      570      580      590      600      610
gi|115 MNRGEALTYNKFNYATLPPIKFTTTEPFIT-LGAIFEAEDFLGIEAYI-DRIEFIPVDET
      620      630      640      650      660
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      620      630      640      650      660      670
gi|115 YEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECLSDDLYPEKRLLFDA
      670      680      690      700      710      720
Cry1Ac VKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFD---
      680      690      700      710      720      730
gi|115 VREAKRLSEARNLLQDPDFQEIN--GENGWTASTGIEVIEGDALFKGRYLRLPGAREIDT
      730      740      750      760      770      780
Cry1Ac ECPYTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTSLWLPLS
      740      750      760      770      780      790
gi|115 ETYPYTYLYQKVEEGLKPYTRYRLRGFVGSQGLEIFTIRHQTNRIVKNVDP--DLLP--
      790      800      810      820      830      840
Cry1Ac AQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSLDIVGCTDLNEDLGWVV
      800      810      820      830      840      850
gi|115 DVSPVNSDGSINRCSEQKYVNSRLEVENRSGE----AHEFSIPIDTGEIDYENAGIIVW
      850      860      870      880      890
Cry1Ac IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKES
      860      870      880      890      900      910
gi|115 GFKITDPEGYATLGNLELVEEGPLSGDALERLQREEQQWKIQMTRRREEDRRYMASKQA
      900      910      920      930      940      950
Cry1Ac VDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPESLVIPGVNAAIFEELEGRIFT
      920      930      940      950      960      970
gi|115 VDRLYADYDQQLNPDVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFTELTDRLQQ
      960      970      980      990      1000      1010
Cry1Ac AFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVVPWEAEVVSQEVRCVCPGR
      980      990      1000      1010      1020      1030

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      1020      1030      1040      1050      1060      1070
gi|115 AWSLYDQRNAIPNGDFRNGLSNWNATPGVEVQ-QINHTSVLVIIPNWEQVVSQQFTVQPQK
      1040      1050      1060      1070      1080      1090
Cry1Ac GYLLRVTAKEYGEGCVTIHEIENNTDELKFSNCVVEE--IYPNNTVTCNDYTVNQEEY
      1080      1090      1100      1110      1120      1130
gi|115 RYVLRVTARKEGVNGYVSIIRDGGNQTETLTFSASDYDTNGMYNTQVSNNTNGYNTNNA-Y
      1100      1110      1120      1130      1140      1150
Cry1Ac GGAYTSRNRNGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGRDYTPLPVGVYTKEL
      1140      1150      1160      1170      1180
gi|115 NTQASSTN-GYN-ANNM---YNT---QASNTNGYNTNSV----YNDQT---GYITKTV
      1160      1170      1180
Cry1Ac EYFPETDKWIEIGETEGTFIVDSVELLLMEE
      1180      1190      1200      1210
gi|115 TFIPTDQMWIEMSETEGTFYIESVELIVDVE
      1180      1190      1200      1210

>>gi|71793186|emb|CAJ21052.1| unnamed protein product [B (1210 aa)
  initn: 1962 initl: 807 opt: 883 Z-score: 1030.1 bits: 202.6 E(): 1.9e-48
Smith-Waterman score: 2605; 40.200% identity (67.389% similar) in 1199 aa overlap
(22-1179:59-1207)

      10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLL
      30      40      50      60      70      80
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
      60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNL
      90      100      110      120      130      140
gi|717 VPFVGPVIVSLYTLQDLIDILWPSGQKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
      120      130      140      150      160      170
Cry1Ac YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
      150      160      170      180      190      200
gi|717 YQLYLTALEEWKENPNRSRALRDVNRNRFELDSLFTQYMPSPFRVTNFVFPFLTVYQAA
      180      190      200      210      220      230
Cry1Ac LHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDW
      210      220      230      240      250      260
gi|717 LHLLLLKDasIPGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSKQW
      240      250      260      270      280
Cry1Ac IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGS
      270      280      290      300      310      320
gi|717 VDYNQFRREMTLTVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDK
      290      300      310      320
Cry1Ac AQG---IEGS-IRSPHLMIDLNSITTYTDAH-----RGEYYWSGHQIMASPVGFSGPEFT

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gi|717 APSFGVIESSVIRPPHVPDYITGLTVYTSRISISSARYIRHWAGHQISYHRI-FSD-NII
330 340 350 360 370 380

Cry1Ac FPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDG
340 350 360 370 380
gi|717 KQMYGTGNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFFMVNQ
390 400 410 420 430 440

Cry1Ac TEFAYGTSSNLPASVYRKSGTVDLSLEIPPQNNVPPRQGFSHRLSHVMSFRSGFSNSSF
390 400 410 420 430 440
gi|717 LNNTRKTLKYNPVSVDIAGTRDSELELPPETSDQPNYESYSHRCHITSIPA--TGSTT
450 460 470 480 490

Cry1Ac SIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLF-----NGSVISGPGFTGGDL
450 460 470 480 490 500
gi|717 GLV--PVFSWTHRSADLINAVHSDKITQIPVVKVSDLAPSITGGPNNTVVS GPGFTGGGI
500 510 520 530 540 550

Cry1Ac VRLNSSGNINQRGYIEVPIHFPSTSTRYRVRVRYASVPIHLNWNWGNSSIFSNTVPAT
510 520 530 540 550 560
gi|717 IKVIRNGVVIS---HMRVKI--SDINKEYSMRIRYASANNTFEFYINPSEENVKSHA-QKT
560 570 580 590 600 610

Cry1Ac ATSLDNLQSSDFGY-----FESANAFTSSLGNIVGVRNFSGTAGVIIDREFEIPVTAT
570 580 590 600 610
gi|717 MNRGEALTYNKFNYATLPPIKFTTTEPFIT-LGAIFEAEFDLGIEAYI-DRIEFIPVDET
620 630 640 650 660

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
620 630 640 650 660 670
gi|717 YEAEQDLEAAKAVNALFTNTKD-GLRPGVTDYEVNQAANLVECLSDLLYPNEKRLFLFA
670 680 690 700 710 720

Cry1Ac VKHAKRSLDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFFD---
680 690 700 710 720 730
gi|717 VREAKRLSEARNLLQDPDFQEI--GENGWASTGIEVIEGDALFKGRYLRLPGAREIDT
730 740 750 760 770 780

Cry1Ac ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNVPGTGLSLWPLS
740 750 760 770 780 790
gi|717 ETYPTYLYQKVEEGVLKPYTRYLRGFGVSSQGLEIFTIRHQTNRIVKNVPD--DLLP--
790 800 810 820 830 840

Cry1Ac AQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIVGCTDLNEDLGWVV
800 810 820 830 840 850
gi|717 DVSPVNSDGSINRCSEQKYVNSRLEVENRSGE----AHEFSIPIDTGEIDYENENAGIWW
850 860 870 880 890

Cry1Ac
860 870 880 890 900 910

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Cry1Ac IFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKES
330 340 350 360 370 380
gi|717 GFKITDPEGYATLGNLELVEEGPLSGDALERLQREEQWKIQMTRRRETDRRYMASKQA
900 910 920 930 940 950

Cry1Ac VDALFVNSQYDQLQADTNIAAMIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFT
920 930 940 950 960 970
gi|717 VDRLYADYDQQLNPDVEITDLTAAQDLIQSIPYVYNEMFPEIPGMNYTKFTLTDRLQQ
960 970 980 990 1000 1010

Cry1Ac AFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQSVLVVPEWAEVSVQEVVCPGR
980 990 1000 1010 1020 1030
gi|717 AWSLYDQRNAIPNGDFRNLGSLNWNATPGVEVQ-QINHTSVLVIPNWEQVVSQOFTVQPNQ
1020 1030 1040 1050 1060 1070

Cry1Ac GYILRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEE--IYPNNTVTCNDYTVNQBEY
1040 1050 1060 1070 1080 1090
gi|717 RYVLRVTARKEGVGNGYVSRDGGNQTETLTFASADYDTNGMYNTQVSNNGYNTNNA-Y
1080 1090 1100 1110 1120 1130

Cry1Ac GGAYTSRNRGYNAPSPADYASVYEEKSYTDGRRENPCFENRGYRDYTPPLVGYVTKEL
1100 1110 1120 1130 1140 1150
gi|717 NTQASSTN-GYN-ANNM---YNT---QASNTNGYNTNSV----YNDQT---GYITKTV
1140 1150 1160 1170

Cry1Ac EYFPETDKVWIEIGETEGTFIVDSVELLLMEE
1160 1170 1180
gi|717 TFIPYTDQMWIEMSETEGTFYIESVELIVDVE
1180 1190 1200 1210

>>gi|25277392|emb|CAD57545.1| unnamed protein product [B (667 aa)
initn: 1161 init1: 807 opt: 874 Z-score: 1023.4 bits: 200.5 E(): 4.4e-48
Smith-Waterman score: 1228; 36.943% identity (66.720% similar) in 628 aa overlap
(22-612:59-666)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
10 20 30 40 50
gi|252 FANEPTNALQNMDYKDYLLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAFVGLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
60 70 80 90 100 110
gi|252 VPFVGPVIVSLYTLQDILWPSGQKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
120 130 140 150 160
gi|252 YQLYLTALEEWKENPNSRALRD-VRNRFIELDSLFTQYMPNFRVTFVFPFLTVVTAQA
150 160 170 180 190 200

170 180 190 200 210 220

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Cry1Ac  NLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD
gi|252  NLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQ
      210      220      230      240      250      260
      230      240      250      260      270      280
Cry1Ac  WIRYNQFRRELTTLVLDIVSLFPNYSRTYPVRTVSQLTREIYTNPVLE-NFD--GSFRG
gi|252  WVDYNQFRREMTLTLVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYD
      270      280      290      300      310      320
      290      300      310      320      330
Cry1Ac  SAQG---IEGS-IRSPHLMdILNSITiYTDah----RGEYyWSGHQIMASpVGFSGPEF
gi|252  KAPsFGVIeSSvIRPPHvFDYITGLTVYtQSRsISSARyIRHWAGHQISYHRI-FSD-NI
      330      340      350      360      370      380
      340      350      360      370      380
Cry1Ac  TFPLYGTMGNAAPQQRIVaQLGQGVYRTLSSTL-----YRRPFNIGINNqQLSVLD
gi|252  IKQMYGTnQNLHSTStF-DFTNYDIYkTLsKDAVLLDlVFPgYtIF-FGMpEVEFFMVN
      390      400      410      420      430      440
      390      400      410      420      430      440
Cry1Ac  GTEFAYGTSSNLpSAVYRkSGTVdSLDEIPpQNNVpPRQGFsHRLSHVSMFRSGFSNSs
gi|252  QLNnTRKtLkYnPVSKDIaGTRdSELELpPETSDQPNyESYSHRLCHITsIPa--TGST
      450      460      470      480      490
      450      460      470      480      490      500
Cry1Ac  VSIIRAPMFSWIHRSAEFNnIIASDSITQIPAVKGNFLF-----NGSVISGPGFTGGD
gi|252  TGLV--PVFSWThRSADLlNAVHSDKITQIPVVKVSDLAPsITGGPNnTVVSGPGFTGGG
      500      510      520      530      540      550
      510      520      530      540      550      560
Cry1Ac  LVRLNssGNnIQnRGYIEVPIHFPSTSTRYRVRVRYASVtPIHLNvNWGNSSIFsNTVPA
gi|252  IIKVIRNGVIIsh----MRVKISdINKEYSMRIRYASANNtEFYINPSEENVKSHA-QK
      560      570      580      590      600      610
      570      580      590      600      610
Cry1Ac  TATSLDNLQSSDFGy-----FESANAFTSSLGnIVGRNfSGTAGVIIDRFEFIPVtA
gi|252  TMNRGEALtYnKfNYATLPPiKfTTPEfFIT-LGAIfeAEDFLGIeAYI-DRIEFIPVD
      620      630      640      650      660
      620      630      640      650      660      670
Cry1Ac  TLEAEYNLERAQkAVNALFTsTNQLGLKtNVTDYHIDQVSNLVtYLSDEfCLDEKRELSE

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>>gi|71793195|emb|CAJ21056.1| unnamed protein product [B (673 aa)
  initn: 1180 initl: 807 opt: 874 Z-score: 1023.3 bits: 200.5 E(): 4.4e-48
Smith-Waterman score: 1247; 37.480% identity (66.614% similar) in 635 aa overlap
(22-619:59-673)

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Cry1Ac  CMQAMDNPNINeCIPYnCLSNPEVEVLGGERIETGYTPIDISLSLTQFLl
gi|717  FANEPTNALQnMDYkDYlKMSAGNASeYpGSPEVLVSGQDAAKAA---IDIVGKLLSGLG

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      30      40      50      60      70      80
      60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
gi|717  VPFVGPiVSLYtQLIDILWpSQKsQWEIfMEQVEELINQkIAeYARNKALeSELEGLNN
      90      100      110      120      130      140
      120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
gi|717  YQLYLtALEEWKENPNgsRALRD-VRNrFEILdSLFTQYMPsFRVtNFVpFLtVYtQAA
      150      160      170      180      190      200
      170      180      190      200      210      220
Cry1Ac  NLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD
gi|717  NLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQ
      210      220      230      240      250      260
      230      240      250      260      270      280
Cry1Ac  WIRYNQFRRELTTLVLDIVSLFPNYSRTYPVRTVSQLTREIYTNPVLE-NFD--GSFRG
gi|717  WVDYNQFRREMTLTLVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYD
      270      280      290      300      310      320
      290      300      310      320      330
Cry1Ac  SAQG---IEGS-IRSPHLMdILNSITiYTDah----RGEYyWSGHQIMASpVGFSGPEF
gi|717  KAPsFGVIeSSvIRPPHvFDYITGLTVYtQSRsISSARyIRHWAGHQISYHRI-FSD-NI
      330      340      350      360      370      380
      340      350      360      370      380
Cry1Ac  TFPLYGTMGNAAPQQRIVaQLGQGVYRTLSSTL-----YRRPFNIGINNqQLSVLD
gi|717  IKQMYGTnQNLHSTStF-DFTNYDIYkTLsKDAVLLDlVFPgYtIF-FGMpEVEFFMVN
      390      400      410      420      430      440
      390      400      410      420      430      440
Cry1Ac  GTEFAYGTSSNLpSAVYRkSGTVdSLDEIPpQNNVpPRQGFsHRLSHVSMFRSGFSNSs
gi|717  QLNnTRKtLkYnPVSKDIaGTRdSELELpPETSDQPNyESYSHRLCHITsIPa--TGST
      450      460      470      480      490
      450      460      470      480      490      500
Cry1Ac  VSIIRAPMFSWIHRSAEFNnIIASDSITQIPAVKGNFLF-----NGSVISGPGFTGGD
gi|717  TGLV--PVFSWThRSADLlNAVHSDKITQIPVVKVSDLAPsITGGPNnTVVSGPGFTGGG
      500      510      520      530      540      550
      510      520      530      540      550      560
Cry1Ac  LVRLNssGNnIQnRGYIEVPIHFPSTSTRYRVRVRYASVtPIHLNvNWGNSSIFsNTVPA
gi|717  IIKVIRNGVIIsh----MRVKISdINKEYSMRIRYASANNtEFYINPSEENVKSHA-QK
      560      570      580      590      600      610
      560      570      580      590      600      610
Cry1Ac  TATSLDNLQSSDFGy-----FESANAFTSSLGnIVGRNfSGTAGVIIDRFEFIPVtA
gi|717  TMNRGEALtYnKfNYATLPPiKfTTPEfFIT-LGAIfeAEDFLGIeAYI-DRIEFIPVD
      620      630      640      650      660
      620      630      640      650      660      670
Cry1Ac  TLEAEYNLERAQkAVNALFTsTNQLGLKtNVTDYHIDQVSNLVtYLSDEfCLDEKRELSE

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gi|115 WVDYNQFRREMLTFLVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYD
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
SAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFSGPEF

gi|115 KAPSPFGVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRI-FSD-NI
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
TFPLYGTMGNAAPQQRIVAQGLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLD

gi|115 IKQMYGTNQLNHSTSTF-DFTNYDIYKTLKSDAVLLDIVFPGYTYIF-FGMPEVEFFMVN
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
GTEFAYGTSSNLPSAVYRKSQTVDSLDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSS

gi|115 QLNNRKTKLKYNPVSKDIIAGTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGST
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLF-----NGSVISGPGFTGGD

gi|115 TGLV--PVFSTWTHRSADLINAVHSDKITQIPVVKVSDLAPSTIGGPNNTVVSQPGFTGGG
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
LVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTPVA

gi|115 IIKVIRNGVII--SHMRVKIS--DINKEYSMRIRYASANNTEFYINPSEENVKSHA-QK
560 570 580 590 600 610

Cry1Ac 570 580 590 600 610
TATSLDNLQSSDFGY-----FESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTA

gi|115 TMNRGEALTYNKFNYATLPPKFTTTEPFIT-LGALFEAEDFLGIEAYI-DRIEFIPVDE
620 630 640 650 660

Cry1Ac 620 630 640 650 660 670
TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSE

gi|115 TYEAE
670

>>gi|25277412|emb|CAD57550.1| unnamed protein product [B (616 aa)
initn: 1159 initl: 787 opt: 866 Z-score: 1014.5 bits: 198.8 E(): 1.4e-47
Smith-Waterman score: 1225; 37.881% identity (67.25% similar) in 623 aa overlap
(22-612:12-615)

Cry1Ac 10 20 30 40 50
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFV-PGAG

gi|252 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVGPVIVS
10 20 30 40

Cry1Ac 60 70 80 90 100 110
FVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEIEFARNQAIISRLEGLSNLYQIYAESFR

gi|252 LYTQLIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
50 60 70 80 90 100

Cry1Ac 120 130 140 150 160 170
EWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD

gi|252 EWEENPNGRALRD-VRNRFEILDLSLFTQYMPSPFRVTNFEVPLFTVYAMAANLHLLKLD
110 120 130 140 150 160

Cry1Ac 180 190 200 210 220 230
VSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRR

gi|252 ASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYQFRR
170 180 190 200 210 220

Cry1Ac 240 250 260 270 280 290
ELTLTVLDIVSLFPPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGSAQG---IE

gi|252 EMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSPGVIE
230 240 250 260 270 280

Cry1Ac 300 310 320 330 340
GS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFSGPEFTFPLYGTMG

gi|252 SSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMVGTONQ
290 300 310 320 330 340

Cry1Ac 350 360 370 380 390
NAAPQQRIVAQGLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDGTEFAYGTS

gi|252 NLHSTSTF-DFTNYDIYKTLKSDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNTRKTL
350 360 370 380 390 400

Cry1Ac 400 410 420 430 440 450
SNLPSAVYRKSQTVDSLDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF

gi|252 KYNPVSVDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGNTTGLV--PVF
410 420 430 440 450

Cry1Ac 460 470 480 490 500 510
SWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNR

gi|252 SWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDLLQYNRSTGSGVTGL
460 470 480 490 500 510

Cry1Ac 520 530 540 550 560 570
GYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFG

gi|252 FLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNPGEDLTSKTFK
520 530 540 550 560 570

Cry1Ac 580 590 600 610 620
YFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAEYNLERAQKA

gi|252 VADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVD
580 590 600 610

Cry1Ac 630 640 650 660 670 680
VNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNL

Regulatory Product Characterization Team

>>gi|71793197|emb|CAJ21057.1| unnamed protein product [B (616 aa)
initn: 1159 initl: 787 opt: 866 Z-score: 1014.5 bits: 198.8 E(): 1.4e-47
Smith-Waterman score: 1225; 37.881% identity (67.255% similar) in 623 aa overlap
(22-612:12-615)

10 20 30 40 50
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFV-PGAG
gi|717 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVFGPIVS
10 20 30 40
60 70 80 90 100 110
Cry1Ac FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFR
gi|717 LYTQLIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
50 60 70 80 90 100
120 130 140 150 160 170
Cry1Ac EWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|717 EWEENPNGSRALRD-VRNRFEILDSLFTQYMPFSFRVTNFEVFPFLTVYAMAANLHLLLLKD
110 120 130 140 150 160
180 190 200 210 220 230
Cry1Ac VSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRR
gi|717 ASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFRR
170 180 190 200 210 220
240 250 260 270 280 290
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--GSFRGSAQG---IE
gi|717 EMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSPGVIE
230 240 250 260 270 280
300 310 320 330 340
Cry1Ac GS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFSGPEFTFPLYGTMG
gi|717 SSVIRPPHFVDYITGLTVYQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMYGTNQ
290 300 310 320 330 340
350 360 370 380 390
Cry1Ac NAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQLSVLDGTEFAYGTS
gi|717 NLHSTSTF-DFTNYDIYKTLSKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNTRKTL
350 360 370 380 390 400
400 410 420 430 440 450
Cry1Ac SNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF
gi|717 KYNPVSKDIIASTRSELELPPETSQDPNYESYSHRLCHITSIPA--TGNTGLV--PVF
410 420 430 440 450
460 470 480 490 500 510
Cry1Ac SWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNR
gi|717 SWTHRSADLNTIYSDKITQIPAVKCDNLPFV-PVVKPGHTGGDLQYNRSTGVSGLT
460 470 480 490 500 510

520 530 540 550 560 570
Cry1Ac GYIEVPIHFPSTSTRVVRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFG
gi|717 FLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPGEDLTSKTFK
520 530 540 550 560 570
580 590 600 610 620
Cry1Ac YFESAN----AFTSSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAEYNLERAQKA
gi|717 VADAITTLNLATDSSSLALKHNLGEDPNSTLSGIVVVDRIEFIPVD
580 590 600 610
630 640 650 660 670 680
Cry1Ac VNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNL

>>gi|115828946|gb|ABJ38784.1| Sequence 16 from patent US (616 aa)
initn: 1159 initl: 787 opt: 866 Z-score: 1014.5 bits: 198.8 E(): 1.4e-47
Smith-Waterman score: 1225; 37.881% identity (67.255% similar) in 623 aa overlap
(22-612:12-615)

10 20 30 40 50
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFV-PGAG
gi|115 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVFGPIVS
10 20 30 40
60 70 80 90 100 110
Cry1Ac FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFR
gi|115 LYTQLIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
50 60 70 80 90 100
120 130 140 150 160 170
Cry1Ac EWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRD
gi|115 EWEENPNGSRALRD-VRNRFEILDSLFTQYMPFSFRVTNFEVFPFLTVYAMAANLHLLLLKD
110 120 130 140 150 160
180 190 200 210 220 230
Cry1Ac VSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERWVGPDSRDWIRYNQFRR
gi|115 ASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFRR
170 180 190 200 210 220
240 250 260 270 280 290
Cry1Ac ELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--GSFRGSAQG---IE
gi|115 EMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSPGVIE
230 240 250 260 270 280
300 310 320 330 340
Cry1Ac GS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFSGPEFTFPLYGTMG
gi|115 SSVIRPPHFVDYITGLTVYQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMYGTNQ
290 300 310 320 330 340
350 360 370 380 390
Cry1Ac NAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQLSVLDGTEFAYGTS
gi|115 NLHSTSTF-DFTNYDIYKTLSKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNTRKTL
350 360 370 380 390 400
400 410 420 430 440 450
Cry1Ac SNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMF
gi|115 KYNPVSKDIIASTRSELELPPETSQDPNYESYSHRLCHITSIPA--TGNTGLV--PVF
410 420 430 440 450
460 470 480 490 500 510
Cry1Ac SWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNR
gi|115 SWTHRSADLNTIYSDKITQIPAVKCDNLPFV-PVVKPGHTGGDLQYNRSTGVSGLT
460 470 480 490 500 510





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500      510      520      530      540      550
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVDPATATSL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  RSTGSVGTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPG
      560      570      580      590      600
      570      580      590      600      610
Cry1Ac  DNLQSSDFGYFESAN----AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  EDLTSKTPKVADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDETYEAE
      610      620      630      640      650      660
      620      630      640      650      660      670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
>>gi|71793193|emb|CAJ21055.1| unnamed protein product [B (669 aa)
  initn: 1190 initl: 799 opt: 866 Z-score: 1013.9 bits: 198.8 E(): 1.5e-47
Smith-Waterman score: 1244; 38.095% identity (67.143% similar) in 630 aa overlap
(22-619:59-669)

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      10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . : : : . . . . : : : : . : . :
gi|717  FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

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      60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      . : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

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      120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
      . : . : : : : . : . . : : . : . : . : : : : : : : : : : : : : :
gi|717  YQLYLTALEEWEENPNGSRALRD-VNRNFEILDSLFTQYMPFRVTNFVFPFLTVYAMAA
      150      160      170      180      190      200

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      170      180      190      200      210      220
Cry1Ac  NLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|717  NLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQ
      210      220      230      240      250      260

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      230      240      250      260      270      280
Cry1Ac  WIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFD--GSFRG
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|717  WVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREYVTDPLGAVNVSSIGSWYD
      270      280      290      300      310      320

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      290      300      310      320      330
Cry1Ac  SAQG---IEGS-IRSPHMLDILNSITTYTDAH----RGEYYSWGSHQIMASVPGFSGPEF
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|717  KAPSPGVISSVIRPPHVFYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSNL
      330      340      350      360      370      380

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      340      350      360      370      380

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Cry1Ac  TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLD
      . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  Q-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFFMVN
      390      400      410      420      430      440
      390      400      410      420      430      440
Cry1Ac  GTEFAYGTSSNLPSSAVYRKSQGVTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  QLNNTKRKTLKYNPVSKDIIASTRDSLELPPETSQPNVYESYSHRLCHITSIPA--TGNT
      450      460      470      480      490
      450      460      470      480      490      500
Cry1Ac  VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  TGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKWDNLPFV-PVVKGPHTGGDLLQYN
      500      510      520      530      540      550
      510      520      530      540      550      560
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVDPATATSL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  RSTGSVGTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPG
      560      570      580      590      600

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      570      580      590      600      610
Cry1Ac  DNLQSSDFGYFESAN----AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAE
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|717  EDLTSKTPKVADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDETYEAE
      610      620      630      640      650      660

```

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      620      630      640      650      660      670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
>>gi|25277395|emb|CAD57546.1| unnamed protein product [s (669 aa)
  initn: 1190 initl: 799 opt: 866 Z-score: 1013.9 bits: 198.8 E(): 1.5e-47
Smith-Waterman score: 1244; 38.095% identity (67.143% similar) in 630 aa overlap
(22-619:59-669)

```

```

      10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . : : : . . . . : : : : . : . :
gi|252  FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

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```

      60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      . : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

      120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|252  YQLYLTALEEWEENPNGSRALRD-VNRNFEILDSLFTQYMPFRVTNFVFPFLTVYAMAA
      150      160      170      180      190      200

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```

      170      180      190      200      210      220
Cry1Ac  NLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . : . : .
gi|252  NLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQ

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Regulatory Product Characterization Team

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210      220      230      240      250      260
230      240      250      260      270      280
Cry1Ac WIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRG
gi|252 WVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYD
270      280      290      300      310      320
290      300      310      320      330
Cry1Ac SAQG---IEGS-IRSPHLMIDILNSITIYTDH-----RGEYYWSGHQIMASPVGFSGPEF
gi|252 KAPSFVGISSVIRPPHVFYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RGSNL
330      340      350      360      370      380
340      350      360      370      380
Cry1Ac TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLD
gi|252 Q-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFFMVN
390      400      410      420      430      440
390      400      410      420      430      440
Cry1Ac GTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSS
gi|252 QLNNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGNT
450      460      470      480      490      500
450      460      470      480      490      500
Cry1Ac VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLN
gi|252 TGLV--PVFSWTHRSADLNNNTIYDKITQIPAVKCDNLFPV-PVVKGPGHTGGDLLQYN
500      510      520      530      540      550
510      520      530      540      550      560
Cry1Ac SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPATATSL
gi|252 RSTGSVGTFLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPG
560      570      580      590      600
570      580      590      600      610
Cry1Ac DNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAE
gi|252 EDLTSKTFKVADAITTLNLATDSSLALKHNLGEPNSTLSGIVYVDRIEFIPVDETYEAE
610      620      630      640      650      660
620      630      640      650      660      670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHA
>>gi|115828940|gb|ABJ38779.1| Sequence 6 from patent US (669 aa)
  initn: 1190 initl: 799 opt: 866 Z-score: 1013.9 bits: 198.8 E(): 1.5e-47
Smith-Waterman score: 1244; 38.095% identity (67.143% similar) in 630 aa overlap
(22-619:59-669)
10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|115 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30      40      50      60      70      80
60      70      80      90      100      110

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Cry1Ac SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115 VPFVGPVIVSLYQLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100      110      120      130      140
120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
gi|115 YQLYLTALEEEENPNNGSRALRD-VRNRFEILDSLFTQYMPSPFRVTNFVPLTVYAMAA
150      160      170      180      190      200
170      180      190      200      210      220
Cry1Ac NLHSLVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRD
gi|115 NLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKTSAQ
210      220      230      240      250      260
230      240      250      260      270      280
Cry1Ac WIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRG
gi|115 WVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYD
270      280      290      300      310      320
290      300      310      320      330
Cry1Ac SAQG---IEGS-IRSPHLMIDILNSITIYTDH-----RGEYYWSGHQIMASPVGFSGPEF
gi|115 KAPSFVGISSVIRPPHVFYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RGSNL
330      340      350      360      370      380
340      350      360      370      380
Cry1Ac TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLD
gi|115 Q-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFFMVN
390      400      410      420      430      440
390      400      410      420      430      440
Cry1Ac GTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSS
gi|115 QLNNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGNT
450      460      470      480      490      500
450      460      470      480      490      500
Cry1Ac VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLN
gi|115 TGLV--PVFSWTHRSADLNNNTIYDKITQIPAVKCDNLFPV-PVVKGPGHTGGDLLQYN
500      510      520      530      540      550
510      520      530      540      550      560
Cry1Ac SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPATATSL
gi|115 RSTGSVGTFLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPG
560      570      580      590      600
570      580      590      600      610
Cry1Ac DNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAE
gi|115 EDLTSKTFKVADAITTLNLATDSSLALKHNLGEPNSTLSGIVYVDRIEFIPVDETYEAE
610      620      630      640      650      660
610      620      630      640      650      660
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHA
510      520      530      540      550      560
Cry1Ac SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPATATSL
gi|115 RSTGSVGTFLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTMNPG
560      570      580      590      600
570      580      590      600      610
Cry1Ac DNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAE
gi|115 EDLTSKTFKVADAITTLNLATDSSLALKHNLGEPNSTLSGIVYVDRIEFIPVDETYEAE
610      620      630      640      650      660

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620      630      640      650      660      670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

>>gi|71793188|emb|CAJ21053.1| unnamed protein product [s (669 aa)
  initn: 1190 initl: 799 opt: 866 Z-score: 1013.9 bits: 198.8 E(): 1.5e-47
Smith-Waterman score: 1244; 38.095% identity (67.143% similar) in 630 aa overlap
(22-619:59-669)

          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
          : : : : :
gi|717  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

          60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          : : : : :
gi|717  VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100     110     120     130     140

          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNP-ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAA
          : : : : :
gi|717  YQLYLTALEEWEENPNSRALRD-VRNRFEILDSLFTQYMPFRVNTNFVFPFLTYYAMAA
          150     160     170     180     190     200

          170     180     190     200     210     220
Cry1Ac  NLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD
          : : : : :
gi|717  NLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQ
          210     220     230     240     250     260

          230     240     250     260     270     280
Cry1Ac  WIRYNQFRRELTTLVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLN-NFD--GSFRG
          : : : : :
gi|717  WVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYD
          270     280     290     300     310     320

          290     300     310     320     330
Cry1Ac  SAQG---IEGS-IRSPHLMIDILNSITTYTDAH----RGEYYWSGHQIMASVPGFSGPEF
          : : : : :
gi|717  KAPSPGVISSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSNL
          330     340     350     360     370     380

          340     350     360     370     380
Cry1Ac  TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLD
          : : : : :
gi|717  Q-QMYGTNQLNHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPVEFFMVN
          390     400     410     420     430     440

          390     400     410     420     430     440
Cry1Ac  GTEFAYGTSSNLPsAVYRKSgtVDSLDEIppQNNVPRQGFshRLSHVSMFRSgFSNss
          : : : : :
gi|717  QLNNRKRtLkYnPVskDIIAsTRDSELELPPETSQDPNYESYSHRLCHITsIPa--TGNT
          450     460     470     480     490

          450     460     470     480     490     500
Cry1Ac  VSIIRAPMfSWIHRsAEFNIIAsDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLN
          : : : : :

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gi|717  TGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKcWdNLpFV-pVVKgPghTgGdLLQYn
          500     510     520     530     540     550

          510     520     530     540     550     560
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTPATATSL
          : : : : :
gi|717  RSTGsvGTLfLaryGLALEKAG-KYRvRLRYATDADIVLHVn--DAQI---QMPKTMNpG
          560     570     580     590     600

          570     580     590     600     610
Cry1Ac  DNLQSSDFGYFESAN---AFTSSLG--NIVGVRNfSGTAGVI-IDRFEfIPVtATLEAE
          : : : : :
gi|717  EDLTSKtFKVADAITTLNlATDSSlALKHNLGEdPNSTLSGIVYVDRIEFIPVDETYEAE
          610     620     630     640     650     660

          620     630     640     650     660     670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

>>gi|71793259|emb|CAJ21082.1| unnamed protein product [B (674 aa)
  initn: 1128 initl: 505 opt: 865 Z-score: 1012.7 bits: 198.6 E(): 1.7e-47
Smith-Waterman score: 1239; 37.323% identity (66.772% similar) in 635 aa overlap
(22-618:59-674)

          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
          : : : : :
gi|717  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

          60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          : : : : :
gi|717  VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100     110     120     130     140

          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTN-----PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
          : : : : :
gi|717  YQLYLTALEEWEENPNSRFRSRGPALRD-VRNRFEILDSLFTQYMPFRVNTNFVFPFLT
          150     160     170     180     190     200

          170     180     190     200     210     220
Cry1Ac  VYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
          : : : : :
gi|717  VYAMAANLHLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKG
          210     220     230     240     250     260

          230     240     250     260     270     280
Cry1Ac  GPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTPYIRTVSQTREIYTNPVLN-NFD-
          : : : : :
gi|717  GTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
          270     280     290     300     310     320

          290     300     310     320     330
Cry1Ac  -GSFRGSAQG---IEGS-IRSPHLMIDILNSITTYTDAH----RGEYYWSGHQIMASVPG
          : : : : :
gi|717  IGSWYDKAPSPGVISSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS
          330     340     350     360     370     380

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          340      350      360      370      380
Cry1Ac FSGPEFTFPFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 -RGSNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEV
          390      400      410      420      430      440

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          390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 EFFMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA
          450      460      470      480      490      500

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          450      460      470      480      490      500
Cry1Ac GFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 --TGNNTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHTGG
          510      520      530      540      550

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          510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 DLLQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
          560      570      580      590      600

```

```

          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 KTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNHGEDPNSTLSGIVYVDRIEFIPVD
          610      620      630      640      650      660

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          620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
          : :
gi|717 ETYEA
          670

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>>gi|115828955|gb|ABJ38793.1| Sequence 46 from patent US (675 aa)
  initn: 1134 initl: 505 opt: 865 Z-score: 1012.7 bits: 198.6 E(): 1.7e-47
Smith-Waterman score: 1246; 37.421% identity (66.824% similar) in 636 aa overlap
(22-619:59-675)

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          10      20      30      40      50
Cry1Ac      CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FANEPTNALQNMDYDKYLKMSAGNASEYPGSPVLSVSGQDAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

```

```

          60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIARLEGLSNL
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VPFVGPVSLYQLIDILWPSGKESQWEIFMEQVEELNQKIAEYARNKALSELEGLGNN
          90      100      110      120      130      140

```

```

          120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTN-----PALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 YQLYLTALEEWEENPNRSRFRSRGPAALRD--VRNRFEILDSLFTQYMPFSFRVTNFEVPLFT
          150      160      170      180      190      200

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          170      180      190      200      210      220
Cry1Ac VYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVM
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VYMAAANLHLLLLKDKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
          210      220      230      240      250      260

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          230      240      250      260      270      280
Cry1Ac GPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD-
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GTSAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSS
          270      280      290      300      310      320

```

```

          290      300      310      320      330
Cry1Ac -GSFRGSAQG---IEGS-IRSPHLMIDLNSITITYTDAH-----RGEYYWSGHQIMASPVG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 IGSWYDKAPSFVGIESSVIRPPHVFYDITGLTYTQSRSSISSARYIRHWAGHQISYHRVS
          330      340      350      360      370      380

```

```

          340      350      360      370      380
Cry1Ac FSGPEFTFPFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 -RGSNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEV
          390      400      410      420      430      440

```

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          390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 EFFMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA
          450      460      470      480      490      500

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          450      460      470      480      490      500
Cry1Ac GFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 --TGNNTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHTGG
          510      520      530      540      550

```

```

          510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVP
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 DLLQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
          560      570      580      590      600

```

```

          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 KTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNHGEDPNSTLSGIVYVDRIEFIPVD
          610      620      630      640      650      660

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          620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
          : : :
gi|115 ETYEAE
          670

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>>gi|115828971|gb|ABJ38809.1| Sequence 78 from patent US (675 aa)
  initn: 1134 initl: 505 opt: 865 Z-score: 1012.7 bits: 198.6 E(): 1.7e-47
Smith-Waterman score: 1245; 37.421% identity (66.824% similar) in 636 aa overlap
(22-619:59-675)

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Cry1Ac      10      20      30      40      50
            CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|115     FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA--IDIVGKLLSGLG
            30      40      50      60      70      80

Cry1Ac      60      70      80      90      100     110
            SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115     VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKAL SELEGLGN
            90      100     110     120     130     140

Cry1Ac      120     130     140     150     160
            YQIYAESFREWEADPTN-----PALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLS
gi|115     YQLYLTALEEWENPNNGSRFRSRG PALRD-VRNRFELDLSLFTQYMPFSFRVTNFV PFLT
            150     160     170     180     190     200

Cry1Ac      170     180     190     200     210     220
            VYVQAANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
gi|115     VYAMAANLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
            210     220     230     240     250     260

Cry1Ac      230     240     250     260     270     280
            GPDSRDWIRYNQFRRELT TLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL E-NFD-
gi|115     GTSAKQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
            270     280     290     300     310     320

Cry1Ac      290     300     310     320     330
            -GSFRGSAQG---IEGS-IRSPHLM DILNSITIYTD A H----RGEYYWSGHQIMASPVG
gi|115     IGSWYDKAPSFVGI ESSVIRPPHVFYDITGLTVYTQSR S ISSARYIRHWAGHQISYHRVS
            330     340     350     360     370     380

Cry1Ac      340     350     360     370     380
            FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQ
gi|115     -RGSNLQ-QMYGTNQN LHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEV
            390     400     410     420     430     440

Cry1Ac      390     400     410     420     430     440
            QLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGF SHRLSHVSMFRS
gi|115     EFFMVNQLNNTKRLTKYNPVSKDI IASTRDSELELPPETSDQPNYESYSHRLCHITSIPA
            450     460     470     480     490     500

Cry1Ac      450     460     470     480     490     500
            GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLNGSVISGPGFTGG
gi|115     --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVK CWDNLPFV-PVKGPGHTGG
            510     520     530     540     550

Cry1Ac      510     520     530     540     550     560
            DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVP
gi|115     DLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRRLRYATDADIVLHV N--DAQI--QMP
            560     570     580     590     600

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Cry1Ac      570     580     590     600     610
            ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
gi|115     KTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHN LGEDPNSTLSGIVVYVDRIEFIPVD
            610     620     630     640     650     660

Cry1Ac      620     630     640     650     660     670
            ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
gi|115     ETYEAE
            670

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>>gi|71793227|emb|CAJ21066.1| unnamed protein product [B (675 aa)  
 initn: 1134 init1: 505 opt: 865 Z-score: 1012.7 bits: 198.6 E(): 1.7e-47  
 Smith-Waterman score: 1246; 37.421% identity (66.824% similar) in 636 aa overlap  
 (22-619:59-675)

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Cry1Ac      10      20      30      40      50
            CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|717     FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA--IDIVGKLLSGLG
            30      40      50      60      70      80

Cry1Ac      60      70      80      90      100     110
            SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717     VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKAL SELEGLGN
            90      100     110     120     130     140

Cry1Ac      120     130     140     150     160
            YQIYAESFREWEADPTN-----PALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLS
gi|717     YQLYLTALEEWENPNNGSRFRSRG PALRD-VRNRFELDLSLFTQYMPFSFRVTNFV PFLT
            150     160     170     180     190     200

Cry1Ac      170     180     190     200     210     220
            VYVQAANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
gi|717     VYAMAANLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
            210     220     230     240     250     260

Cry1Ac      230     240     250     260     270     280
            GPDSRDWIRYNQFRRELT TLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL E-NFD-
gi|717     GTSAKQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
            270     280     290     300     310     320

Cry1Ac      290     300     310     320     330
            -GSFRGSAQG---IEGS-IRSPHLM DILNSITIYTD A H----RGEYYWSGHQIMASPVG
gi|717     IGSWYDKAPSFVGI ESSVIRPPHVFYDITGLTVYTQSR S ISSARYIRHWAGHQISYHRVS
            330     340     350     360     370     380

Cry1Ac      340     350     360     370     380
            FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQ
gi|717     -RGSNLQ-QMYGTNQN LHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEV
            390     400     410     420     430     440

Cry1Ac      390     400     410     420     430     440
            QLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGF SHRLSHVSMFRS
gi|717     EFFMVNQLNNTKRLTKYNPVSKDI IASTRDSELELPPETSDQPNYESYSHRLCHITSIPA
            450     460     470     480     490     500

Cry1Ac      450     460     470     480     490     500
            GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLNGSVISGPGFTGG
gi|717     --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVK CWDNLPFV-PVKGPGHTGG
            510     520     530     540     550

Cry1Ac      510     520     530     540     550     560
            DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVP
gi|717     DLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRRLRYATDADIVLHV N--DAQI--QMP
            560     570     580     590     600

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          390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDELPPQNNVPPRQGFSHRLSHVSMFRS
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 EFFMVNQLNNTTRKTLKYNPVSVDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA
          450      460      470      480      490      500

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          450      460      470      480      490      500
Cry1Ac GFSNssSVSIIRAPMFSWIHRSAEFNNIASDSITQIPAVK--GNFLFNGSVISGPGFTGG
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV--PVVKGPGHTGG
          510      520      530      540      550

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          510      520      530      540      550      560
Cry1Ac DLVRLNssGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTPV
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 DLLQYNRSTGsvgtLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
          560      570      580      590      600

```

```

          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 KTMNPGEDLTSKTFKVADAITVNLATDSSVAVKHNVGSDPNSTLSGIVYVDRIEFIPVD
          610      620      630      640      650      660

```

```

          620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
          : : :
gi|717 ETYEAE
          670

```

>>gi|25277457|emb|CAD57559.1| unnamed protein product [B (617 aa)  
 initn: 1107 initl: 505 opt: 862 Z-score: 1009.7 bits: 197.9 E(): 2.5e-47  
 Smith-Waterman score: 1221; 37.821% identity (66.987% similar) in 624 aa overlap  
 (22-612:12-616)

```

          10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFV-PGAG
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVGPPIVS
          10      20      30      40

```

```

          60      70      80      90      100      110
Cry1Ac FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFR
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LYTQLIDILWPSSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
          50      60      70      80      90      100

```

```

          120      130      140      150      160      170
Cry1Ac EWEADPT--NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLR
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 EWEENPLRMSRALRD--VRNRFIELDSLFTQYMPFRVTFVFPFLTVYAMAANLHLLLLK
          110      120      130      140      150      160

```

```

          180      190      200      210      220      230
Cry1Ac DVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFR
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYINQFR
          170      180      190      200      210      220

```

```

          240      250      260      270      280      290
Cry1Ac RELTLTFLVDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLNFD--GSFRGSAQG---I
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 REMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAPSFVGI
          230      240      250      260      270      280

```

```

          300      310      320      330      340
Cry1Ac EGS-IRSPHLMIDLNSITITYTDAH-----RGEYYWSGHQIMASPVGFSGPEFTFPLYGTM
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 ESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMYGTN
          290      300      310      320      330      340

```

```

          350      360      370      380      390
Cry1Ac GNAAPQQRIVAQLGQGVYRTLSTL-----YRRPFNIGLNQQLSVLDGTEFAYGT
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 QNLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNNTTRKT
          350      360      370      380      390      400

```

```

          400      410      420      430      440      450
Cry1Ac SSNLPsAVYRKSGTVDSLDELPPQNNVPPRQGFSHRLSHVSMFRSGFSNssSVSIIRAPM
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LKYNPVSVDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--TGNTTGLV--PV
          410      420      430      440      450

```

```

          460      470      480      490      500      510
Cry1Ac FSWIHRSAEFNNIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNssGNNIQN
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 FSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV--PVVKGPGHTGGDLLQYNRSTGsvgt
          460      470      480      490      500      510

```

```

          520      530      540      550      560      570
Cry1Ac RGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDF
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNPGEDLTSKTF
          520      530      540      550      560      570

```

```

          580      590      600      610      620
Cry1Ac GYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAEYNLERAQK
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 KVADAITTLNLATDSSLALKHNLGSDPNSTLSGIVYVDRIEFIPVD
          580      590      600      610

```

```

          630      640      650      660      670      680
Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN

```

>>gi|25277434|emb|CAD57555.1| unnamed protein product [B (617 aa)  
 initn: 1107 initl: 505 opt: 862 Z-score: 1009.7 bits: 197.9 E(): 2.5e-47  
 Smith-Waterman score: 1221; 37.821% identity (66.987% similar) in 624 aa overlap  
 (22-612:12-616)

```

          10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFV-PGAG
          . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVGPPIVS
          10      20      30      40

```

```

          60      70      80      90      100      110
Cry1Ac FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFR

```

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```

gi|252 LYTQLIDLILWPSGSEKSWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
      50      60      70      80      90      100
Cry1Ac EWEADPT--NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 EWEENPLKMSRALRD-VRNRFELDLSLFTQYMPSFRVTNFEVFPFLTVYAMAANLHLLLLK
      110     120     130     140     150     160
Cry1Ac 180     190     200     210     220     230
Cry1Ac DVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRWIRYNQFR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYNQFR
      170     180     190     200     210     220
Cry1Ac 240     250     260     270     280     290
Cry1Ac RELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGSAQG---I
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 REMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAPSGFVI
      230     240     250     260     270     280
Cry1Ac 300     310     320     330     340
Cry1Ac EGS-IRSPHLMIDLNSITIIYTDH-----RGEYYWSGHQIMASPVGFGSGPEFTFPLYGTM
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 ESSVIRPPHVFDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMYGTN
      290     300     310     320     330     340
Cry1Ac 350     360     370     380     390
Cry1Ac GNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDGTEFAYGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 QNLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNTRKT
      350     360     370     380     390     400
Cry1Ac 400     410     420     430     440     450
Cry1Ac SSNLPSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSIIRAPM
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LKYNPVSKDIIASTRDELELPPETSQPNYESYSHRLCHITSIPA--TGNNTGLV--PV
      410     420     430     440     450
Cry1Ac 460     470     480     490     500     510
Cry1Ac FSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 FSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLLQYNRSTGSGVT
      460     470     480     490     500     510
Cry1Ac 520     530     540     550     560     570
Cry1Ac RGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNPGEDLTSKTF
      520     530     540     550     560     570
Cry1Ac 580     590     600     610     620
Cry1Ac GYFESAN----AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEAEYNLERAQK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 KVADAITTLNLATDSSLALKHNLGEDPNSTLSGIYVVDRIEPIFIPV
      580     590     600     610
Cry1Ac 630     640     650     660     670     680

```

```

Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
>>gi|25277454|emb|CAD57558.1| unnamed protein product [B (670 aa)
      initn: 1129 initl: 505 opt: 862 Z-score: 1009.2 bits: 197.9 E(): 2.7e-47
      Smith-Waterman score: 1240; 38.035% identity (66.878% similar) in 631 aa overlap
      (22-619:59-670)
Cry1Ac 10      20      30      40      50
      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80
Cry1Ac 60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 VPFVGPVIVSLYTLQIDILWPSGSEKSWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90     100     110     120     130     140
Cry1Ac 120     130     140     150     160
Cry1Ac YQIYAESFREWEADPT--NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 YQLYLTALEEWEENPLRMSRALRD-VRNRFELDLSLFTQYMPSFRVTNFEVFPFLTVYAMA
      150     160     170     180     190     200
Cry1Ac 170     180     190     200     210     220
Cry1Ac ANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 ANLHLLLLKDAISIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAK
      210     220     230     240     250     260
Cry1Ac 230     240     250     260     270     280
Cry1Ac DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 QWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWY
      270     280     290     300     310     320
Cry1Ac 290     300     310     320     330
Cry1Ac GSAQG---IEGS-IRSPHLMIDLNSITIIYTDH-----RGEYYWSGHQIMASPVGFGSPE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 DKAPSGVIESSVIRPPHVFDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSN
      330     340     350     360     370     380
Cry1Ac 340     350     360     370     380
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 LQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFFMV
      390     400     410     420     430     440
Cry1Ac 390     400     410     420     430     440
Cry1Ac DGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 NQLNTRKTLKYNPVSKDIIASTRDELELPPETSQPNYESYSHRLCHITSIPA--TGN
      450     460     470     480     490
Cry1Ac 450     460     470     480     490     500
Cry1Ac SVSIIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252 TTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLLQY

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```

500      510      520      530      540      550
Cry1Ac  NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGSSIFSNTVPATATS
gi|252  NRSTGSVGTFLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNP
560      570      580      590      600

```

```

570      580      590      600      610
Cry1Ac  LDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEA
gi|252  GEDLTSKTFKVADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDETYEA
610      620      630      640      650      660

```

```

620      630      640      650      660      670
Cry1Ac  EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKH
gi|252  E
670

```

>>gi|25277419|emb|CAD57552.1| unnamed protein product [B (670 aa)  
initn: 1129 initl: 505 opt: 862 Z-score: 1009.2 bits: 197.9 E(): 2.7e-47  
Smith-Waterman score: 1240; 38.035% identity (66.878% similar) in 631 aa overlap  
(22-619:59-670)

```

10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|252  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLN
gi|252  VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100      110      120      130      140

```

```

120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPT--NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQA
gi|252  YQLYLTALEEWEEENPLKMSRALRD--VRNRFEILDSLTQYMPFSFRVTNFVEPFLTVYAMA
150      160      170      180      190      200

```

```

170      180      190      200      210      220
Cry1Ac  ANLHLSVLRDVSVFQGRWFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR
gi|252  ANLHLLLLKDISIFGEEWGWTSTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAK
210      220      230      240      250      260

```

```

230      240      250      260      270      280
Cry1Ac  DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFR
gi|252  QWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYTDPLGAVNVSSIGSWY
270      280      290      300      310      320

```

```

290      300      310      320      330
Cry1Ac  GSAQG---IEGS-IRSPHLMIDILNSITYTDAH----RGEYYSWGHQIMASPVGFSGPE
gi|252  DKAPSGFVIESSVIRPPHVFYDITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RGSN

```

```

330      340      350      360      370      380
Cry1Ac  FTFPLYGTMGNAAPQQRIVAQLGQGVYRSTLSSTL-----YRRPFNIGINNQQLSVL
gi|252  LQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFFMV
390      400      410      420      430      440

```

```

390      400      410      420      430      440
Cry1Ac  DGTEFAYGTSSNLPSAVYRKSQVSDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNS
gi|252  NQLNNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGN
450      460      470      480      490

```

```

450      460      470      480      490      500
Cry1Ac  SVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGTGGDLVRL
gi|252  TTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDLLQY
500      510      520      530      540      550

```

```

510      520      530      540      550      560
Cry1Ac  NSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGSSIFSNTVPATATS
gi|252  NRSTGSVGTFLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNP
560      570      580      590      600

```

```

570      580      590      600      610
Cry1Ac  LDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTATLEA
gi|252  GEDLTSKTFKVADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDETYEA
610      620      630      640      650      660

```

```

620      630      640      650      660      670
Cry1Ac  EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKH
gi|252  E
670

```

>>gi|115828952|gb|ABJ38790.1| Sequence 40 from patent US (676 aa)  
initn: 1129 initl: 505 opt: 862 Z-score: 1009.1 bits: 197.9 E(): 2.7e-47  
Smith-Waterman score: 1243; 37.363% identity (66.562% similar) in 637 aa overlap  
(22-619:59-676)

```

10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLN
gi|115  VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100      110      120      130      140

```

```

120      130      140      150      160
Cry1Ac  YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
gi|115  YQLYLTALEEWEEENPFRSRGFRSRGPALRD--VRNRFEILDSLTQYMPFSFRVTNFVEPFL

```

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```

150      160      170      180      190      200
Cry1Ac  170      180      190      200      210      220
SVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERV
gi|115  TVYAMAANLHLLLLKDAIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKL
210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac  WGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD
gi|115  KGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVS
270      280      290      300      310      320

290      300      310      320      330
Cry1Ac  --GSFRGSAQG---IEGS-IRSPHLM DILNSITIIYTDH----RGEYYWSGHQIMASPV
gi|115  SIGSWYDKAPSPFVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRV
330      340      350      360      370      380

340      350      360      370      380
Cry1Ac  GFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSLT-----YRRPFNIGINN
gi|115  S-RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVYPGYTYIF-FGMPE
390      400      410      420      430      440

390      400      410      420      430      440
Cry1Ac  QQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFR
gi|115  VEFFMVNQLNNTKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIP
450      460      470      480      490      500

450      460      470      480      490
Cry1Ac  SGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTG
gi|115  A--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV-PVVKGPGHTG
510      520      530      540      550

500      510      520      530      540      550
Cry1Ac  GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTV
gi|115  GDLLQYNRSTGSVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QM
560      570      580      590      600

560      570      580      590      600      610
Cry1Ac  PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPV
gi|115  PKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPV
610      620      630      640      650      660

620      630      640      650      660      670
Cry1Ac  TATLEAYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
gi|115  DETYEAE
670

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>>gi|71793253|emb|CAJ21079.1| unnamed protein product [B (676 aa)  
 initn: 1129 initl: 505 opt: 862 Z-score: 1009.1 bits: 197.9 E(): 2.7e-47

Smith-Waterman score: 1242; 37.363% identity (66.562% similar) in 637 aa overlap  
 (22-619:59-676)

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10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIEFPARNQAI SRLEGLSNL
gi|717  VPFVGPVIVSLYTLQIDLILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100      110      120      130      140

120      130      140      150      160
Cry1Ac  YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLL
gi|717  YQLYLTALEEWEENPFRRSRGFRSRGPALRD-VNRNFEILDSLFTQYMPFRVTNFVPPFL
150      160      170      180      190      200

170      180      190      200      210      220
Cry1Ac  SVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERV
gi|717  TVYAMAANLHLLLLKDAIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKL
210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac  WGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD
gi|717  KGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVS
270      280      290      300      310      320

290      300      310      320      330
Cry1Ac  --GSFRGSAQG---IEGS-IRSPHLM DILNSITIIYTDH----RGEYYWSGHQIMASPV
gi|717  SIGSWYDKAPSPFVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRV
330      340      350      360      370      380

340      350      360      370      380
Cry1Ac  GFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSLT-----YRRPFNIGINN
gi|717  S-RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVYPGYTYIF-FGMPE
390      400      410      420      430      440

390      400      410      420      430      440
Cry1Ac  QQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFR
gi|717  VEFFMVNQLNNTKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIP
450      460      470      480      490      500

450      460      470      480      490
Cry1Ac  SGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTG
gi|717  A--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV-PVVKGPGHTG
510      520      530      540      550

500      510      520      530      540      550
Cry1Ac  GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTV
gi|717  GDLLQYNRSTGSVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QM
560      570      580      590      600

560      570      580      590      600      610
Cry1Ac  PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPV
gi|717  PKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPV
610      620      630      640      650      660

620      630      640      650      660      670
Cry1Ac  TATLEAYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
gi|717  DETYEAE
670
500      510      520      530      540      550
Cry1Ac  GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTV

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Regulatory Product Characterization Team

gi|717 GDLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QM
560 570 580 590 600

Cry1Ac PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPV
560 570 580 590 600 610

gi|717 PKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPV
610 620 630 640 650 660

Cry1Ac TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
620 630 640 650 660 670

gi|717 DETYEAE
670

>>gi|71793221|emb|CAJ21063.1| unnamed protein product [B (676 aa)
initn: 1129 initl: 505 opt: 862 Z-score: 1009.1 bits: 197.9 E(): 2.7e-47
Smith-Waterman score: 1243; 37.363% identity (66.562% similar) in 637 aa overlap
(22-619:59-676)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
10 20 30 40 50

gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWIFGQSDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNL
60 70 80 90 100 110

gi|717 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLL
120 130 140 150 160

gi|717 YQLYLTALEEWEENPFRRSRGFRSRGPALRD-VNRNFEILDSLFTQYMPFRVNTFVFPFL
150 160 170 180 190 200

Cry1Ac SVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERV
170 180 190 200 210 220

gi|717 TVYAMAANLHLLLDKASIFGEEWGSVTTINNYDRQMKLTAEYSDHCVKWYETGLAKL
210 220 230 240 250 260

Cry1Ac WGPDSRDWIRYNQFRRELTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD
230 240 250 260 270 280

gi|717 KGTSKQKWDVYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVS
270 280 290 300 310 320

Cry1Ac --GSFRGSAQG---IEGS-IRSPHLMIDLNSITITYTDAH----RGEYYWSGHQIMASPV
290 300 310 320 330

gi|717 SIGSWYDKAPSGVIESSVIRPPHFVDYITGLTVYTSRISISSARYIRHWAGHQISYHRV
330 340 350 360 370 380

Cry1Ac GFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRILSSTL-----YRRPFNIGINN
340 350 360 370 380

gi|717 S-RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPE
390 400 410 420 430 440

Cry1Ac QQLSVLDGTEFAYGTSSNLPASAVYRKSQTVDSLDEIPQNNVPPRQGFHLSHVSFMR
390 400 410 420 430 440

gi|717 VEFFMVNQLNNTKRLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIP
450 460 470 480 490 500

Cry1Ac SGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTG
450 460 470 480 490

gi|717 A--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWDLPFV-PVVKGPGHTG
510 520 530 540 550

Cry1Ac GDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSISFNTV
500 510 520 530 540 550

gi|717 GDLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QM
560 570 580 590 600

Cry1Ac PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPV
560 570 580 590 600 610

gi|717 PKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPV
610 620 630 640 650 660

Cry1Ac TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
620 630 640 650 660 670

gi|717 DETYEAE
670

>>gi|115828968|gb|ABJ38806.1| Sequence 72 from patent US (676 aa)
initn: 1129 initl: 505 opt: 862 Z-score: 1009.1 bits: 197.9 E(): 2.7e-47
Smith-Waterman score: 1242; 37.363% identity (66.562% similar) in 637 aa overlap
(22-619:59-676)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
10 20 30 40 50

gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWIFGQSDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNL
60 70 80 90 100 110

gi|115 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLL
120 130 140 150 160

gi|115 YQLYLTALEEWEENPFRRSRGFRSRGPALRD-VNRNFEILDSLFTQYMPFRVNTFVFPFL
150 160 170 180 190 200

Cry1Ac SVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERV
170 180 190 200 210 220

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gi|115 TVYAMAANLHLLLDKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKL
210 220 230 240 250 260

Cry1Ac WGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD
230 240 250 260 270 280

gi|115 KGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNV
270 280 290 300 310 320

Cry1Ac --GSFRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPV
290 300 310 320 330

gi|115 SIGSWYDKAPSPFVIESSVIRPPHFVDYITGLTVYTSRISISSARYIRHWAGHQISYHRV
330 340 350 360 370 380

Cry1Ac GFSGPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSSSTL-----YRRPFNIGINN
340 350 360 370 380

gi|115 S-RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLTKDAVLLDIVPGYTYIF-FGMPE
390 400 410 420 430 440

Cry1Ac QQLSVDLGTTEFAYGTSNLPASAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFR
390 400 410 420 430 440

gi|115 VEFFMVNQLNTRKTLKYNPVSKDIIASTRDELELPPETSQPNYESYSHRLCHITSIP
450 460 470 480 490 500

Cry1Ac SGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLPNGSVISGPGFTG
450 460 470 480 490

gi|115 A--TGNTTGLV--PVFWSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTG
510 520 530 540 550

Cry1Ac GDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGSSIFSNTV
500 510 520 530 540 550

gi|115 GDLLQYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QM
560 570 580 590 600

Cry1Ac PATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPV
560 570 580 590 600 610

gi|115 PKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPV
610 620 630 640 650 660

Cry1Ac TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
620 630 640 650 660 670

gi|115 DETYEAE
670

>>gi|115828954|gb|ABJ38792.1| Sequence 44 from patent US (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1240; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
10 20 30 40 50

gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
60 70 80 90 100 110

gi|115 VPFVGPVIVSLYTLQILIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNPALR----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
120 130 140 150 160

gi|115 YQLYLTALEEEENPNNGSRFRSRGALRDVRNRFELLDLSLFTQYMPFRVTFNFEVFPFLTVY
150 160 170 180 190 200

Cry1Ac VQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLEERVWGP
170 180 190 200 210 220

gi|115 AMAANLHLLLDKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT
210 220 230 240 250 260

Cry1Ac DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
230 240 250 260 270 280

gi|115 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASVGVGS
290 300 310 320 330

gi|115 SWYDKAPSPFVIESSVIRPPHFVDYITGLTVYTSRISISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSSSTL-----YRRPFNIGINNQQL
340 350 360 370 380

gi|115 GSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLTKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac SVLDGTEFAYGTSNLPASAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSFG
390 400 410 420 430 440

gi|115 FMVNQLNTRKTLKYNPVSKDIIASTRDELELPPETSQPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLPNGSVISGPGFTGGDL
450 460 470 480 490 500

gi|115 TGNTTGLV--PVFWSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
500 510 520 530 540 550

Cry1Ac VRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGSSIFSNTVPAT
510 520 530 540 550 560

gi|115 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKT
560 570 580 590 600 610

570 580 590 600 610

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Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGST-----AGVI-IDRFEFIPVTAT
gi|115 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPVDET

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|115 YEAE

>>gi|115828970|gb|ABJ38808.1| Sequence 76 from patent US (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1239; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115 VPFVGPVIVSLYQLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKAL SELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|115 YQLYLTALEEWEENPNRSRFRSRGALRDVNRNFEILDSLFTQYMP SFRVTFNFEVPLTVY

Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|115 AMAANLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT

Cry1Ac DSRDWIRYNQFRRELTTLTVL DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|115 SAKQWVDYVQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG

Cry1Ac SFRGSAQG---IEGS-IRSPHLM DILNSIT IYTD AH-----RGEY YWSGHQIMASPVGFS
gi|115 SWYDKAPSGFVI ESSVIRPPHFVDYITGLTVYTQSR SISSARYIRHWAGHQISYHRVS-R

Cry1Ac GPEFTFPLYGTMGNAAPQQRIV AQLGQGVYRTLSSTL-----YRRPFNIGINNQQQL
gi|115 GSNLQ-QMYGTNQN LHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEVEF

Cry1Ac GPEFTFPLYGTMGNAAPQQRIV AQLGQGVYRTLSSTL-----YRRPFNIGINNQQQL

Cry1Ac SVLDGTEFAYGTSSNLP S AVYRKS GTVDSLDEIPPQNNVPPRQGF SHRLSHVSMFRSGF
gi|115 FMVNQLNNTKRKTLKYNPVSKDIIASTRDSELELP PETS DQPNYESYSHRLCHITSIPA--

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|115 TGNTTGLV--PVFSWTHRSADLNNTIYS DKITQIPAVK CWDNLPFV-PVVKGPGHTGGDL

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWGNS SIFSNIVPAT
gi|115 LQYNRSTG SVGTLFLARYGLALEKAG-KYRVRLRYATDADIVLHV N--DAQI---QMPKT

Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGST-----AGVI-IDRFEFIPVTAT
gi|115 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHN LGEDPNSTLSGIVYVDRIEFIPVDET

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|115 YEAE

>>gi|115828957|gb|ABJ38795.1| Sequence 50 from patent US (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1240; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115 VPFVGPVIVSLYQLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKAL SELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|115 YQLYLTALEEWEENPNRSRFRSRQALRDVNRNFEILDSLFTQYMP SFRVTFNFEVPLTVY

Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|115 AMAANLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT

Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP

Regulatory Product Characterization Team

Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|115 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREIYTNPVLE-NFD--G

Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH----RGEYYWSGHQIMASPVGF
gi|115 SWYDKAPSGFVIESSVIRPPHVFYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAVLQGGVYRSLSSSTL-----YRRPFNIGINNQQ
gi|115 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEF

Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
gi|115 FMVNLNNTKTLKYNPVSKDIIASTRDELELPPETSQDPNYESYSHRCLCHITSIPA--

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|115 TGNNTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV-PVVKGPGHTGGDL

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPAT
gi|115 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKT

Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|115 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDET

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|115 YEAE

>>gi|71793231|emb|CAJ21068.1| unnamed protein product [B (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1240; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|717 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG

Cry1Ac SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEAFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYQLDILWPSGKESQWEIFMEQVEELINQKLA EYARNKALSELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEEWENPNNGSRFRSRQALRDVRNRFEILDSLFTQYMPFSFRVTNFEVPLTVY

Cry1Ac VQAAHLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLKLDASIFGEEWGWSTTTINNYDRQMKLTA EYSDHCWKVYETGLAKLKG

Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREIYTNPVLE-NFD--G

Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH----RGEYYWSGHQIMASPVGF
gi|717 SWYDKAPSGFVIESSVIRPPHVFYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAVLQGGVYRSLSSSTL-----YRRPFNIGINNQQ
gi|717 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEF

Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
gi|717 FMVNLNNTKTLKYNPVSKDIIASTRDELELPPETSQDPNYESYSHRCLCHITSIPA--

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|717 TGNNTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV-PVVKGPGHTGGDL

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPAT
gi|717 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKT

Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDET

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Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSK
gi|717 YEAE

>>gi|71793263|emb|CAJ21084.1| unnamed protein product [B (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1239; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEWEENPNRSRFRSRQALRDVNRNRFELDSLFTQYMPFSFRVTNFEVPLFTVY

Cry1Ac VQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT

Cry1Ac DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--G
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVYTDPLGAVNVSSIG

Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITYTDAH----RGEYYSWGHQIMASPVGFS
gi|717 SWYDKAPSFVGISSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R

Cry1Ac GPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|717 GSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLSDAVLLDIVPGYTYIF-FGMPEVEVF

Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDLSLDEIPPQNNVPRQGFSHRLSHVSMFRSGF
gi|717 FMVNLQNLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWGSSIFSNTVPAT
gi|717 LQYNRSTGVSGLTFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKT

Cry1Ac ATSLDNLQSSDFGYFESANAFSSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDET

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSK
gi|717 YEAE

>>gi|115828973|gb|ABJ38811.1| Sequence 82 from patent US (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1239; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
gi|115 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|115 YQLYLTALEEWEENPNRSRFRSRQALRDVNRNRFELDSLFTQYMPFSFRVTNFEVPLFTVY

Cry1Ac VQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|115 AMAANLHLLLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT

Cry1Ac DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--G
gi|115 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVYTDPLGAVNVSSIG

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          290          300          310          320          330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITITYTDAH----RGEYYWSGHQIMASPVGFS
gi|115 SWYDKAPSFVGISSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R
          330          340          350          360          370          380

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          340          350          360          370          380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|115 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEF
          390          400          410          420          430          440

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          390          400          410          420          430          440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDLDEIPPQNNVPPRQGFSHRLSHVMFRRSGF
gi|115 FMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
          450          460          470          480          490

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          450          460          470          480          490          500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGTGGDL
gi|115 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
          500          510          520          530          540          550

```

```

          510          520          530          540          550          560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPAT
gi|115 LQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
          560          570          580          590          600          610

```

```

          570          580          590          600          610
Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|115 MNPGEDELTSKTFKVAADITVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDET
          620          630          640          650          660          670

```

```

          620          630          640          650          660          670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|115 YEAE

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>>gi|71793257|emb|CAJ21081.1| unnamed protein product [B (674 aa)
  initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1239; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

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          10          20          30          40          50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
          30          40          50          60          70          80

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```

          60          70          80          90          100          110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLINQRIEIEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYQLIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90          100          110          120          130          140

```

```

          120          130          140          150          160
Cry1Ac YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEWEENPNNGSRFRSRGALRDVRNRFEILDSLFTQYMPFRVNTFVFPFLTVY
          150          160          170          180          190          200

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```

          170          180          190          200          210          220
Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKG
          210          220          230          240          250          260

```

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          230          240          250          260          270          280
Cry1Ac DSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE--NFD--G
gi|717 SAKQWVDYNQFRREMLTAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
          270          280          290          300          310          320

```

```

          290          300          310          320          330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITITYTDAH----RGEYYWSGHQIMASPVGFS
gi|717 SWYDKAPSFVGISSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R
          330          340          350          360          370          380

```

```

          340          350          360          370          380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|717 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEF
          390          400          410          420          430          440

```

```

          390          400          410          420          430          440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDLDEIPPQNNVPPRQGFSHRLSHVMFRRSGF
gi|717 FMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
          450          460          470          480          490

```

```

          450          460          470          480          490          500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGTGGDL
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
          500          510          520          530          540          550

```

```

          510          520          530          540          550          560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPAT
gi|717 LQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
          560          570          580          590          600          610

```

```

          570          580          590          600          610
Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDELTSKTFKVAADITVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDET
          620          630          640          650          660          670

```

```

          620          630          640          650          660          670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|717 YEAE

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>>gi|71793225|emb|CAJ21065.1| unnamed protein product [B (674 aa)
initn: 1134 initl: 505 opt: 859 Z-score: 1005.6 bits: 197.3 E(): 4.3e-47
Smith-Waterman score: 1240; 37.066% identity (66.877% similar) in 634 aa overlap
(22-619:59-674)

Cry1Ac 10 20 30 40 50
CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDLILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNPALR-----EEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEWENPNNGSRFRSRGALRDVNRFEILDLSFTQYMPFRVTFVFPFLTVY
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
VQAAHLHLSVLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLLLKDKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKG
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
SFRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGF
gi|717 SWYDKAPSGVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|717 GSNLQ-QMYGNTQNLHSTSF-DFTNVDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
gi|717 FMVNLQNNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
SNSSVSIIRAPMFSWHRSAEFNIIASDSITQIPAVK--GNFLPFGSVISGPGFTGGDL
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
500 510 520 530 540 550

510 520 530 540 550 560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHILNVNMGNSSIFSNTVPAT
gi|717 LQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
560 570 580 590 600 610

570 580 590 600 610
Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTSKTFKVAIDAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPVDE
620 630 640 650 660 670

620 630 640 650 660 670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|717 YEAE

>>gi|71793201|emb|CAJ21058.1| unnamed protein product [B (620 aa)
initn: 1098 initl: 505 opt: 858 Z-score: 1005.0 bits: 197.0 E(): 4.7e-47
Smith-Waterman score: 1217; 37.640% identity (66.826% similar) in 627 aa overlap
(22-612:12-619)

10 20 30 40 50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFV-PGAG
gi|717 MSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLGVFPVFPVIVS
10 20 30 40

60 70 80 90 100 110
Cry1Ac FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFR
gi|717 LYTQLIDLILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
50 60 70 80 90 100

120 130 140 150 160 170
Cry1Ac EWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAHLHLS
gi|717 EWEENPNNGSRNGSRALRD-VNRNFEILDLSFTQYMPFRVTFVFPFLTVYAMAANLHLL
110 120 130 140 150 160

180 190 200 210 220 230
Cry1Ac VLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYN
gi|717 LKDKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSKQWVDYN
170 180 190 200 210 220

240 250 260 270 280 290
Cry1Ac QFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGSAQG-
gi|717 QFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGSWYDKAPSF
230 240 250 260 270 280

300 310 320 330 340
Cry1Ac --IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFSGPEFTFPLY
gi|717 GVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMY
290 300 310 320 330 340

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          350      360      370      380      390
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSL-----YRRPFNIGINNQQLSVLDGTEFA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 GTNQNHLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNNT
      350      360      370      380      390      400

          400      410      420      430      440      450
Cry1Ac YGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFShRLSHVSMFRSGFSNssVSIIR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 RKTlKYNpVSKDIIAsTRDSELELPPeTSDQPNyESySHRLCHITSIPA--TGNTTGLV-
      410      420      430      440      450

          460      470      480      490      500      510
Cry1Ac APMFswIHRSaEFNnIIASDSITQIPAVK--GNfLfnGsvISGPGfTGGDLVRLNssGNn
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 -PVfSwTHRSADLnnTIYSdKITQIPAVKcWdNLPfV-PVvKGPgHTGGDLlQYnrSTGS
      460      470      480      490      500      510

          520      530      540      550      560      570
Cry1Ac IQNRgyIEVPIHfPSTsTRyRVRVRYASVtPIHLNvNwGnssIFsNTVPATATsLDNLQs
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 VGTlFLARyGLALEKAG-KYrVRLRYATDADIVLHVn--DAQI---QMPKTMNpGEDLTS
      520      530      540      550      560      570

          580      590      600      610      620
Cry1Ac SDFGyFESAN----AFTSSlG--NIVGVRnFSGTAGVI-IDRFefIPVtATLEAEYNLER
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 KTFKvADAItTLNlATDSSlALKHnLGEDPNsTLsGIVyVDRIEFIPVD
      580      590      600      610      620

          630      640      650      660      670      680
Cry1Ac AQKAVNALFTsTNQLGLKtNVTdYHIDQVSNlVtYLSDEfCLDEKRELSEKVKHAKRLSD

>>gi|115828947|gb|ABJ38785.1| Sequence 20 from patent US (620 aa)
  initn: 1098 initl: 505 opt: 858 Z-score: 1005.0 bits: 197.0 E(): 4.7e-47
Smith-Waterman score: 1217; 37.640% identity (66.826% similar) in 627 aa overlap
(22-612:12-619)

          10      20      30      40      50
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFV-PGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115      MSAGNASEYPGSPeVLVSGQDAAKAA---IDIVGkLLSGLGVPfVFGPIVS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          10      20      30      40

          60      70      80      90      100      110
Cry1Ac FVLGLVDIIWIGfGpSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESFR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 LYtQLIDILWPsgEKsQWEIfMEQVEELINQKIAEYARnKALSELEGLGNyQLYlTALe
      50      60      70      80      90      100

          120      130      140      150      160      170
Cry1Ac EWEADPTNP----ALREEMRIQFNdMNSALtTAIPLfAVQNYQVPLLSVYVQAANLHLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 EWEENPNgsRngSRALRD-VRNRFELDSLFTQYMPsFRVtNFVEPFLTVYAMAANLHLl
      110      120      130      140      150      160

          180      190      200      210      220      230
Cry1Ac VLrDVsVfGQRWGFDAAtINSRYNDLTRLIGNyTDHAvRWYNTGLERVWGPDSRDWIRYn

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          170      180      190      200      210      220
gi|115 LLKDasIFGEEWGWSTTTInNYDRQMKLTAeYSDHCvKWYETGLAKLkGTsAKQWVDYn
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

          240      250      260      270      280      290
Cry1Ac QFRRELTlTVLDIVSLFPNyDSRTYPiRTVSQLTReIYtNPVLE-NFD--GSFRGSAQg-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 QFRREMTLAVLDVVALFPNyDTRTYPMETKAQLTReVYtDPLGAVNVSSIGsWYDKAPsF
      230      240      250      260      270      280

          300      310      320      330      340
Cry1Ac --IEGS-IRSPHLMDILNSITtYtDAH----RGEYyWsgHQIMAsPVGFSGPEfTFPLy
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GVIESSVIRPPHVFdyITGLtVYtQSRsISSARyIRHWAGHQISYHRVs-RGSNLQ-QMy
      290      300      310      320      330      340

          350      360      370      380      390
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSL-----YRRPFNIGINNQQLSVLDGTEFA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GTNQNHLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVYPGYTYIF-FGMPEVEFFMVNQLNNT
      350      360      370      380      390      400

          400      410      420      430      440      450
Cry1Ac YGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFShRLSHVSMFRSGFSNssVSIIR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 RKTlKYNpVSKDIIAsTRDSELELPPeTSDQPNyESySHRLCHITSIPA--TGNTTGLV-
      410      420      430      440      450

          460      470      480      490      500      510
Cry1Ac APMFswIHRSaEFNnIIASDSITQIPAVK--GNfLfnGsvISGPGfTGGDLVRLNssGNn
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 -PVfSwTHRSADLnnTIYSdKITQIPAVKcWdNLPfV-PVvKGPgHTGGDLlQYnrSTGS
      460      470      480      490      500      510

          520      530      540      550      560      570
Cry1Ac IQNRgyIEVPIHfPSTsTRyRVRVRYASVtPIHLNvNwGnssIFsNTVPATATsLDNLQs
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VGTlFLARyGLALEKAG-KYrVRLRYATDADIVLHVn--DAQI---QMPKTMNpGEDLTS
      520      530      540      550      560      570

          580      590      600      610      620
Cry1Ac SDFGyFESAN----AFTSSlG--NIVGVRnFSGTAGVI-IDRFefIPVtATLEAEYNLER
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 KTFKvADAItTLNlATDSSlALKHnLGEDPNsTLsGIVyVDRIEFIPVD
      580      590      600      610      620

          630      640      650      660      670      680
Cry1Ac AQKAVNALFTsTNQLGLKtNVTdYHIDQVSNlVtYLSDEfCLDEKRELSEKVKHAKRLSD

>>gi|25277428|emb|CAD57553.1| unnamed protein product [B (620 aa)
  initn: 1098 initl: 505 opt: 858 Z-score: 1005.0 bits: 197.0 E(): 4.7e-47
Smith-Waterman score: 1217; 37.640% identity (66.826% similar) in 627 aa overlap
(22-612:12-619)

          10      20      30      40      50
Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFV-PGAG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|252      MSAGNASEYPGSPeVLVSGQDAAKAA---IDIVGkLLSGLGVPfVFGPIVS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          10      20      30      40

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60      70      80      90      100     110
Cry1Ac FVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQALSRLEGLSNLQYIYAESFR
      . : : : : . : : : . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 252 LYTQLIDLILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNNYQLYLTALE
      50      60      70      80      90      100

120     130     140     150     160     170
Cry1Ac EWEADPTNP----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLS
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 EWEENPNGSRNGSRALRD-VRRNRFELDSLFTQYMPSPFRVTNFEVFPFLTIVYAMAANLHLL
      110     120     130     140     150     160

180     190     200     210     220     230
Cry1Ac VLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYN
      . : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 LLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTSAKQWVDYN
      170     180     190     200     210     220

240     250     260     270     280     290
Cry1Ac QFRRELTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GSFRGSAQG-
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 QFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGSWYDKAPSF
      230     240     250     260     270     280

300     310     320     330     340
Cry1Ac --IEGS-IRSPHLMIDLNSITYTDAH----RGEYYWSGHQIMASPVGFSGPEFTFPLY
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 GVISSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RGSNLQ-QMY
      290     300     310     320     330     340

350     360     370     380     390
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDGTEFA
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 GTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEFFMVNQLNNT
      350     360     370     380     390     400

400     410     420     430     440     450
Cry1Ac YGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIR
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 RKTLYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--TGNVTTGLV-
      410     420     430     440     450

460     470     480     490     500     510
Cry1Ac APMFVSIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLVRLNSSGNN
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 -PVFSWTHRSADLNNIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLLQYNRSTGS
      460     470     480     490     500     510

520     530     540     550     560     570
Cry1Ac IQNRGYIEVPIHPFSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTPATATSLDNLQS
      . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 VGTFLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTMNPGEDLTS
      520     530     540     550     560     570

580     590     600     610     620
Cry1Ac SDFGYFESAN----AFTSSLG--NIVGVNRFSGTAGVI-IDRFEFIPVTATLEAEYNLER
      . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 252 KTFKVADAITTLNLATDSSLALKHNLGEPNSTLSGIVYVDRIEPIFVD

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580     590     600     610     620
Cry1Ac AQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSD
      630     640     650     660     670     680

>>gi|71793215|emb|CAJ21062.1| unnamed protein product [B (673 aa)
      initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1239; 37.382% identity (66.877% similar) in 634 aa overlap
(22-619:59-673)

10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFFLL
      . : : : . : : : . : : : . : : : . : : :

gi | 717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQALSRLEGLSNL
      : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 VPFVGPVIVSLYTLQIDLILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90     100     110     120     130     140

120     130     140     150     160
Cry1Ac YQIYAESFREWADPTNP----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 YQLYLTALEEWEENPNGSRNGSRALRD-VRRNRFELDSLFTQYMPSPFRVTNFEVFPFLTIVY
      150     160     170     180     190     200

170     180     190     200     210     220
Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
      . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 AMAANLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
      210     220     230     240     250     260

230     240     250     260     270     280
Cry1Ac DSRDWIRYNQFRRELTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
      . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIG
      270     280     290     300     310     320

290     300     310     320     330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITYTDAH----RGEYYWSGHQIMASPVGFS
      : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 SWYDKAPSGVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-R
      330     340     350     360     370     380

340     350     360     370     380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
      : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEF
      390     400     410     420     430     440

390     400     410     420     430     440
Cry1Ac SVLDGTEFAFGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
      . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : : . : : :
gi | 717 FMVNQLNNTRKTLYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--
      450     460     470     480     490

450     460     470     480     490     500

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Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|717 TGNTTGLV--PVFSTWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDL
500 510 520 530 540 550

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPAT
gi|717 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
560 570 580 590 600

Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTskTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRLEFIPVDET
610 620 630 640 650 660

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|717 YEAE
670

>>gi|71793249|emb|CAJ21077.1| unnamed protein product [B (673 aa)
initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1238; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA--IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|717 YQLYLTALEEWENPFRRGFRGALRDVRNFEILDSLFTQYMPFRVTVNFVFPFLTVYA
150 160 170 180 190 200

Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|717 MAANLHLLLLK DASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210 220 230 240 250 260

Cry1Ac SRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFD--GS
gi|717 AKQWVDYDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKALQTLREYVTDPLGAVNVSSIGS
270 280 290 300 310 320

290 300 310 320 330

Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITIYTDH----RGEYYWSGHQIMASPVGFSG
gi|717 WYDKAPSFVGISSVIRPPHVFYITGLTVYTSRSISSARYIRHWAGHQIYHRVRS-RG
330 340 350 360 370 380

Cry1Ac PEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGVYIYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
gi|717 MVNQLNTRKTLKYNPVSQDI IASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNNTTGLV--PVFSTWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
560 570 580 590 600 610

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTskTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRLEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|717 EAE

>>gi|71793211|emb|CAJ21061.1| unnamed protein product [B (673 aa)
initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1240; 38.013% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA--IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

120 130 140 150 160

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Cry1Ac YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEWEENPNNGSRNGSRALRD--VRNRFEILDSLFTQYMPFSFRVTNFEVPLTVY
150 160 170 180 190 200
Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCWKYETGLAKLKG
210 220 230 240 250 260
Cry1Ac DSRDWIRYNQFRRELTLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIG
270 280 290 300 310 320
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH-----RGEYYWSGHQIMASVPGFS
gi|717 SWYDKAPSFVGISSVIRPPHVDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|717 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRSHVSMFRSGF
gi|717 FMVNQLNNTKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--
450 460 470 480 490
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNQSVISGPGFTGGDL
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDL
500 510 520 530 540 550
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVPIHLNVNWNSSIFSNTVPAT
gi|717 LQYNRSTGSVGLTFLARYGLALEKAG-KYRVRLRYATDADIVLHVY--DAQI---QMPKT
560 570 580 590 600
Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTSKTFKVADAITTLNLTADSSSLAVKHNVGEPNLSLGIIVVDRIEFIPVDET
610 620 630 640 650 660
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSK
gi|717 YEAE
670

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>>gi|115828965|gb|ABJ38803.1| Sequence 66 from patent US (673 aa)
initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNMDYKDYLLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80
Cry1Ac SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLGLSNL
gi|115 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
90 100 110 120 130 140
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|115 YQLYLTALEEWEENPFRGFRGALRDVNRFEILDSLFTQYMPFSFRVTNFEVPLTVYA
150 160 170 180 190 200
Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|115 MAANLHLLLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCWKYETGLAKLKG
210 220 230 240 250 260
Cry1Ac SRDWIRYNQFRRELTLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIG
270 280 290 300 310 320
Cry1Ac FRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH-----RGEYYWSGHQIMASVPGFSG
gi|115 WYDKAPSFVGISSVIRPPHVDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RG
330 340 350 360 370 380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
gi|115 SNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRSHVSMFRSGFS
gi|115 MVNQLNNTKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNQSVISGPGFTGGDLV
gi|115 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDL
500 510 520 530 540 550

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510      520      530      540      550      560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  QYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
560      570      580      590      600      610

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570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEPFIVPTATL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVVYDRIEFIPVDETY
620      630      640      650      660      670

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620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      : : :
gi|115  EAE

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>>gi|115828950|gb|ABJ38788.1| Sequence 30 from patent US (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1240; 38.013% identity (66.719% similar) in 634 aa overlap  
 (22-619:59-673)

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10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

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60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLN
      : : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100     110     120     130     140

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120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      : : : . . . : : : . . . : : : . . . : : : . . . : : : . . . : : :
gi|115  YQLYLTALEEWEENPNRSRNGSRALRD-VRNRFEILDLSLFTQYMPFSFRVTNFEVFPFLTVY
150     160     170     180     190     200

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170     180     190     200     210     220
Cry1Ac VQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  AMAANLHLLLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKG
210     220     230     240     250     260

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230     240     250     260     270     280
Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTRBIYTNPVLE-NFD--G
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTRVYVYDPLGAVNVSSIG
270     280     290     300     310     320

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290     300     310     320     330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDILNSITYTDAH-----RGEYYSWGHQIMASPVGF
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  SWYDKAPSGFVIESSVIRPPHFVDYITGLTVYTSQRSISSARYIRHWAGHQISYHRVS-R
330     340     350     360     370     380

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```

340     350     360     370     380
Cry1Ac GPEFTTPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGLINNQQL
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  GSNLQ-QMYGTNQLNHSTSTF-DFTNYDIYKTLSKDAVLLDIVPGYTYIF-FGMPEVEF
390     400     410     420     430     440

```

```

390     400     410     420     430     440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPNQNNVPPRQGFSHRLSHVSMFRSGF
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  FMVNQLNNTKTLKYNPVSKDIIASTRDELELPPETSQDPNYESYSHRLCHITSIPA--
450     460     470     480     490

```

```

450     460     470     480     490     500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  TGNTTGLV--PVFSWTHRSADLNNNTIYSDKITQIPAVKCDWNLPPFV-PVVKGPGHTGGDL
500     510     520     530     540     550

```

```

510     520     530     540     550     560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPAT
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  LQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
560     570     580     590     600

```

```

570     580     590     600     610
Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEPFIVPTAT
      . . . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  MNPGEDLTSKTFKVADAITTLNLATDSSLAVKHNVGEDPNSTLSGIVVYDRIEFIPVDET
610     620     630     640     650     660

```

```

620     630     640     650     660     670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      : : :
gi|115  YEAE
670

```

>>gi|115828964|gb|ABJ38802.1| Sequence 64 from patent US (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap  
 (22-619:59-673)

```

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLN
      : : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100     110     120     130     140

```

```

120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      : : : . . . : : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  YQLYLTALEEWEENPFRGRFRGALRDVRNRFEILDLSLFTQYMPFSFRVTNFEVFPFLTVYA
150     160     170     180     190     200

```

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```

170      180      190      200      210      220
Cry1Ac Q AANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115 MAANLHLLLLK DASFGE EWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210      220      230      240      250      260

```

```

230      240      250      260      270      280
Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|115 AKQWVDYDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGS
270      280      290      300      310      320

```

```

290      300      310      320      330
Cry1Ac FRGSAQG---IEGS-IRSPHLM DILNSIT IYTD A H----RGEYYWSGHQIMASVPGFSG
gi|115 WYDKAPSFVGI ESSVIRPPHVF DYITGLTVYTQSR S ISSARYIRHWAGHQISYHRVS-RG
330      340      350      360      370      380

```

```

340      350      360      370      380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
gi|115 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEVEFF
390      400      410      420      430      440

```

```

390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHR LSHVSMFRSGFS
gi|115 MVNQLNNTKRTLKYNPVSKDIIASTRDSELELPPETS DQP NYESYSHRLCHITSIPA--T
450      460      470      480      490

```

```

450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|115 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVK CWDNLPFV-PVVKGP GHTGGDLL
500      510      520      530      540      550

```

```

510      520      530      540      550      560
Cry1Ac R LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWGNSSIFSNTV PATA
gi|115 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHV N--DAQI---QMPKTM
560      570      580      590      600      610

```

```

570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|115 NPGEDLT SKTFKVADAI'TVNLATDSSVAVKHNVGEDPNSTLSGVIYVDRIEFIPVDETY
620      630      640      650      660      670

```

```

620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD EFC LDEKRELSEKV
gi|115 EAE

```

>>gi|71793271|emb|CAJ21088.1| unnamed protein product [B (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1238; 37.125% identity (66.825% similar) in 633 aa overlap  
 (22-619:59-673)

```

10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKAL SELEGLGN
90      100      110      120      130      140

```

```

120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|717 YQLYLTALEEWEEENPFRFRGFRGALRDVRNRFEILDSLFTQYMP SFRVTNFVEVPFLTVYA
150      160      170      180      190      200

```

```

170      180      190      200      210      220
Cry1Ac Q AANLHLSVLRDVS VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|717 MAANLHLLLLK DASFGE EWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210      220      230      240      250      260

```

```

230      240      250      260      270      280
Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|717 AKQWVDYDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGS
270      280      290      300      310      320

```

```

290      300      310      320      330
Cry1Ac FRGSAQG---IEGS-IRSPHLM DILNSIT IYTD A H----RGEYYWSGHQIMASVPGFSG
gi|717 WYDKAPSFVGI ESSVIRPPHVF DYITGLTVYTQSR S ISSARYIRHWAGHQISYHRVS-RG
330      340      350      360      370      380

```

```

340      350      360      370      380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEVEFF
390      400      410      420      430      440

```

```

390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHR LSHVSMFRSGFS
gi|717 MVNQLNNTKRTLKYNPVSKDIIASTRDSELELPPETS DQP NYESYSHRLCHITSIPA--T
450      460      470      480      490

```

```

450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVK CWDNLPFV-PVVKGP GHTGGDLL
500      510      520      530      540      550

```

```

510      520      530      540      550      560
Cry1Ac R LNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWGNSSIFSNTV PATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHV N--DAQI---QMPKTM
560      570      580      590      600      610

```

```

          570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLDGDPNSTLSGIVYVDRIEFIPVDETY
          620      630      640      650      660      670

```

```

          620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|717 EAE

```

>>gi|71793245|emb|CAJ21075.1| unnamed protein product [B (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap  
 (22-619:59-673)

```

          10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

```

```

          60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100      110      120      130      140

```

```

          120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|717 YQLYLTALBEWEENPFRRGFRRGALRDVNRNFEILDSLFTQYMPFRVNTNFVFPFLTVYA
          150      160      170      180      190      200

```

```

          170      180      190      200      210      220
Cry1Ac QAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|717 MAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
          210      220      230      240      250      260

```

```

          230      240      250      260      270      280
Cry1Ac SRDWIRYNQFRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|717 AKQWVDYDQFREMFLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGS
          270      280      290      300      310      320

```

```

          290      300      310      320      330
Cry1Ac FRGSAQG---IEGS-IRSPHLDILNSITIYTDH----RGEYWSGHQIMASVPGFSG
gi|717 WYDKAPSGVIESSVIRPPHFVDYITGLTVYTSRSISSARYIRHWAGHQAISYHRVS-RG
          330      340      350      360      370      380

```

```

          340      350      360      370      380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
gi|717 SNLQ-QMYGTNQLNHSTTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPVEVFF
          390      400      410      420      430      440

```

```

          390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
gi|717 MVNQLNTRKTKLYNPNVSKDIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPA--T
          450      460      470      480      490

```

```

          450      460      470      480      490      500
Cry1Ac NSSVSIIRAMPFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDLL
          500      510      520      530      540      550

```

```

          510      520      530      540      550      560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNVTPATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
          560      570      580      590      600      610

```

```

          570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLDGDPNSTLSGIVYVDRIEFIPVDETY
          620      630      640      650      660      670

```

```

          620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|717 EAE

```

>>gi|115828967|gb|ABJ38805.1| Sequence 70 from patent US (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1238; 37.382% identity (66.877% similar) in 634 aa overlap  
 (22-619:59-673)

```

          10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

```

```

          60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
gi|115 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100      110      120      130      140

```

```

          120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|115 YQLYLTALBEWEENPNPNSRRGSRALRD-VNRNFEILDSLFTQYMPFRVNTNFVFPFLTVYA
          150      160      170      180      190      200

```

```

          170      180      190      200      210      220
Cry1Ac VQAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115 AMAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
          210      220      230      240      250      260

```

```

                230      240      250      260      270      280
Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE--NFD--G
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
      270      280      290      300      310      320

```

```

                290      300      310      320      330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITIYTDH----RGEYVWSGHQIMASPVGFS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 SWYDKAPSGVGISSVIRPPHFVDYITGLTVYTSQRSISSARYIRHWAGHQISYHRVS-R
      330      340      350      360      370      380

```

```

                340      350      360      370      380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQQL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPVEVEF
      390      400      410      420      430      440

```

```

                390      400      410      420      430      440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
      450      460      470      480      490

```

```

                450      460      470      480      490      500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
      500      510      520      530      540      550

```

```

                510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPAT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
      560      570      580      590      600

```

```

                570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGYFESANAFSTSSLGIVGVNRFSGT-----AGVI-IDRFEFIPVTAT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 MNPGEDLTSTKTFKVADAITVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDET
      610      620      630      640      650      660

```

```

                620      630      640      650      660      670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 YEAE
      670

```

```

>>gi|71793190|emb|CAJ21054.1| unnamed protein product [B (673 aa)
  initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1236; 37.855% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

```

```

                10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSEVLVSGQDAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

                60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 VPFVGPVIVSLYTLQILDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
      90      100      110      120      130      140

```

```

                120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 YQLYLTALEEWEENPNNGSRNGSRALRD-VRNRFELLDLSLFTQYMPFRVNTNFVFPFLTVY
      150      160      170      180      190      200

```

```

                170      180      190      200      210      220
Cry1Ac VQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 AMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT
      210      220      230      240      250      260

```

```

                230      240      250      260      270      280
Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE--NFD--G
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
      270      280      290      300      310      320

```

```

                290      300      310      320      330
Cry1Ac SFRGSAQG---IEGS-IRSPHLMIDLNSITIYTDH----RGEYVWSGHQIMASPVGFS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 SWYDKAPSGVGISSVIRPPHFVDYITGLTVYTSQRSISSARYIRHWAGHQISYHRVS-R
      330      340      350      360      370      380

```

```

                340      350      360      370      380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQQL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : ~
gi|717 GSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPVEVEF
      390      400      410      420      430      440

```

```

                390      400      410      420      430      440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
      . . . . . : : : : ~ : : : : : : : : : : : : : : : : : : : : ~
gi|717 FMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
      450      460      470      480      490

```

```

                450      460      470      480      490      500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : :
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDL
      500      510      520      530      540      550

```

```

                510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPAT
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : :
gi|717 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
      560      570      580      590      600

```

```

                570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVNRFSGTAGVI-IDRFEFIPVTAT
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : :
gi|717 MNPGEDLTSTKTFKVADAITVNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDET

```

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```

610      620      630      640      650      660
Cry1Ac  LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      :::
gi|717 YEAE
      670

>>gi|115828942|gb|ABJ38780.1| Sequence 8 from patent US (673 aa)
      initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1236; 37.855% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

```

```

      10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      ::: : : . . . . . : : : : :
gi|115  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

      60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      : : . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  VPFVGPVIVSLYTLIDILWPSGKESQWEIFMQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

      120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNP----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|115  YQLYLTALEEWEENPNRSRNGSRALRD--VRNRFELDSLFTQYMPSPFRVTFEVPFLTVY
      150      160      170      180      190      200

```

```

      170      180      190      200      210      220
Cry1Ac  VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  AMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
      210      220      230      240      250      260

```

```

      230      240      250      260      270      280
Cry1Ac  DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  SAKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVIYDPLGAVNVSSIG
      270      280      290      300      310      320

```

```

      290      300      310      320      330
Cry1Ac  SFRGSAQG---IEGS-IRSPHLMIDILNSITTYTDAH----RGEYWSGHQIMASPVGF
      : . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  SWYDKAPSGFVIESSVIRPPHVFYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVRS-R
      330      340      350      360      370      380

```

```

      340      350      360      370      380
Cry1Ac  GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
      : . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEF
      390      400      410      420      430      440

```

```

      390      400      410      420      430      440
Cry1Ac  SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGF
      . . . : : : : : : : : : : : : : : : : : : : : : : :
gi|115  FMVNQLNNTTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--

```

```

      450      460      470      480      490
Cry1Ac  SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|115  TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDL
      500      510      520      530      540      550

```

```

      510      520      530      540      550      560
Cry1Ac  VRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWGNSSIFSNTVPAT
      . . : : . . . . . : : . . . : : : : : : : : : : : : : :
gi|115  LQYNRSTGTVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
      560      570      580      590      600

```

```

      570      580      590      600      610
Cry1Ac  ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFGTAGVI-IDRFEFIPVTAT
      . . . : : . . . : : : : : : : : : : : : : : : : : : :
gi|115  MNPGEDLTSKTFKVADAITTLNLATDSSLALKHNLGEDPNSTLSGIVYVDRIEFIPVDET
      610      620      630      640      650      660

```

```

      620      630      640      650      660      670
Cry1Ac  LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      :::
gi|115 YEAE
      670

```

```

>>gi|71793203|emb|CAJ21059.1| unnamed protein product [B (673 aa)
      initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

```

```

      10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      : : : : : : : . . . : : : : : : :
gi|717  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

      60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      : : . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  VPFVGPVIVSLYTLIDILWPSGKESQWEIFMQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

      120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . : :
gi|717  YQLYLTALEEWEENPFRGFRGALRDVRNRFELDSLFTQYMPSPFRVTFEVPFLTVYA
      150      160      170      180      190      200

```

```

      170      180      190      200      210      220
Cry1Ac  QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  MAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
      210      220      230      240      250      260

```

```

      230      240      250      260      270      280
Cry1Ac  SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717  AKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVIYDPLGAVNVSSIG

```

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```

270      280      290      300      310      320
Cry1Ac 290      300      310      320      330
FRGSAQG---IEGS-IRSPHLMILNSITITDAH----RGEYYWSGHQIMASVPGFSG
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 WYDKAPSFVIESSVIRPPHVFYDITGLTVYTSRSISSARYIRHWAGHGISYHRVS-RG
330      340      350      360      370      380

```

```

340      350      360      370      380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390      400      410      420      430      440

```

```

390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 MVNQLNNTKTKYNPVSVDIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPA--T
450      460      470      480      490

```

```

450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGGHTGGDLL
500      510      520      530      540      550

```

```

510      520      530      540      550      560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTVPATA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI--QMPKTM
560      570      580      590      600      610

```

```

570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEIPVDETY
620      630      640      650      660      670

```

```

620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 EAE

```

```

>>gi|76360363|emb|CAJ32199.1| unnamed protein product [B (673 aa)
initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

```

```

10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIARLEGLSNL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 VPFVGPVLSLYTQLDILWPSGEEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN

```

```

90      100     110     120     130     140
Cry1Ac 120     130     140     150     160
YQIYAESFREWEADPTNPALRE----EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 YQLYLTALEEEENPFRGFRGALRDVNRNFEILDLSLFTQYMPSFRVNFVFPFLTVYA
150     160     170     180     190     200

```

```

170     180     190     200     210     220
Cry1Ac QAANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 MAANLHLLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCWKWYETGLAKLKGTS
210     220     230     240     250     260

```

```

230     240     250     260     270     280
Cry1Ac SRDWIRYQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 AKQWVDYQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGS
270     280     290     300     310     320

```

```

290     300     310     320     330
Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITITDAH----RGEYYWSGHQIMASVPGFSG
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 WYDKAPSFVIESSVIRPPHVFYDITGLTVYTSRSISSARYIRHWAGHGISYHRVS-RG
330     340     350     360     370     380

```

```

340     350     360     370     380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390     400     410     420     430     440

```

```

390     400     410     420     430     440
Cry1Ac VLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 MVNQLNNTKTKYNPVSVDIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPA--T
450     460     470     480     490

```

```

450     460     470     480     490     500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGGHTGGDLL
500     510     520     530     540     550

```

```

510     520     530     540     550     560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTVPATA
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI--QMPKTM
560     570     580     590     600     610

```

```

570     580     590     600     610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|763 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEIPVDETY
620     630     640     650     660     670

```

```

620     630     640     650     660     670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :

```



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gi|115 SWYDKAPSGFVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
340 350 360 370 380

gi|115 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSFMFRSGF
390 400 410 420 430 440

gi|115 FMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
450 460 470 480 490 500

gi|115 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV-PVVKGPGHTGGDL
500 510 520 530 540 550

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPAT
510 520 530 540 550 560

gi|115 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
560 570 580 590 600

Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTAT
570 580 590 600 610

gi|115 MNPGEDLTSKTFKVADAITTLNLTADSSSLALKHNVGEPNSTLSGIVYVDRIEFIPVDET
610 620 630 640 650 660

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
620 630 640 650 660 670

gi|115 YEAE
670

>>gi|71793207|emb|CAJ21060.1| unnamed protein product [B (673 aa)
initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1240; 38.013% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
10 20 30 40 50

gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPVLSVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIFGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAIARLEGLSNL
60 70 80 90 100 110

gi|717 VPFVGPVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESPFEWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
120 130 140 150 160

gi|717 YEAE
670

gi|717 YQLYLTALEEEWENPNNGSRNGSRALRD-VNRNFEILDSLFTQYMPFRVTVNFVFPFLTVY
150 160 170 180 190 200

Cry1Ac VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
170 180 190 200 210 220

gi|717 AMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT
210 220 230 240 250 260

Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLE-NFD--G
230 240 250 260 270 280

gi|717 SAKQWVDYNQFRREMLAVLDVVALFPNYDTRTPYMETKAQLTREYVTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac SFRGSAQG---IEGS-IRSPHMLDILNSITITYTDAH----RGEYYSWGHQIMASVPGFS
290 300 310 320 330

gi|717 SWYDKAPSGFVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQ
340 350 360 370 380

gi|717 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSFMFRSGF
390 400 410 420 430 440

gi|717 FMVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
450 460 470 480 490 500

gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCWDNLPFV-PVVKGPGHTGGDL
500 510 520 530 540 550

Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTVPAT
510 520 530 540 550 560

gi|717 LQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKT
560 570 580 590 600

Cry1Ac ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFSGTAGVI-IDRFEFIPVTAT
570 580 590 600 610

gi|717 MNPGEDLTSKTFKVADAITTLNLTADSSSLALKHNVGEPNSTLSGIVYVDRIEFIPVDET
610 620 630 640 650 660

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
620 630 640 650 660 670

gi|717 YEAE
670

>>gi|25277399|emb|CAD57547.1| unnamed protein product [B (673 aa)
initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47

Regulatory Product Characterization Team

Smith-Waterman score: 1236; 37.855% identity (66.719% similar) in 634 aa overlap (22-619:59-673)

Sequence alignment for gi|252 vs Cry1Ac. Shows amino acid sequences with positions 10-50, 60-110, 120-170, 180-220, 230-280, 290-330, 340-380, 390-440, 450-500, 510-560. Includes gaps and alignment markers.

Sequence alignment for gi|252 vs Cry1Ac. Shows amino acid sequences with positions 560-600, 570-610, 620-660, 670. Includes gaps and alignment markers.

>>gi|71793239|emb|CAJ21072.1| unnamed protein product [B (673 aa) initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47 Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap (22-619:59-673)

Sequence alignment for gi|717 vs Cry1Ac. Shows amino acid sequences with positions 30-80, 90-140, 150-200, 210-260, 270-320, 330-380, 390-440, 450-500, 510-560. Includes gaps and alignment markers.

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gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFVSHRSHVSMFRSGFS
390 400 410 420 430 440

gi|717 MVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--T
450 460 470 480 490

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
450 460 470 480 490 500

gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV--PVVKGPGHTGGDLL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATA
510 520 530 540 550 560

gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
560 570 580 590 600 610

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
570 580 590 600 610

gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
620 630 640 650 660 670

gi|717 EAE

>>gi|76360359|emb|CAJ32197.1| unnamed protein product [B (673 aa)
initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1238; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
10 20 30 40 50

gi|763 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
60 70 80 90 100 110

gi|763 VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMQVEELNQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
120 130 140 150 160

gi|763 YQLYLTALEEWEEENFRRGFRRGALRDVNRNFEILDLSFTQYMPFSFRVTFNFEVPPFLTUYA
150 160 170 180 190 200

Cry1Ac QANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
170 180 190 200 210 220

gi|763 MAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210 220 230 240 250 260

Cry1Ac SRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTPYRTVSQLTREIYTNPVLE-NFD--GS
230 240 250 260 270 280

gi|763 AKQWVDYNGFRREMTLAVLDVVALFPNYDTRTPYMETKAQLTREVYTDPLGAVNVSSIGS
270 280 290 300 310 320

Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITITYTDAH-----RGEYVWSGHQIMASPVGFSG
290 300 310 320 330

gi|763 WYDKAPSFVGISSVIRPPHVPDYITGLTVYTSRISISSARYIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
340 350 360 370 380

gi|763 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFVSHRSHVSMFRSGFS
390 400 410 420 430 440

gi|763 MVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--T
450 460 470 480 490

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
450 460 470 480 490 500

gi|763 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV--PVVKGPGHTGGDLL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVPATA
510 520 530 540 550 560

gi|763 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
560 570 580 590 600 610

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
570 580 590 600 610

gi|763 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
620 630 640 650 660 670

gi|763 EAE

>>gi|115828966|gb|ABJ38804.1| Sequence 68 from patent US (673 aa)
initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1238; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
10 20 30 40 50



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Cry1Ac VLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFsHRLSHVSMFRSGFS
gi|717 MVNQLNNTKRLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
      450      460      470      480      490
Cry1Ac 450 460 470 480 490 500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLDPFV--PVVKGPGHTGGDLL
      500      510      520      530      540      550
Cry1Ac 510 520 530 540 550 560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNIVPATA
gi|717 QYNRSTGSVGTFLFARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610
Cry1Ac 570 580 590 600 610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAIITVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670
Cry1Ac 620 630 640 650 660 670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|717 EAE

```

>>gi|76360361|emb|CAJ32198.1| unnamed protein product [B (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap  
 (22-619:59-673)

```

Cry1Ac 10 20 30 40 50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLL
gi|763 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80
Cry1Ac 60 70 80 90 100 110
Cry1Ac SEFV-PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIIEFARNQAI SRLEGLSNL
gi|763 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140
Cry1Ac 120 130 140 150 160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|763 YQLYLTALEEWENEFRRGFRGALRDVNRNFEILDLSLFTQYMPFRVTVNFVPLTVYA
      150      160      170      180      190      200
Cry1Ac 170 180 190 200 210 220
Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVWGP
gi|763 MAANLHLLLLKDasIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
      210      220      230      240      250      260
Cry1Ac 230 240 250 260 270 280

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Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|763 AKQWVDYNQFRREMTLAVLDVVALFPNYDTRTPMETKAQLTREVYTDPLGAVNVSSIGS
      270      280      290      300      310      320
Cry1Ac 290 300 310 320 330
Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITIIYTDAAH----RGEYVWSGHQIMASPVGFSG
gi|763 WYDKAPSFVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQI SYHRVS-RG
      330      340      350      360      370      380
Cry1Ac 340 350 360 370 380
Cry1Ac PEFTFFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|763 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEVFF
      390      400      410      420      430      440
Cry1Ac 390 400 410 420 430 440
Cry1Ac VLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFsHRLSHVSMFRSGFS
gi|763 MVNQLNNTKRLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
      450      460      470      480      490
Cry1Ac 450 460 470 480 490 500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|763 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLDPFV--PVVKGPGHTGGDLL
      500      510      520      530      540      550
Cry1Ac 510 520 530 540 550 560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNIVPATA
gi|763 QYNRSTGSVGTFLFARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610
Cry1Ac 570 580 590 600 610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|763 NPGEDLTSKTFKVADAIITVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670
Cry1Ac 620 630 640 650 660 670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|763 EAE

```

>>gi|71793251|emb|CAJ21078.1| unnamed protein product [B (673 aa)  
 initn: 1129 initl: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1238; 37.382% identity (66.877% similar) in 634 aa overlap  
 (22-619:59-673)

```

Cry1Ac 10 20 30 40 50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80
Cry1Ac 60 70 80 90 100 110

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Cry1Ac SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|717 VPFVGPVIVSLYTLQDLIDLWPSGKQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|717 YQLYLTALEEWEENPNRSRNGSRALRD-VRNRFEILDSLFTQYMPSPFRVTNFVFPFLTIVY
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|717 AMAANLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGST
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--G
gi|717 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH-----RGEYIWSGHQIMASPVGFSG
gi|717 SWYDKAPSFVGISSVIRPPHVFYITGLTVYTSRISISSARYIRHWAGHQISYHRVRS-R
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
GPEFTFPLYGTMGNAAPQQRIVAVQLGQGVYRTLSSTL-----YRRPFNIGINNQQL
gi|717 GSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEVF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
SVLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGF
gi|717 FMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGTGGDL
gi|717 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV-PVVGKPGHTGGDL
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
VRLNSSGNIQNRGYIEVPIHFPSTSTRYRVRYASVPIHLNWNWGNSSIFSNTPVAT
gi|717 LQYNRSTGSVGLTFLARYGLALEKAG-KYRVRLRYATDADIVLHVY--DAQI---QMPKT
560 570 580 590 600

Cry1Ac 570 580 590 600 610
ATSLDNLQSSDFGYFESANAFSTSSLGNI VGVVRFSGT-----AGVI-IDRFEFIPVTAT
gi|717 MNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLDGPNSTLSGIVYVDRIEFIPVDET
610 620 630 640 650 660

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Cry1Ac 620 630 640 650 660 670
LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|717 YEAE
670

>>gi|115828978|gb|ABJ38815.1| Sequence 90 from patent US (673 aa)
initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47
Smith-Waterman score: 1238; 37.125% identity (66.825% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac 10 20 30 40 50
CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115 VPFVGPVIVSLYTLQDLIDLWPSGKQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNPALRE----EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|115 YQLYLTALEEWEENPFRFRGALRDVNRNFEILDSLFTQYMPSPFRVTNFVFPFLTIVYA
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115 MAANLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGST
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIGS
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
FRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH-----RGEYIWSGHQIMASPVGFSG
gi|115 WYDKAPSFVGISSVIRPPHVFYITGLTVYTSRISISSARYIRHWAGHQISYHRVRS-RG
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
PEFTFPLYGTMGNAAPQQRIVAVQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|115 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEVF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
VLDGTEFAYGTSSNLPSAVYRKS GMTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
gi|115 MVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490

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      450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV--PVVKGPGHTGGDLL
      500      510      520      530      540      550

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      510      520      530      540      550      560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 QYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610

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      570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 NPGEDLTSKTFKVADAITVNLATDSSVAVKHNLGDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670

```

```

      620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      : : :
gi|115 EAE

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>>gi|115828951|gb|ABJ38789.1| Sequence 34 from patent US (673 aa)  
 initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1239; 37.382% identity (66.877% similar) in 634 aa overlap  
 (22-619:59-673)

```

      10      20      30      40      50
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

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      60      70      80      90      100      110
Cry1Ac SEFV--PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
      : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VPFVGPVIVSLYTQLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

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      120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFVAVQYQVPLLSVY
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 YQLYLTALEEWEENPNSRNGSRALRD--VRNRFEILDLSLFTQYMPSPFRVTNFEVFPFLTIVY
      150      160      170      180      190      200

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      170      180      190      200      210      220
Cry1Ac VQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 AMAANLHLLLDASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKG
      210      220      230      240      250      260

```

```

      230      240      250      260      270      280
Cry1Ac DSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE--NFD--G
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 SAKQWVDYVQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSSIG
      270      280      290      300      310      320

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```

      290      300      310      320      330
Cry1Ac SFRGSAQG---IEGS-IRSPHMDILNSITTYTDAH----RGEYYSWGHQIMASPVGF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 SWYDKAPSGVIESSVIRPPHFVDYITGLTVYVYQSRSSISSARYIRHWAGHQISYHRVS-R
      330      340      350      360      370      380

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```

      340      350      360      370      380
Cry1Ac GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRVLSSSTL-----YRRPFNIGINNQQ
      . . . . . : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 GSNLQ-QMYGTNQLNHSTSTF-DFTNYDIYKTLSKDAVLLDIVYPGYTYIF-FGMPEVEF
      390      400      410      420      430      440

```

```

      390      400      410      420      430      440
Cry1Ac SVLDGTEFAYGTSSNLPSAVYRKSQTVDLDEIPPQNNVPPRQGFSHRLSHVSMFRSGF
      . . . . . : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 FMVNQLNNTKTLKYNPVSKDIIASTRDESELEPPETSQDPNYESYSHRLCHITSIPA--
      450      460      470      480      490

```

```

      450      460      470      480      490      500
Cry1Ac SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV--PVVKGPGHTGGDL
      500      510      520      530      540      550

```

```

      510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPAT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 LQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPK
      560      570      580      590      600

```

```

      570      580      590      600      610
Cry1Ac ATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTAT
      . . . . . : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 MNPGEDLTSKTFKVADAITVNLATDSSVAVKHNVGDPNSTLSGIVYVDRIEFIPVDE
      610      620      630      640      650      660

```

```

      620      630      640      650      660      670
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      : : :
gi|115 YEAE
      670

```

>>gi|115828961|gb|ABJ38799.1| Sequence 58 from patent US (673 aa)  
 initn: 1129 init1: 505 opt: 858 Z-score: 1004.4 bits: 197.0 E(): 5e-47  
 Smith-Waterman score: 1239; 37.125% identity (66.825% similar) in 633 aa overlap  
 (22-619:59-673)

```

      10      20      30      40      50
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

      60      70      80      90      100      110
Cry1Ac SEFV--PGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 VPFVGPVIVSLYTQLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

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120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 YQLYLTALEEWEEENPFRRGFRRGALRDVRRRFEILDSLFTQYMPFSFRVTNFVFPFLTVA
      150      160      170      180      190      200

170      180      190      200      210      220
Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWVWGP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 MAANLHLLLLLKDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTS
      210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE--NFD--GS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 AKQWVDYDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVTDPLGAVNVSSIGS
      270      280      290      300      310      320

290      300      310      320      330
Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITITYTDAH----RGEYYWSGHQIMASPVGFSG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 WYDKAPSPFGVIESSVIRPPHVFYDITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RG
      330      340      350      360      370      380

340      350      360      370      380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 SNLQ-QMYGTNQLNHSSTF-DFTNYDIYKTLKSKDVAFLDIVYPGYTYIF-FGMPEVEVFF
      390      400      410      420      430      440

390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 MVNQLNNTKRLTKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
      450      460      470      480      490

450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 GNTTGLV--PVFSWTHRSADLNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLL
      500      510      520      530      540      550

510      520      530      540      550      560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVDPATA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 QYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610

570      580      590      600      610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEPVPTATL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 NPGEDLTSKTKFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670

620      630      640      650      660      670
Cry1Ac EAENLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKRELSEKV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |115 EAE

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>>gi|17385648|dbj|BAB78602.1| crystal protein CryE6Q [Ba (1254 aa)
      initn: 1567 initl: 360 opt: 860 Z-score: 1002.8 bits: 197.6 E(): 6.2e-47
      Smith-Waterman score: 1795; 32.814% identity (57.096% similar) in 1219 aa overlap
      (77-1182:112-1237)

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50      60      70      80      90      100
Cry1Ac TQFLLESEFVPGAGFVGLVDIIWGIFFGSPQWDAFLVQIEQLINQRIEEFARNQAIARLEG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 AAVQVLNTVIKLLWPDPEKPSSEPAYDIDFIWKELIGRVEILIEEKIDREAYNAIARLRS
      90      100      110      120      130      140

110      120      130      140      150      160
Cry1Ac LSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 LKRALSLEYQESFETWIDDENDPELQEDVRRMRTSTLFLVLTITETFKYSQELNLLTVFV
      150      160      170      180      190      200

170      180      190      200      210      220
Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRY-ND----LTRLIGNYTDHAVRWYNTGLER
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 QAADPHMLLQGVVGVVWGFQDRTVDSFYQNDRGEGLKNLLPKYSDYCTYWDYDQGLNR
      210      220      230      240      250      260

230      240      250
Cry1Ac V-----WGPDSR-----DWIRYNQFRRELTTLVLDIVSLFPNYDSRT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 AKNLKANLSDTVRYPAANLENMSVLQLELDWNLYNDRDMDITLVDLIVAVWPTYDLHY
      270      280      290      300      310      320

260      270      280      290      300      310
Cry1Ac YPIRTV---SQLTREIYTNPVLENFDGSAQGIIEGSIIRSPHLMILNSITITYTDAHR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 YDNGNYGVQSELTRSIYSQAV-GNVMGTVFTKEQYEVSVFVRPPHVLVWLEKMFQIRPTE
      330      340      350      360      370      380

320      330      340      350      360      370
Cry1Ac GEYYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 ----QGAPIDATMAGVS----LYYSYSGWDNIVDD----ILLGYPTYSSSEIRVLKSKS
      390      400      410      420

380      390      400      410      420      430
Cry1Ac NIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDE-EIPPQNNVPPRQGFSHRL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 VIVQDQEKRAIYNTDLQHDKLVDR-FVVFYQNSGVEVNYAGRDNPPSSYKTFAWDITITNYS
      430      440      450      460      470      480

440      450      460      470      480      490
Cry1Ac SHVSMFRSGFSNSSVSIIRAPMFSWIHRSAE-FNNII-ASDSITQIPAVKGNFLFNLS-V
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 SQMTWINGVNVNHFHGYIQAYAPWIPASCEPFNNIVDAEDVITQIPAVKARELYRGARV
      490      500      510      520      530      540

500      510      520      530      540      550
Cry1Ac ISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLNVNWGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi |173 IKGVNNTGGDLV-----SIAPHGLCELYVSPVNVVRYQVRIHACQDPKINLNIGD
      550      560      570      580      590

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Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDGTEFA
gi|252 GTNQNLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEFFMVNQLNNT
350 360 370 380 390 400

Cry1Ac YGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFShRLSHVSMFRSGFSNssVSIIR
gi|252 RkTLKYNpVSKDIIAsTRDSELELPPETSdQPnyESySHRLCHITSIPA--TGNTTGLV-
410 420 430 440 450

Cry1Ac APMFswIHRSAEFNnIIASDSITQIPAVK--GNFLFNgsVIsGPGFTGGDLVRLNssGNn
gi|252 -PVfSWThRSADLNNtIYsDKITQIPAVKcWdNLPfV-PVVKGPgHTGGDLQYnrSTGS
460 470 480 490 500 510

Cry1Ac IQNRgyIEVPIHfPSTSTRYrVRVRYASVtPIHLNvNWGNssIFsNTVPATATSLDNLQs
gi|252 VGTlFLARyGLALEKAG-KYrVRLRYATDADIVLHVn--DAQI---QMPKTMNPGEDLTS
520 530 540 550 560 570

Cry1Ac SDFgyfESAN---AFTSSLG--NIVGVRNfSGTAGVI-IDRFEFIPVtATLEAEYNLER
gi|252 KTFKvADAIITTLNlATdSSlALKHNLGEdPNStLSGIVyVDRIEFIPVD
580 590 600 610 620

Cry1Ac AQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSD

>>gi|25277450|emb|CAD57557.1| unnamed protein product [B (620 aa)
initn: 1098 initl: 505 opt: 856 Z-score: 1002.6 bits: 196.6 E(): 6.3e-47
Smith-Waterman score: 1215; 37.640% identity (66.667% similar) in 627 aa overlap
(22-612:12-619)

Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFV-PGAG
gi|252 MSAGNASEYPGSPeVLVSGQDAAKAA---IDIVGKLLSGLGVFPVFGPIVS
10 20 30 40 50

Cry1Ac FVLGLVDIIWIGfGPsQWDAFLVQIEQLINQRIEEFARNQAIsrLEGLSNlyQIYAESFR
gi|252 LYtQLIDILWpSGEKsQWEIFMEQVEELINQKIAEYARnkALSELEGLGNnyQLYLtALE
60 70 80 90 100 110

Cry1Ac EWEADPT-----NPALREEMRIQFNdmNSALtTAIPLFAVQNYQVPLLSVYVQAANLHLS
gi|252 EWEENPLRMSNGSRALRD-VRNRFELDSLFTQYMPsFRVtNFVFPFLtVYAMAANLHLL
120 130 140 150 160 170

Cry1Ac VLrDVsVfGQRWGFDAATINSRYNDLTRLIGNyTDHAVRwYNTGLERVwGpDSRDWIRYn
gi|252 LLKDasIFGEEWGWStTtINnyDRQMKLTAeYSDHCvKwYETGLAKLkGtSAKQwVDYn
180 190 200 210 220 230

170 180 190 200 210 220
Cry1Ac 240 250 260 270 280 290
QFRRELTlTVLDIVSLFPnyDSrTYPIrTVSQtLREIYtNPVLE-NFD--GSFRGSAQg-

gi|252 QFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVVYTDPLGAVNVSSIGSWYDKAPSF
230 240 250 260 270 280

Cry1Ac --IEGS-IRSPHLMDILNSITITyTDAH----RGEYyWsgHQImAsPvGfSGPEfTFpPly
gi|252 GVIESSVIRPPHFVDYITGLTVYTQSRsISSARyIRHWAGHQISYHRVs-RGSNLQ-QMY
290 300 310 320 330 340

Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLSVLDGTEFA
gi|252 GTNQNLHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEFFMVNQLNNT
350 360 370 380 390 400

Cry1Ac YGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFShRLSHVSMFRSGFSNssVSIIR
gi|252 RkTLKYNpVSKDIIAsTRDSELELPPETSdQPnyESySHRLCHITSIPA--TGNTTGLV-
410 420 430 440 450

Cry1Ac APMFswIHRSAEFNnIIASDSITQIPAVK--GNFLFNgsVIsGPGFTGGDLVRLNssGNn
gi|252 -PVfSWThRSADLNNtIYsDKITQIPAVKcWdNLPfV-PVVKGPgHTGGDLQYnrSTGS
460 470 480 490 500 510

Cry1Ac IQNRgyIEVPIHfPSTSTRYrVRVRYASVtPIHLNvNWGNssIFsNTVPATATSLDNLQs
gi|252 VGTlFLARyGLALEKAG-KYrVRLRYATDADIVLHVn--DAQI---QMPKTMNPGEDLTS
520 530 540 550 560 570

Cry1Ac SDFgyfESAN---AFTSSLG--NIVGVRNfSGTAGVI-IDRFEFIPVtATLEAEYNLER
gi|252 KTFKvADAIITTLNlATdSSlALKHNLGEdPNStLSGIVyVDRIEFIPVD
580 590 600 610 620

Cry1Ac AQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSD

>>gi|25277446|emb|CAD57556.1| unnamed protein product [B (673 aa)
initn: 1129 initl: 505 opt: 856 Z-score: 1002.1 bits: 196.6 E(): 6.8e-47
Smith-Waterman score: 1234; 38.013% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFV-PGAG
gi|252 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPeVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

60 70 80 90 100 110

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Cry1Ac SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|252 VPFVGPVIVSLYTLQIDLILWPSGEKQWEIFMEQVEELINQKIAEYARNKAL SELEGLGNN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADP---TNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|252 YQLYLTALEEWEENPLRMSNGSRALRD-VRNRFEILDSLFTQYMPFSFRVTNFVFPFLTIVY
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|252 AMAANLHLLKLDASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--G
gi|252 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVVYTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH----RGEYYWSGHQIMASVPGFS
gi|252 SWYDKAPSFVGISSVIRPPHFVDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQQL
gi|252 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
gi|252 FMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|252 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPV-PVVGPGGHTGGDL
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
VRLNSSGNIQNRGYIEVPIHFPSTSTRYRVRYASVPIHLNWNWGNSSIFSNTVPAT
gi|252 LQYNRSTGSVGLTFLARYGLALEKAG-KYRVRLRYATDADIVLHVY--DAQI---QMPKT
560 570 580 590 600

Cry1Ac 570 580 590 600 610
ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFGSTAGVI-IDRFEFIPVTAT
gi|252 MNPGEDLTSKTFKVAADAITTLNATDSSSLALKHNLGEPNLSLGIYVVDRIEFIPVDET
610 620 630 640 650 660

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Cry1Ac 620 630 640 650 660 670
LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDEFCLDEKRELSEK
gi|252 YEAE
670

>>gi|25277416|emb|CAD57551.1| unnamed protein product [B (673 aa)
initn: 1129 init1: 505 opt: 856 Z-score: 1002.1 bits: 196.6 E(): 6.8e-47
Smith-Waterman score: 1234; 38.013% identity (66.719% similar) in 634 aa overlap
(22-619:59-673)

Cry1Ac 10 20 30 40 50
CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|252 FANEPTNALQNMDYKDYLLKMSAGNASEYPGSPPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|252 VPFVGPVIVSLYTLQIDLILWPSGEKQWEIFMEQVEELINQKIAEYARNKAL SELEGLGNN
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADP---TNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
gi|252 YQLYLTALEEWEENPLKMSNGSRALRD-VRNRFEILDSLFTQYMPFSFRVTNFVFPFLTIVY
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP
gi|252 AMAANLHLLKLDASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGT
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLE-NFD--G
gi|252 SAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVVYTDPLGAVNVSSIG
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
SFRGSAQG---IEGS-IRSPHLMIDLNSITIIYTDH----RGEYYWSGHQIMASVPGFS
gi|252 SWYDKAPSFVGISSVIRPPHFVDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-R
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
GPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQQL
gi|252 GSNLQ-QMYGTNQNHLHSTSTF-DFTNYYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEVEF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGF
gi|252 FMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRLCHITSIPA--
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
SNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDL
gi|252 TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPV-PVVGPGGHTGGDL
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
VRLNSSGNIQNRGYIEVPIHFPSTSTRYRVRYASVPIHLNWNWGNSSIFSNTVPAT
gi|252 LQYNRSTGSVGLTFLARYGLALEKAG-KYRVRLRYATDADIVLHVY--DAQI---QMPKT
560 570 580 590 600

Cry1Ac 570 580 590 600 610
ATSLDNLQSSDFGYFESAN---AFTSSLG--NIVGVRNFGSTAGVI-IDRFEFIPVTAT
gi|252 MNPGEDLTSKTFKVAADAITTLNATDSSSLALKHNLGEPNLSLGIYVVDRIEFIPVDET
610 620 630 640 650 660

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          510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 DLLQYNRSTGSGVGLTFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMP
          560      570      580      590      600

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          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 KTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNGLGDPNSTLSGIVYVDRIEFIPVD
          610      620      630      640      650      660

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          620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 ETYEAE
          670

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>>gi|71793261|emb|CAJ21083.1| unnamed protein product [B (675 aa)  
 initn: 1129 initl: 505 opt: 854 Z-score: 999.7 bits: 196.2 E(): 9.2e-47  
 Smith-Waterman score: 1234; 37.421% identity (66.667% similar) in 636 aa overlap  
 (22-619:59-675)

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          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

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          60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 VPFVGPVIVSLYTLQDLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100      110      120      130      140

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          120      130      140      150      160
Cry1Ac YQIYAESFREWEADP---TNP---ALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YQLYLTALEEWEENPFRRSGPNSRALRD--VRNRFEILDSLFTQYMPSFRVTFNFEVFPFLT
          150      160      170      180      190      200

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          170      180      190      200      210      220
Cry1Ac VYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 VYAMAANLHLLLLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
          210      220      230      240      250      260

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          230      240      250      260      270      280
Cry1Ac GPDSDRWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLE-NFD-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 GTSARQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
          270      280      290      300      310      320

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          290      300      310      320      330
Cry1Ac -GSFRGSAQG---IEGS-IRSPHLMIDILNSITITYDAH----RGEYYWSGHQIMASPVG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 IGSWDKAPSFVGIESSVIRPPHVFDYITGLTVYQSRSSISSARYIRHWAGHQISYHRVS
          330      340      350      360      370      380

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          340      350      360      370      380
Cry1Ac FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRFPNIGINNO
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 -RGSNLQ-QMYGTNQNLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVYPGTYIF-FGMPEV
          390      400      410      420      430      440

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          390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSGTVDLSLEIPPQNNNVPPRQGFSHRLSHVMFRS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 EFFMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYEESYSHRLCHITSIPA
          450      460      470      480      490      500

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          450      460      470      480      490      500
Cry1Ac GFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLNGSVISGPGFTGG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGG
          510      520      530      540      550

```

```

          510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 DLLQYNRSTGSGVGLTFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMP
          560      570      580      590      600

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```

          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 KTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNGLGDPNSTLSGIVYVDRIEFIPVD
          610      620      630      640      650      660

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          620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 ETYEAE
          670

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>>gi|71793229|emb|CAJ21067.1| unnamed protein product [B (675 aa)  
 initn: 1129 initl: 505 opt: 854 Z-score: 999.7 bits: 196.2 E(): 9.2e-47  
 Smith-Waterman score: 1235; 37.421% identity (66.667% similar) in 636 aa overlap  
 (22-619:59-675)

```

          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

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          60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 VPFVGPVIVSLYTLQDLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100      110      120      130      140

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          120      130      140      150      160
Cry1Ac YQIYAESFREWEADP---TNP---ALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YQLYLTALEEWEENPFRRSGPNSRALRD--VRNRFEILDSLFTQYMPSFRVTFNFEVFPFLT
          150      160      170      180      190      200

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      170      180      190      200      210      220
Cry1Ac VVYQANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 VYAMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
      210      220      230      240      250      260

      230      240      250      260      270      280
Cry1Ac GPDSDRDIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 GTSAKQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
      270      280      290      300      310      320

      290      300      310      320      330
Cry1Ac -GSFRGSAQG---IEGS-IRSPHLM DILNSIT IYTD AH----RGEYYWSGHQIMASPVG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 IGSWYDKAPSPFVIESSVIRPPHVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS
      330      340      350      360      370      380

      340      350      360      370      380
Cry1Ac FSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 -RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEV
      390      400      410      420      430      440

      390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 EFFMVNQLNNTRKTLYKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA
      450      460      470      480      490      500

      450      460      470      480      490      500
Cry1Ac GFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKWDNLFPV-PVVKPGHTGG
      510      520      530      540      550

      510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 DLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
      560      570      580      590      600      610

      570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 KTMNPGEDLTSKTFKVADAITVNLATDSSVAVKHNVGDPNSTLSGIVYVDRIEFIPVD
      610      620      630      640      650      660

      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELS
      : : :
gi|717 ETYEAE
      670

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>>gi|115828972|gb|ABJ38810.1| Sequence 80 from patent US (675 aa)
  initn: 1129 initl: 505 opt: 854 Z-score: 999.7 bits: 196.2 E(): 9.2e-47
Smith-Waterman score: 1234; 37.421% identity (66.667% similar) in 636 aa overlap
(22-619:59-675)

```

```

      10      20      30      40      50
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

      60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VPFVGPVIVSLYTLQILIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

      120      130      140      150      160
Cry1Ac YQIYAESFREWEADP---TNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 YQLYLTALEEEWENPFRRGPNRSRALRD-VRNRFELDSLFTQYMPSFRVTFNFEVPLT
      150      160      170      180      190      200

      170      180      190      200      210      220
Cry1Ac VVYQANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VYAMAANLHLLLLKASIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
      210      220      230      240      250      260

      230      240      250      260      270      280
Cry1Ac GPDSDRDIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 GTSAKQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
      270      280      290      300      310      320

      290      300      310      320      330
Cry1Ac -GSFRGSAQG---IEGS-IRSPHLM DILNSIT IYTD AH----RGEYYWSGHQIMASPVG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 IGSWYDKAPSPFVIESSVIRPPHVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS
      330      340      350      360      370      380

      340      350      360      370      380
Cry1Ac FSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 -RGSNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTL SKDAVLLDIVPGYTYIF-FGMPEV
      390      400      410      420      430      440

      390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 EFFMVNQLNNTRKTLYKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA
      450      460      470      480      490      500

      450      460      470      480      490      500
Cry1Ac GFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKWDNLFPV-PVVKPGHTGG
      510      520      530      540      550

      510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTVP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 DLLQYNRSTGSGVGLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
      560      570      580      590      600      610

      570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 KTMNPGEDLTSKTFKVADAITVNLATDSSVAVKHNVGDPNSTLSGIVYVDRIEFIPVD
      610      620      630      640      650      660

      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELS
      : : :
gi|115 ETYEAE
      670

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```

560      570      580      590      600
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|115 KTMNPGEDLTSKTFKVADAITTVNLTADSSVAVKHNHGDPNSTLSGIVYVDRIEFIPVD
      610      620      630      640      650      660

      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
      : : :
gi|115 ETYEAE
      670

```

>>gi|115828956|gb|ABJ38794.1| Sequence 48 from patent US (675 aa)  
 initn: 1129 initl: 505 opt: 854 Z-score: 999.7 bits: 196.2 E(): 9.2e-47  
 Smith-Waterman score: 1235; 37.421% identity (66.667% similar) in 636 aa overlap  
 (22-619:59-675)

```

      10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

      60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLN
      : : . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

      120      130      140      150      160
Cry1Ac YQIYAESFREWEADP---TNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 YQLYLTALEEWEENPFRSRGPNRSRALRD-VNRNFEILDSLFTQYMPFRVNTFVEPPLT
      150      160      170      180      190      200

```

```

      170      180      190      200      210      220
Cry1Ac VYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 VYAMAANLHLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCWKYETGLAKLK
      210      220      230      240      250      260

```

```

      230      240      250      260      270      280
Cry1Ac GPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLE-NFD-
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 GTSARQWVDYNGFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREYVYTDPLGAVNVSS
      270      280      290      300      310      320

```

```

      290      300      310      320      330
Cry1Ac -GSFRGSAQG---IEGS-IRSPHLMIDILNSITITDAH-----RGEYYSQGHQIMASVPG
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 IGSWDKAPSGVGISSVIRPPHVDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS
      330      340      350      360      370      380

```

```

      340      350      360      370      380
Cry1Ac FSGPEFTFPFLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQ
      : . . . . : : . . . : : . . . : : . . . : : . . . :

```

```

gi|115 -RGSNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEV
      390      400      410      420      430      440

      390      400      410      420      430      440
Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSLDEIPPQNNVPPRQGFSHRSLSHVSMFRS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|115 EFFMVNQLNTRKTLKYNPVSQKDI IASTRDSELELPPETSQDPNYESYSHRLCHITSIPA
      450      460      470      480      490      500

      450      460      470      480      490      500
Cry1Ac GFSNNSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNPLFNGSVISGPGFTGG
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|115 --TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLPPFV-PVVKGPGHTGG
      510      520      530      540      550

```

```

      510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPTSTRYRVRVRYASVTPIHNLVNVNWNSSIFSNTVVP
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 DLLQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMP
      560      570      580      590      600

```

```

      570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVT
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|115 KTMNPGEDLTSKTFKVADAITTVNLTADSSVAVKHNHGDPNSTLSGIVYVDRIEFIPVD
      610      620      630      640      650      660

      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELS
      : : :
gi|115 ETYEAE
      670

```

>>gi|71793223|emb|CAJ21064.1| unnamed protein product [B (675 aa)  
 initn: 1129 initl: 505 opt: 854 Z-score: 999.7 bits: 196.2 E(): 9.2e-47  
 Smith-Waterman score: 1235; 37.264% identity (66.509% similar) in 636 aa overlap  
 (22-619:59-675)

```

      10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

      60      70      80      90      100      110
Cry1Ac SEFV-PGAGFVLGLVDIIWIFGPSQWDAFLVQIEQLINQRIEERFARNQAIISRLGLESLN
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|717 VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

      120      130      140      150      160
Cry1Ac YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLS
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :
gi|717 YQLYLTALEEWEENPFRSRGFRSRGALRD-VNRNFEILDSLFTQYMPFRVNTFVEPPLT
      150      160      170      180      190      200

```

```

      170      180      190      200      210      220
Cry1Ac VYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVW
      : : . . . : : . . . : : . . . : : . . . : : . . . : : . . . :

```

gi|717 VYAMAANLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLK
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
GPDSRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNFVLE-NFD-

gi|717 GTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNVSS
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
-GSFRGSAQG---IEGS-IRSPHLMdILNSITiYTDah----RGEYYWSGHQIMASpVG

gi|717 IGSWYDKAPSFVGISSVIRPPHVFDYITGLTVYtQSRsISSARyIRHWAGHQISYHRVS
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
FSGPEFTFPLYGTMGNAAPQQRIVaQLGQGVYRTLSSTL-----YRRPFNIGINNq

gi|717 -RGSNLQ-QMYGTNQNlHSTStF-DFTNYDIYKTLsKDAVLLDlVYPGYTYIF-FGMPEV
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
QLSVLDGTEFAYGTSSNLPSAVYRkSGTVDSLDEIPPQNNVPPRQGFShRLSHVSMFRS

gi|717 EFFMVNQLNnTRKTLKYNpVSKDIaSTRDSELELPPETSDQPNYEsYSHRLCHITSIPa
450 460 470 480 490 500

Cry1Ac 450 460 470 480 490 500
GFSNSSVSIIRAPMFSWIHRSAEFNNIaSDSITQIPAVK--GNFLFNGSVISGPGFTGG

gi|717 --TGNTTGLV--PVFSWThRSADLNNTIYSDKITQIPAVKcWdNLPFV-PVVKGPgHTGG
510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
DLVRLNssGNNIQNRgyIEVPIHFPStSTRYRVRVRYASVtPIHLNVNwGNSsIFsNTVpT

gi|717 DLLQYnRStGsvGTLFLARyGLALEKAG-KYRVRLRYATDADIVLHVn--DAQI---QMP
560 570 580 590 600

Cry1Ac 570 580 590 600 610
ATATSLDNLQSSDFGYFESANAFTSSLGNIvGVRNFSGT-----AGVI-IDRFEFIPVt

gi|717 KTMNPGEDLTskTFKvADAITVnLATDSSvAVKHnVGEDPNStLSGIVYVDRIEFIPVd
610 620 630 640 650 660

Cry1Ac 620 630 640 650 660 670
ATLEAEYNLERaQkAVNALFTStnQLGLKtnVtDyHIDQVSNLVtYLSDFECLDEKRELS

gi|717 ETYEAE
670

>>gi|115828960|gb|ABJ38798.1| Sequence 56 from patent US (673 aa)
initn: 1121 initl: 497 opt: 850 Z-score: 995.0 bits: 195.3 E(): 1.7e-46
Smith-Waterman score: 1231; 37.125% identity (66.667% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac 10 20 30 40 50
CMQAMDNPNINeCIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLL

gi|115 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPeVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIrLEGLSNL

gi|115 VPFVGPiVSLYtQLIDILWPSGekSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNn
90 100 110 120 130 140

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNPALRE---EMRIQFNdMNSALtTAIPLFAVQNYQVPLLSVYV

gi|115 YQLYLtALEEWEENPFrRGFRrGALRDVrNRFEILDsLFTQYMPsFRVtNFVEVpFLTVYA
150 160 170 180 190 200

Cry1Ac 170 180 190 200 210 220
QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAvRWYNTGLERVWGPd

gi|115 MAANLHLLLLKDasIFGEEGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTs
210 220 230 240 250 260

Cry1Ac 230 240 250 260 270 280
SRDWIRYNQFRRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNFVLE-NFD--GS

gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDITTYPIETKAQLTREVYTDPLGAVNVSSIGs
270 280 290 300 310 320

Cry1Ac 290 300 310 320 330
FRGSAQG---IEGS-IRSPHLMdILNSITiYTDah----RGEYYWSGHQIMASpVGFSG

gi|115 WYDKAPSFVGISSVIRPPHVFDYITGLTVYtQSRsISSARyIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

Cry1Ac 340 350 360 370 380
PEFTFPLYGTMGNAAPQQRIVaQLGQGVYRTLSSTL-----YRRPFNIGINNqQLS

gi|115 SNLQ-QMYGTNQNlHSTStF-DFTNYDIYKTLsKDAVLLDlVYPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac 390 400 410 420 430 440
VLDGTEFAYGTSSNLPSAVYRkSGTVDSLDEIPPQNNVPPRQGFShRLSHVSMFRSGFS

gi|115 MVNQLNnTRKTLKYNpVSKDIaSTRDSELELPPETSDQPNYEsYSHRLCHITSIPa--T
450 460 470 480 490

Cry1Ac 450 460 470 480 490 500
NSSVSIIRAPMFSWIHRSAEFNNIaSDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV

gi|115 GNtTGLV--PVFSWThRSADLNNTIYSDKITQIPAVKcWdNLPFV-PVVKGPgHTGGDLl
500 510 520 530 540 550

Cry1Ac 510 520 530 540 550 560
RLNssGNNIQNRgyIEVPIHFPStSTRYRVRVRYASVtPIHLNVNwGNSsIFsNTVpATa

gi|115 QYnRStGsvGTLFLARyGLALEKAG-KYRVRLRYATDADIVLHVn--DAQI---QMPKtM
560 570 580 590 600 610

Cry1Ac 570 580 590 600 610
TSLDNLQSSDFGYFESANAFTSSLGNIvGVRNFSGT-----AGVI-IDRFEFIPVtATL

gi|115 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGVIYVDRIEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
EAE

>>gi|71793237|emb|CAJ21071.1| unnamed protein product [B (673 aa)
initn: 1121 initl: 497 opt: 850 Z-score: 995.0 bits: 195.3 E(): 1.7e-46
Smith-Waterman score: 1231; 37.125% identity (66.667% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL

gi|717 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL

gi|717 VPFVGPVIVSLYTLQDIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV

gi|717 YQLYLTALEEWEENPFRRGFRRGALRDVRNRFEILDSLFTQYMPFSRVTVNFVPLTVYA
150 160 170 180 190 200

Cry1Ac QAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPD

gi|717 MAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTGTS
210 220 230 240 250 260

Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS

gi|717 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREYVTDPLGAVNVSSIGS
270 280 290 300 310 320

Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITTYTDAH---RGEYYWSGHQIMASVPGFSG

gi|717 WYDKAPSPGVIESSVIRPPHVFDYITGLTVYTSRSISSARIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS

gi|717 SNLQ-QMYGTNQLNHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGSFHRLSHVSMPFRSGFS

gi|717 MVNQLNTRKTKLYNEVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV

gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPGHTGGDLL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSIFSNVTPATA

gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
560 570 580 590 600 610

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL

gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGVIYVDRIEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
EAE

>>gi|71793269|emb|CAJ21087.1| unnamed protein product [B (673 aa)
initn: 1121 initl: 497 opt: 850 Z-score: 995.0 bits: 195.3 E(): 1.7e-46
Smith-Waterman score: 1230; 37.125% identity (66.667% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL

gi|717 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL

gi|717 VPFVGPVIVSLYTLQDIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV

gi|717 YQLYLTALEEWEENPFRRGFRRGALRDVRNRFEILDSLFTQYMPFSRVTVNFVPLTVYA
150 160 170 180 190 200

Cry1Ac QAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPD

gi|717 MAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAKLKGTGTS
210 220 230 240 250 260

Cry1Ac SRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS

```

gi|717 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREVYTDPLGAVNVSSIGS
      270      280      290      300      310      320

```

```

Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITIYTDH----RGEYVWSGHQIMASPVGFSG
      290      300      310      320      330

```

```

gi|717 WYDKAPSPFVIESSVIRPPHVFYDITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RG
      330      340      350      360      370      380

```

```

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
      340      350      360      370      380

```

```

gi|717 SNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEFF
      390      400      410      420      430      440

```

```

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSHVSMFRSGFS
      390      400      410      420      430      440

```

```

gi|717 MVNQLNNTKTKLYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
      450      460      470      480      490

```

```

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
      450      460      470      480      490      500

```

```

gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKWDNLPFV-PVVKGPHTGGDLL
      500      510      520      530      540      550

```

```

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVWGNSSIFSNTVPATA
      510      520      530      540      550      560

```

```

gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610

```

```

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
      570      580      590      600      610

```

```

gi|717 NPGEDLTSKTFKVADAITVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670

```

```

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      620      630      640      650      660      670

```

gi|717 EAE

```

>>gi|115828977|gb|ABJ38814.1| Sequence 88 from patent US (673 aa)
  initn: 1121 initl: 497 opt: 850 Z-score: 995.0 bits: 195.3 E(): 1.7e-46
  Smith-Waterman score: 1230; 37.125% identity (66.667% similar) in 633 aa overlap
  (22-619:59-673)

```

```

Cry1Ac      10      20      30      40      50
      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL

```

```

gi|115 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

Cry1Ac      60      70      80      90      100     110
      SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLBGLSNL

```

```

gi|115 VPFVGVIVSLYTLQILIDLWPSGGEKSQWEIFMEQVELINQKTAEYARNKALSELEGLGNN
      90      100      110      120      130      140

```

```

Cry1Ac YQIYAESFREWEADPTNPALRE----EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
      120      130      140      150      160

```

```

gi|115 YQLYLTALEEEWENPFRRGFRGALRDVNRNFEILDLSLFTQMPSFRVTFVFPPLTVYA
      150      160      170      180      190      200

```

```

Cry1Ac QAANLHLSVLRDVSFVQQRWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
      170      180      190      200      210      220

```

```

gi|115 MAANLHLLLLKASIFGEEWGSTTTINNYDRQMKLTAEYSDHCVKWKYETGLAKLKGTS
      210      220      230      240      250      260

```

```

Cry1Ac SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
      230      240      250      260      270      280

```

```

gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREVYTDPLGAVNVSSIGS
      270      280      290      300      310      320

```

```

Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITIYTDH----RGEYVWSGHQIMASPVGFSG
      290      300      310      320      330

```

```

gi|115 WYDKAPSPFVIESSVIRPPHVFYDITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RG
      330      340      350      360      370      380

```

```

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
      340      350      360      370      380

```

```

gi|115 SNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEFF
      390      400      410      420      430      440

```

```

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSHVSMFRSGFS
      390      400      410      420      430      440

```

```

gi|115 MVNQLNNTKTKLYNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
      450      460      470      480      490

```

```

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
      450      460      470      480      490      500

```

```

gi|115 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKWDNLPFV-PVVKGPHTGGDLL
      500      510      520      530      540      550

```

```

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVWGNSSIFSNTVPATA
      510      520      530      540      550      560

```

```

gi|115 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
      560      570      580      590      600      610

```

```

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
      570      580      590      600      610

```

```

gi|115 NPGEDLTSKTFKVADAITVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDETY
      620      630      640      650      660      670

```

```

      620      630      640      650      660      670

```



```

Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITIYTDH-----RGEYYWSGHQIMASPVGFSG
gi|717 WYDKAPSFVGISSVIRPPHVFDYITGLTVYTSQRSISSARYIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

```

```

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

```

```

Cry1Ac VLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
gi|717 MVNQLNTRKTLKYNPVSVDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490

```

```

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLL
500 510 520 530 540 550

```

```

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSIFSNIVPATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI--QMPKTM
560 570 580 590 600 610

```

```

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDETY
620 630 640 650 660 670

```

```

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKV
gi|717 EAE

```

>>gi|115828979|gb|ABJ38816.1| Sequence 92 from patent US (673 aa)  
 initn: 1118 initl: 494 opt: 847 Z-score: 991.5 bits: 194.6 E(): 2.6e-46  
 Smith-Waterman score: 1227; 36.967% identity (66.667% similar) in 633 aa overlap  
 (22-619:59-673)

```

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|115 FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

```

```

Cry1Ac SEFV-PGAGFVLGLVDIIWGIIFGSPQWDAFLVQIEQLINQRIIEFARNQAIRLEGLSNL
gi|115 VFGPIVSLYTLQIDILWPSGKQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

```

```

120 130 140 150 160

```

```

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|115 YQLYLTALEEWENPFRGRGALRDVNRFEILDSLFTQYMPSPFRVTFNFEVFPFLTVYA
150 160 170 180 190 200

```

```

Cry1Ac QAANLHLSVLRDVSVPFQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115 MAANLHLLLLKASIFGEEWGWSTTTINNYDRQMKLTAEYSDDHCVKWYETGLAKLKGTS
210 220 230 240 250 260

```

```

Cry1Ac SRDWIRYQFRRELTTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDTIITYPMETKAQLTREVYTDPLGAVNVSSIGS
270 280 290 300 310 320

```

```

Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITIYTDH-----RGEYYWSGHQIMASPVGFSG
gi|115 WYDKAPSFVGISSVIRPPHVFDYITGLTVYTSQRSISSARYIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

```

```

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|115 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

```

```

Cry1Ac VLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
gi|115 MVNQLNTRKTLKYNPVSVDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450 460 470 480 490

```

```

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|115 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV-PVVKGPHTGGDLL
500 510 520 530 540 550

```

```

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSIFSNIVPATA
gi|115 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI--QMPKTM
560 570 580 590 600 610

```

```

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|115 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEDPNSTLSGIVYVDRIEFIPVDETY
620 630 640 650 660 670

```

```

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKV
gi|115 EAE

```

Regulatory Product Characterization Team

>>gi|71793241|emb|CAJ21073.1| unnamed protein product [B (673 aa)
initn: 1118 initl: 494 opt: 847 Z-score: 991.5 bits: 194.6 E(): 2.6e-46
Smith-Waterman score: 1228; 36.967% identity (66.667% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIIRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

Cry1Ac YQIYAESFREWEADTPNALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|717 YQLYLTALEEWEENPFRRGFRGALRDVNRNFEILDSLFTQYMPFRVNFVFPFLTVA
150 160 170 180 190 200

Cry1Ac QAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|717 MAANLHLLLLKDAISFGEEWGWSTTTINNYDRQMKLTAEYSDHCWKWYETGLAKLKGTS
210 220 230 240 250 260

Cry1Ac SRDWIRYNQFRRELTLTVDIVSLFPNYDSRTYPIRTVSQLTREIYTNFVLE--NFD--GS
gi|717 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPMETKAQLTREYVYTDPLGAVNVSSIGS
270 280 290 300 310 320

Cry1Ac FRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASVPGFSG
gi|717 WYDKAPSPFVIESSVIRPPHVFDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RG
330 340 350 360 370 380

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRFPNIGINNQQLS
gi|717 SNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKDAVLLDIVYPGYTYIF-FGMPEVEFF
390 400 410 420 430 440

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPQNNVPPRQGFVSHRSLSHVSMFRSGFS
gi|717 MVNQLNNTTRKTLKYNPVSKDIIASTRDSELELPPETSQPNYESYSHRSLCHITSIPA--T
450 460 470 480 490

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|717 GNTTGLV--PVFSWTHRSADLNTIYSDKITQIPAVKCDWNLPPFV-PVVKGPHTGGDLL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNVNWNSSIFSNTVPATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---QMPKTM
560 570 580 590 600 610

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
620 630 640 650 660 670

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKV
gi|717 EAE

>>gi|110734457|gb|ABG88862.1| Cry1-like Bt toxin 3 [Baci (144 aa)
initn: 478 initl: 478 opt: 836 Z-score: 988.5 bits: 191.9 E(): 3.9e-46
Smith-Waterman score: 836; 87.413% identity (93.706% similar) in 143 aa overlap
(1043-1181:1-143)

Cry1Ac LVVPEWEAEVSEQVRVCPGRGYLLRVTAKEGYGEGCVTIHEIENNTDELKFSNCVVEEI
gi|110 EGYGEGCVTIHEIENNTDELKFSNCVVEEV
1020 1030 1040 1050 1060 1070
10 20 30

Cry1Ac YPNNVTTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRREN
gi|110 YPNNVTTCNDYTATQEEYEGTYTSRNRGYDYGAYESNSSVPADYASAYEKAYTDGRRDNP
1080 1090 1100 1110 1120
40 50 60 70 80 90

Cry1Ac CEFNRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|110 CESNRGYGDTPLPAGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEN
1130 1140 1150 1160 1170 1180
100 110 120 130 140

>>gi|71793265|emb|CAJ21085.1| unnamed protein product [B (677 aa)
initn: 1129 initl: 505 opt: 842 Z-score: 985.5 bits: 193.5 E(): 5.7e-46
Smith-Waterman score: 1242; 37.304% identity (66.458% similar) in 638 aa overlap
(22-619:59-677)

Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80

Cry1Ac SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIIRLEGLSNL
gi|717 VPFVGPVIVSLYTLQIDILWPSGEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90 100 110 120 130 140

120 130 140 150 160

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Cry1Ac YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPL
gi|717 YQLYLTALEEWEENPFRRSRLNGSRPALRD--VRRNFELDSLFTQYMPFVRVTFNEVVPF
150 160 170 180 190 200
Cry1Ac 170 180 190 200 210 220
LSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|717 LTVYAMAANLHLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAK
210 220 230 240 250 260
Cry1Ac 230 240 250 260 270 280
VWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLN-FN
gi|717 LKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNV
270 280 290 300 310 320
Cry1Ac 290 300 310 320
D--GSFRGSAQG---IEGS-IRSPHLMIDLNSITIYTDH-----RGEYYWSGHQIMASP
gi|717 SSGISWYDKAPSFVGISSVIRPPHVFYITGLTVYDQSRSSISSARYIRHWAGHQSIVYHR
330 340 350 360 370 380
Cry1Ac 330 340 350 360 370 380
VGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRITLSSTL-----YRRPFNIGIN
gi|717 VS-RGSNLQ-QMYGTNQNLHSTSTF-DFTNYDIYKTLSKDAVLLDIVPGYTYIF-FGMP
390 400 410 420 430 440
Cry1Ac 390 400 410 420 430 440
NQQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFsHRLSHVSMF
gi|717 EVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSDQPNYESYSHRLCHITSI
450 460 470 480 490 500
Cry1Ac 450 460 470 480 490
RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFT
gi|717 PA--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHT
510 520 530 540 550
Cry1Ac 500 510 520 530 540 550
GGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYVRVRYASVTPIHNLVNWGNSISFNSNT
gi|717 GDDLQYNRSTGSVGTFLFLARYGLALEKAG-KYRVRRLRYATDADIVLHVN--DAQI---Q
560 570 580 590 600
Cry1Ac 560 570 580 590 600 610
VPATATSLDNLQSSDFGYFESANAFTSSLGNIIVGRNFSGT-----AGVI-IDRFEFIP
gi|717 MPKTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLGEPNNTLSGIVYVDRIEFIP
610 620 630 640 650 660
Cry1Ac 620 630 640 650 660 670
VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
gi|717 VDETYEAE
670

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>>gi|115828974|gb|ABJ38812.1| Sequence 84 from patent US (677 aa)
initn: 1129 init1: 505 opt: 842 Z-score: 985.5 bits: 193.5 E(): 5.7e-46
Smith-Waterman score: 1242; 37.304% identity (66.458% similar) in 638 aa overlap
(22-619:59-677)
Cry1Ac 10 20 30 40 50
CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPPEVLVSGQDAAKAA---IDIVGKLLSGLG
30 40 50 60 70 80
Cry1Ac 60 70 80 90 100 110
SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|115 VPFVGPVIVSLYTLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGN
90 100 110 120 130 140
Cry1Ac 120 130 140 150 160
YQIYAESFREWEADP-----TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPL
gi|115 YQLYLTALEEWEENPFRRSRLNGSRPALRD--VRRNFELDSLFTQYMPFVRVTFNEVVPF
150 160 170 180 190 200
Cry1Ac 170 180 190 200 210 220
LSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|115 LTVYAMAANLHLLKLDASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAK
210 220 230 240 250 260
Cry1Ac 230 240 250 260 270 280
VWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLN-FN
gi|115 LKGTSAKQWVDYNQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNV
270 280 290 300 310 320
Cry1Ac 290 300 310 320
D--GSFRGSAQG---IEGS-IRSPHLMIDLNSITIYTDH-----RGEYYWSGHQIMASP
gi|115 SSGISWYDKAPSFVGISSVIRPPHVFYITGLTVYDQSRSSISSARYIRHWAGHQSIVYHR
330 340 350 360 370 380
Cry1Ac 330 340 350 360 370 380
VGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRITLSSTL-----YRRPFNIGIN
gi|115 VS-RGSNLQ-QMYGTNQNLHSTSTF-DFTNYDIYKTLSKDAVLLDIVPGYTYIF-FGMP
390 400 410 420 430 440
Cry1Ac 390 400 410 420 430 440
NQQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFsHRLSHVSMF
gi|115 EVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSDQPNYESYSHRLCHITSI
450 460 470 480 490 500
Cry1Ac 450 460 470 480 490
RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFT
gi|115 PA--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHT
510 520 530 360 370 380
Cry1Ac 330 340 350 360 370 380
VGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRITLSSTL-----YRRPFNIGIN
gi|115 VS-RGSNLQ-QMYGTNQNLHSTSTF-DFTNYDIYKTLSKDAVLLDIVPGYTYIF-FGMP
390 400 410 420 430 440
Cry1Ac 390 400 410 420 430 440
NQQLSVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEIPPQNNVPPRQGFsHRLSHVSMF
gi|115 EVEFFMVNQLNTRKTLKYNPVSKDIIASTRDSELELPPETSDQPNYESYSHRLCHITSI
450 460 470 480 490 500
Cry1Ac 450 460 470 480 490
RSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFT
gi|115 PA--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV--PVVKGPGHT
510 520 530 540 550

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170      180      190      200      210      220
Cry1Ac  LSVYYQAAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|115  LTVYAMAANLHLLLLKDKASIFGEEWGWSTTTINNYDRQMKLTAEYSDHCVKWYETGLAK
210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac  VWGPDSDRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NF
gi|115  LKGTSAKQWVDYDQFRREMTLAVLDVVALFPNYDTRTYPMETKAQLTREVYTDPLGAVNV
270      280      290      300      310      320

290      300      310      320
Cry1Ac  D--GSFRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASP
gi|115  SSIGSWYDKAPSFVGISSVIRPPHVFDYITGLTVYTQSRSSISSARYIRHWAGHQISYHR
330      340      350      360      370      380

330      340      350      360      370      380
Cry1Ac  VGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGIN
gi|115  VS-RGSNLQ-QMYGTNQNLSHSTSTF-DFTNYDIYKTLSKDAVLLDIVPGYTYIF-FGMP
390      400      410      420      430      440

390      400      410      420      430      440
Cry1Ac  NQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSHVSMF
gi|115  EVEFFMVNQLNNTKTLKYNPVSKDIIASTRDELELPPETSQDPNYESYSHRLCHITSI
450      460      470      480      490      500

450      460      470      480      490
Cry1Ac  RSGFSSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFT
gi|115  PA--TGNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV--PVVKPGHGT
510      520      530      540      550

500      510      520      530      540      550
Cry1Ac  GGDVLRNLSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNT
gi|115  GGDLLQYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---Q
560      570      580      590      600

560      570      580      590      600      610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTSSLGNIIVGVRNFSGT-----AGVI-IDRFEFIP
gi|115  MKPTMNPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGDPNSTLSGVIYVVDRIEFIP
610      620      630      640      650      660

620      630      640      650      660      670
Cry1Ac  VTATLEAEYNLERAQAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRE
gi|115  VDETYEAE
670

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>>gi|115828963|gb|ABJ38801.1| Sequence 62 from patent US (673 aa)  
 initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46  
 Smith-Waterman score: 1220; 36.967% identity (66.509% similar) in 633 aa overlap  
 (22-619:59-673)

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10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115  FANEPTNALQNMDYKDYLKMSAGNASEYPGSPPEVLVSGQDAAKAA---IDIVGKLLSGLG
30      40      50      60      70      80

60      70      80      90      100      110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNL
gi|115  VPFVGPVIVSLYTLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
90      100      110      120      130      140

120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|115  YQLYLTALEEWEEENPFRFRGFRGALRDVRNRFELDLSLFTQYMPFSRVTNFVFPFLTVYA
150      160      170      180      190      200

170      180      190      200      210      220
Cry1Ac  QAAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115  MAANLHLLLLKDKASIFGEEWGWSTTTINNVDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210      220      230      240      250      260

230      240      250      260      270      280
Cry1Ac  SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE--NFD--GS
gi|115  AKQWVDYDQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREVYTDPLGAVNVSSIGS
270      280      290      300      310      320

290      300      310      320      330
Cry1Ac  FRGSAQG---IEGS-IRSPHLMIDLNSITTYTDAH----RGEYYWSGHQIMASPVGFGS
gi|115  WYDKAPSFVGISSVIRPPHVFDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RG
330      340      350      360      370      380

340      350      360      370      380
Cry1Ac  PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
gi|115  SNLQ-QMYGTNQNLSHSTSTF-DFTNYDIYKTLKDAVLLDIVPGYTYIF-FGMPEVEFF
390      400      410      420      430      440

390      400      410      420      430      440
Cry1Ac  VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSHVSMFRSGFS
gi|115  MVNQLNNTKTLKYNPVSKDIIASTRDELELPPETSQDPNYESYSHRLCHITSIIPA--T
450      460      470      480      490

450      460      470      480      490      500
Cry1Ac  NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|115  GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLPFV--PVVKPGHGTGGDLL
500      510      520      530      540      550

510      520      530      540      550      560
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNTVPATA
gi|115  QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
560      570      580      590      600      610

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          570      580      590      600      610
Cry1Ac  TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
          620      630      640      650      660      670

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          620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKRELSEKV
          :::
gi|115  EAE

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>>gi|115828975|gb|ABJ38813.1| Sequence 86 from patent US (673 aa)  
 initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46  
 Smith-Waterman score: 1219; 36.967% identity (66.509% similar) in 633 aa overlap  
 (22-619:59-673)

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          10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

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          60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100     110     120     130     140

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          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  YQLYLTALEEWEENPFRRGFRRGALRDVRRNFEILDSLFTQYMPFRVTFVFPFLTVYA
          150     160     170     180     190     200

```

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          170     180     190     200     210     220
Cry1Ac  QAAHLHLSVLRDVSVFGQRFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPD
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  MAANLHLLLLKASIFGEEWGWSTTTINNVDVRQMKLTAEYSDHCVKWYETGLAKLKGTG
          210     220     230     240     250     260

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          230     240     250     260     270     280
Cry1Ac  SRDWIRYNQFRELTLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFD--GS
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  AKQWVDYNQFREMFLAVLDVVALFPNYDTITYPLETQAQLTREVYTDPLGAVNVSSIGS
          270     280     290     300     310     320

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          290     300     310     320     330
Cry1Ac  FRGSAQG---IEGS-IRSPHLDILNSITTYTDAH----RGEYWSGHQIMASVPGFSG
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  WYDKAPSGVIESSVIRPPHFVDYITGLTVYTSRSISSARYIRHWAGHQAISYHRVS-RG
          330     340     350     360     370     380

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          340     350     360     370     380
Cry1Ac  PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  SNLQ-QMVGYNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPYGYTYIF-FGMPVEVFF
          390     400     410     420     430     440

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          390     400     410     420     430     440
Cry1Ac  VLDGTEFAYGTSSNLPSAVYRKSGTVDLSLEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  MVNQLNTRKTKLYNPNVSKDIIASTRDSELELPPETSDQPNYESYSHRLCHITSIPA--T
          450     460     470     480     490

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          450     460     470     480     490     500
Cry1Ac  NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPV-PVVKGPGHTGGDLL
          500     510     520     530     540     550

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          510     520     530     540     550     560
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNVTPATA
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM
          560     570     580     590     600     610

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```

          570     580     590     600     610
Cry1Ac  TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|115  NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
          620     630     640     650     660     670

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```

          620     630     640     650     660     670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKRELSEKV
          :::
gi|115  EAE

```

>>gi|71793235|emb|CAJ21070.1| unnamed protein product [B (673 aa)  
 initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46  
 Smith-Waterman score: 1220; 36.967% identity (66.509% similar) in 633 aa overlap  
 (22-619:59-673)

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          10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|717  FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
          30      40      50      60      70      80

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          60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|717  VPFVGPVIVSLYTLQIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN
          90      100     110     120     130     140

```

```

          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|717  YQLYLTALEEWEENPFRRGFRRGALRDVRRNFEILDSLFTQYMPFRVTFVFPFLTVYA
          150     160     170     180     190     200

```

```

          170     180     190     200     210     220
Cry1Ac  QAAHLHLSVLRDVSVFGQRFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPD
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|717  MAANLHLLLLKASIFGEEWGWSTTTINNVDVRQMKLTAEYSDHCVKWYETGLAKLKGTG
          210     220     230     240     250     260

```



```

        620      630      640      650      660      670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      :::
gi|717 EAE

>>gi|71793243|emb|CAJ21074.1| unnamed protein product [B (673 aa)
  initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46
Smith-Waterman score: 1220; 36.967% identity (66.509% similar) in 633 aa overlap
(22-619:59-673)

```

```

          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      ::::: : : . . . . . ::::: : : :
gi|717 FANEPTNALQNMDYKDYLKMSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

          60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      :: : . . . . . ::::: : : : : : : : : : : : : : : : :
gi|717 VPFVGPVIVSLYQLIDILWPSGKESQWEIFMQVEELINQKIAEYARNKALSELEGLGNN
      90      100     110     120     130     140

```

```

          120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
      ::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YQLYLTALEEWEENPFRRGFRGALRDVRRNRFELDLSLFTQYMPFSFRVTFEVPFLTVYA
      150     160     170     180     190     200

```

```

          170     180     190     200     210     220
Cry1Ac QAAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
      ::::: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 MAANLHLLLLKASIFGEEGWSTTTINNVDQRMKLTAEYSDHCVKWYETGLAKLKGTS
      210     220     230     240     250     260

```

```

          230     240     250     260     270     280
Cry1Ac SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREYVTDPLGAVNVSSIGS
      270     280     290     300     310     320

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```

          290     300     310     320     330
Cry1Ac FRGSAQG---IEGS-IRSPHLMIDILNSITITYTDAH----RGEYWSGHQIMASVGVFSG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 WYDKAPSGVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQSISYHRVS-RG
      330     340     350     360     370     380

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          340     350     360     370     380
Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSDAVLLDIVPGYTYIF-FGMPEVEVFF
      390     400     410     420     430     440

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```

          390     400     410     420     430     440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 MVNQLNNTKTLKYNPVSKDIIASTRDSLELPPETSDQPNYESYSHRLCHITSIPA--T

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```

          450     460     470     480     490
Cry1Ac NSSVSIIRAPMPSWIHRSAEFNNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|717 GNTTGLV--PVFSWTHRSADLNNIIYSDKITQIPAVKWDNLFFV-PVVKGPGHTGGDLL
      500     510     520     530     540     550

```

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          510     520     530     540     550     560
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNVTPATA
      . : : . . . . . . . . . . . : : : : : : : : : : : : : : : : :
gi|717 QYNRSTGSVGTFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI--QMPKTM
      560     570     580     590     600     610

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```

          570     580     590     600     610
Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
      . : : : : . . . . . . . . . . . : : : : : . . . . . : : : : :
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVGEDPNSTLSGVIYVDRIEFIPVDETY
      620     630     640     650     660     670

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          620     630     640     650     660     670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      :::
gi|717 EAE

```

```

>>gi|115828959|gb|ABJ38797.1| Sequence 54 from patent US (673 aa)
  initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46
Smith-Waterman score: 1220; 36.967% identity (66.509% similar) in 633 aa overlap
(22-619:59-673)

```

```

          10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      ::::: : : . . . . . ::::: : : :
gi|115 FANEPTNALQNMDYKDYAVGSAGNASEYPGSPEVLVSGQDAAKAA---IDIVGKLLSGLG
      30      40      50      60      70      80

```

```

          60      70      80      90      100     110
Cry1Ac SEFV-PGAGFVLGLVDIIWGI FGP SQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
      :: : . . . . . ::::: : : : : : : : : : : : : : : : :
gi|115 VPFVGPVIVSLYQLIDILWPSGKESQWEIFMQVEELINQKIAEYARNKALSELEGLGNN
      90      100     110     120     130     140

```

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          120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
      ::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 YQLYLTALEEWEENPFRRGFRGALRDVRRNRFELDLSLFTQYMPFSFRVTFEVPFLTVYA
      150     160     170     180     190     200

```

```

          170     180     190     200     210     220
Cry1Ac QAAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
      ::::: : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 MAANLHLLLLKASIFGEEGWSTTTINNVDQRMKLTAEYSDHCVKWYETGLAKLKGTS
      210     220     230     240     250     260

```

```

          230     240     250     260     270     280
Cry1Ac SRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREYVTDPLGAVNVSSIGS

```

```

270      280      290      300      310      320
Cry1Ac  290      300      310      320      330
FRGSAQG---IEGS-IRSPHLMILNSITITYTDAH----RGEYYWSGHQIMASVPGFSG
gi|115  WYDKAPSFVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RG
330      340      350      360      370      380

```

```

340      350      360      370      380
Cry1Ac  PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|115  SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390      400      410      420      430      440

```

```

390      400      410      420      430      440
Cry1Ac  VLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
gi|115  MVNQLNNTKTKLKNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450      460      470      480      490

```

```

450      460      470      480      490      500
Cry1Ac  NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|115  GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV-PVKGPGHTGGDLL
500      510      520      530      540      550

```

```

510      520      530      540      550      560
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTVPATA
gi|115  QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI--QMPKTM
560      570      580      590      600      610

```

```

570      580      590      600      610
Cry1Ac  TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|115  NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
620      630      640      650      660      670

```

```

620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|115  EAE

```

>>gi|115828980|gb|ABJ38817.1| Sequence 94 from patent US (673 aa)  
 initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46  
 Smith-Waterman score: 1219; 36.967% identity (66.509% similar) in 633 aa overlap  
 (22-619:59-673)

```

10      20      30      40      50
Cry1Ac  CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
gi|115  FANEPTNALQNM DYKDYLKMSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLSGLG
30      40      50      60      70      80

```

```

60      70      80      90      100     110
Cry1Ac  SEFV-PGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI RLEGLSNL
gi|115  VPFVGPVIVSLYTLQDLIDLWPSGEEKSQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN

```

```

90      100     110     120     130     140
Cry1Ac  120     130     140     150     160
YQIYAESFREWEADPTNPALRE----EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|115  YQLYLTALEEEENPFRGRFRRGALRDVNRNFEILDLSLFTQYMPSFRVNFVFPFLTVA
150     160     170     180     190     200

```

```

170     180     190     200     210     220
Cry1Ac  QAAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|115  MAANLHLLLKLDASIFGEEWGWSTTTINNVDVDRQMKLTAEYSDHCVKWYETGLAKLKGTS
210     220     230     240     250     260

```

```

230     240     250     260     270     280
Cry1Ac  SRDWIRYQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLE-NFD--GS
gi|115  AKQWVDYNQFRREMTLAVLDVVALFPNYDTITYPIETKAQLTREVYTDPLGAVNVSSIGS
270     280     290     300     310     320

```

```

290     300     310     320     330
Cry1Ac  FRGSAQG---IEGS-IRSPHLMILNSITITYTDAH----RGEYYWSGHQIMASVPGFSG
gi|115  WYDKAPSFVIESSVIRPPHVFDYITGLTVYTSRSISSARYIRHWAGHQISYHRVS-RG
330     340     350     360     370     380

```

```

340     350     360     370     380
Cry1Ac  PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL-----YRRPFNIGINNQQLS
gi|115  SNLQ-QMYGTNQLHSTSTF-DFTNYDIYKTLKSKDAVLLDIVPGYTYIF-FGMPEVEFF
390     400     410     420     430     440

```

```

390     400     410     420     430     440
Cry1Ac  VLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
gi|115  MVNQLNNTKTKLKNPVSKDIIASTRDSELELPPETSQPNYESYSHRLCHITSIPA--T
450     460     470     480     490

```

```

450     460     470     480     490     500
Cry1Ac  NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV
gi|115  GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDNLFPV-PVKGPGHTGGDLL
500     510     520     530     540     550

```

```

510     520     530     540     550     560
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNVWGNSSIFSNTVPATA
gi|115  QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI--QMPKTM
560     570     580     590     600     610

```

```

570     580     590     600     610
Cry1Ac  TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|115  NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNVEDPNSTLSGIVYVDRIEFIPVDETY
620     630     640     650     660     670

```

```

620     630     640     650     660     670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV

```

gi|115 EAE

>>gi|71793267|emb|CAJ21086.1| unnamed protein product [B (673 aa)
initn: 1110 initl: 486 opt: 839 Z-score: 982.0 bits: 192.9 E(): 8.9e-46
Smith-Waterman score: 1219; 36.967% identity (66.509% similar) in 633 aa overlap
(22-619:59-673)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
gi|717 FANEPTNALQNDYKDYAVGSAGNASEYPGSPEVLVSGQDAKAA---IDIVGKLLSGLG
Cry1Ac SEFV-PGAGFVLGVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGSLN
gi|717 VPFVGPVIVSLYTLIDILWPSGKESQWEIFMEQVEELINQKIAEYARNKALSELEGLGNN

Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYV
gi|717 YQLYLTALEWEENPFRGFRGALRDVNRNRFELDSLFTQYMPFRVNTFEVPLTVYA

Cry1Ac QAAHLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPD
gi|717 MAANLHLLLLKASIFGEEWGSTTTINNVDVDRQMKLTAEYSDHCVKWYETGLAKLKGT

Cry1Ac SRDWIRYNQFRELTLTVDIVSLFPNYDSRTYPIRTVSQLTREIYTNFVLE-NFD--GS
gi|717 AKQWVDYNQFREMFLAVLDVVALFPNYDTITYPITKAQLTREVYTDPLGAVNVSSIGS

Cry1Ac FRGSAQG---IEGS-IRSPHLMILNSITITYTDAH----RGEYYWSGHQIMASVPGFSG
gi|717 WYDKAPSPGVIESSVIRPPHFVDYITGLTVYTQSRSSISSARYIRHWAGHQISYHRVS-RG

Cry1Ac PEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL-----YRRPFNIGINNQQLS
gi|717 SNLQ-QMYGTNQNHLSTSTF-DFTNYDIYKTLKDAVLLDIVPYGYTYIF-FGMPEVEFF

Cry1Ac VLDGTEFAYGTSSNLPASVYRKSQVVDLSDLEIPPQNNVPPRQGFSHRSLSHVSMFRSGFS
gi|717 MVNQLNNTTRKTLKYNPVSKDIIASTRDSELELPPETSQDPNYESYSHRSLCHITSIPA--T

Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK--GNFLFNGSVISGPGFTGGDLV

gi|717 GNTTGLV--PVFSWTHRSADLNNTIYSDKITQIPAVKCDWNLFPFV-PVVKGPHTGGDLL
500 510 520 530 540 550

Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHLNVNWNSSIFSNTVPATA
gi|717 QYNRSTGSGVTLFLARYGLALEKAG-KYRVRLRYATDADIVLHVN--DAQI---QMPKTM

Cry1Ac TSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGT-----AGVI-IDRFEFIPVTATL
gi|717 NPGEDLTSKTFKVADAITTVNLATDSSVAVKHNLDGEPNSTLSGIVYVDRIEFIPVDETY

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
gi|717 EAE

>>gi|110734455|gb|ABG88861.1| Cry1-like Bt toxin 2 [Baci (144 aa)
initn: 478 initl: 478 opt: 820 Z-score: 969.6 bits: 188.4 E(): 4.4e-45
Smith-Waterman score: 820; 86.014% identity (93.007% similar) in 143 aa overlap
(1043-1181:1-143)

Cry1Ac LVVPEWEAEVSEQVRVCPGRGYLLRVTAAYKEGYGECVTHIEIENNTDELKFSNCEVEEI
gi|110 EGYGECVTHIEIENNTDELKFSNCEVEEI

Cry1Ac YPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEKSYTDGRRNP
gi|110 YPNNTVTCINATQEEYEGTYTSRNRGYDGAYESNSSVVPADYASAYEKAYTDGRRNP

Cry1Ac CEFNRGYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|110 CESNRGYGDTPLPAGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEN

>>gi|15110444|gb|AAE68108.1| Sequence 27 from patent US (655 aa)
initn: 726 initl: 400 opt: 819 Z-score: 958.6 bits: 188.5 E(): 1.8e-44
Smith-Waterman score: 904; 32.063% identity (61.746% similar) in 630 aa overlap
(20-617:57-655)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|151 YPLASDPNAAFQNMNYKEYLQTYDGYTGSGLINPNSINPRDLVQTG---INIVGRILGF

Cry1Ac LLESEFVPGAG---FVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRL
gi|151 LG---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEBELIDQKISAQVVRNALDDLT

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          90      100      110      120      130      140
Cry1Ac  110      120      130      140      150      160
GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPL
gi|151  GLHDYEEYLAALEEWLERP-NGARANLVTQRFENLHTAFVTRMPSFGTGPQSQRDAVAL
          150      160      170      180      190
Cry1Ac  170      180      190      200      210      220
LSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|151  LTVYAQAANLHLLKDAEIIYGARWGLQQGQINLYFNAQQERTRIIYTNHCVETYNRGLSD
          200      210      220      230      240      250
Cry1Ac  230      240      250      260      270      280
VWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNLF-
gi|151  VRGTNTESWLNHYHRFRREMTLMAMDVLALFPFYNVRYQYPNGANPQLTREIYTDPIVYNPP
          260      270      280      290      300      310
Cry1Ac  290      300      310      320
--DGSFR-----GSAQIEGS-IRSPHLMIDLNSITI---YTDHRGEY--YWSGHQ
gi|151  ANQGCRRWGNPNYNTFSELENAFIRPPHLFERLNRLTISRNYTAPTNTSFLDYWSGHT
          320      330      340      350      360      370
Cry1Ac  330      340      350      360      370      380
IMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSITLYRRPF-NIGINNQ
gi|151  LQSQHA--NNPTTYETSQGITS---NTRLFNTTNGA--RAIDSRA--RNFGNLYANLYG
          380      390      400      410      420      430
Cry1Ac  390      400      410      420      430      440
LSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIIPPQNNVPPRQGFSHRLSHVSMFRSG
gi|151  VSSLNI--FPTGMSEITNAANTCRQDLTTEELPLENNNF-----NLLSHVTFLRFN
          440      450      460      470      480
Cry1Ac  450      460      470      480      490      500
FSNSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGG
gi|151  TTQGGPLATLGFVPTYVWTRVDVFTNTITADRITQLPWVKASEIGGGTTVVKGPGFTGG
          490      500      510      520      530      540
Cry1Ac  510      520      530      540      550      560
DLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRYASVTPHILNVNWNWSSIFSNTVVP
gi|151  DILR-RTDGGAV---GTIRANVNAPLTQ-QYRIRIRYASTTSFVNVNL-FVNNSAAGFTLP
          550      560      570      580      590
Cry1Ac  570      580      590      600      610
ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEPVTTATLE
gi|151  STMAQNGSLTYESFNTLEVHTHTIRFSQSDTTLRLNIFPISISGQEVVYVDKLEIVPINPTRE
          600      610      620      630      640      650
Cry1Ac  620      630      640      650      660      670
AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK

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>>gi|42682722|gb|AAS28785.1| Sequence 27 from patent US (655 aa)
  initn: 726 initl: 400 opt: 819 Z-score: 958.6 bits: 188.5 E(): 1.8e-44
Smith-Waterman score: 904; 32.063% identity (61.746% similar) in 630 aa overlap
(20-617:57-655)
          10      20      30      40
Cry1Ac  CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
          50      60      70      80
gi|426  YPLASDPNAAFQNMNYKEYLQTYDGYTGSLINPNLSINPRDVLQGTG---INIVGRILGF
          30      40      50      60      70      80
Cry1Ac  50      60      70      80      90      100
LLSEFVPGAG---FVLGLVDIIWGFIFGSPQWDAFLVQIEQLINQRIIEEFARNQAISRLE
gi|426  LG---VPFAGQLVTFYTFLLNQLWPTNDNAVWEAFMAQIEELIDQKISAQVVRNALDDLT
          90      100      110      120      130      140
Cry1Ac  110      120      130      140      150      160
GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPL
gi|426  GLHDYEEYLAALEEWLERP-NGARANLVTQRFENLHTAFVTRMPSFGTGPQSQRDAVAL
          150      160      170      180      190
Cry1Ac  170      180      190      200      210      220
LSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLER
gi|426  LTVYAQAANLHLLKDAEIIYGARWGLQQGQINLYFNAQQERTRIIYTNHCVETYNRGLSD
          200      210      220      230      240      250
Cry1Ac  230      240      250      260      270      280
VWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNLF-
gi|426  VRGTNTESWLNHYHRFRREMTLMAMDVLALFPFYNVRYQYPNGANPQLTREIYTDPIVYNPP
          260      270      280      290      300      310
Cry1Ac  290      300      310      320
--DGSFR-----GSAQIEGS-IRSPHLMIDLNSITI---YTDHRGEY--YWSGHQ
gi|426  ANQGCRRWGNPNYNTFSELENAFIRPPHLFERLNRLTISRNYTAPTNTSFLDYWSGHT
          320      330      340      350      360      370
Cry1Ac  330      340      350      360      370      380
IMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSITLYRRPF-NIGINNQ
gi|426  LQSQHA--NNPTTYETSQGITS---NTRLFNTTNGA--RAIDSRA--RNFGNLYANLYG
          380      390      400      410      420      430
Cry1Ac  390      400      410      420      430      440
LSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIIPPQNNVPPRQGFSHRLSHVSMFRSG
gi|426  VSSLNI--FPTGMSEITNAANTCRQDLTTEELPLENNNF-----NLLSHVTFLRFN
          440      450      460      470      480
Cry1Ac  450      460      470      480      490      500
FSNSS--VSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGG
gi|426  TTQGGPLATLGFVPTYVWTRVDVFTNTITADRITQLPWVKASEIGGGTTVVKGPGFTGG
          490      500      510      520      530      540
Cry1Ac  510      520      530      540      550      560
DLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRYASVTPHILNVNWNWSSIFSNTVVP
gi|426  DILR-RTDGGAV---GTIRANVNAPLTQ-QYRIRIRYASTTSFVNVNL-FVNNSAAGFTLP
          550      560      570      580      590
Cry1Ac  570      580      590      600      610
ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEPVTTATLE
gi|426  STMAQNGSLTYESFNTLEVHTHTIRFSQSDTTLRLNIFPISISGQEVVYVDKLEIVPINPTRE
          600      610      620      630      640      650
Cry1Ac  620      630      640      650      660      670
AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK

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Regulatory Product Characterization Team

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          510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPHILNVLNWNSSIFSNTVPT
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|426 DILR-RTDGGAV---GTIRANVNAPLTQ-QYRIRLRYASTTSFVVNL-FVNNSAAGFTLP
          550      560      570      580      590

          570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLE
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|426 STMAQNGSLTYESFNTLEVTHTIRFSQSDTTLRLNIFPISISGQEVVYDKLEIVPINPTRE
          600      610      620      630      640      650

          620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK

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>>gi|19386614|dbj|BAB72016.2|mosquitocidal toxin [Bacil (660 aa)
  initn: 677 initl: 183 opt: 809 Z-score: 946.8 bits: 186.3 E(): 8.2e-44
Smith-Waterman score: 954; 31.520% identity (63.520% similar) in 625 aa overlap
(33-635:64-660)

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          10      20      30      40      50      60
Cry1Ac QAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEFVPGAGFVL
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 SLASMQNTNYKDWLTMCDRTDLDVLSRRGAVSTGVMLSTLSSL--FGIPLIGEGIDL
          40      50      60      70      80      90

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          70      80      90      100     110
Cry1Ac GLVDIIWGF-GPSQ--WDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFR
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 GAADFLWPESDGGHQYTWEDLMNHIEELMDERLETEKRTTALDDLRGLKALLGLFRDAFD
          100     110     120     130     140     150

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          120     130     140     150     160     170
Cry1Ac EWEADPTNPALREEMRIQFNDMNSALTTAIP-LFAVQNYQVPLLSVYVQAANLHLSVLRD
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 SWEKNQNDPIAKNRVGGYFEDVHTHFVKDMASIFSATNIEVLLLPVYAQAANLHLLLLRE
          160     170     180     190     200     210

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          180     190     200     210     220     230
Cry1Ac VSVFQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL--ERVWGPDSRDWIRYNQF
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 GVIYGSRWGI-APAADFVYHDQLLKYTAIYANHCVTWYNNGLAQQKELFAKSPNWNRFNAY
          220     230     240     250     260     270

```

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          240     250     260     270     280     290
Cry1Ac RRELTLTVDLIVSLFPNYSRTY--PIRTVSQLTREIYTNPLENFDGSRFGSAQIEGS
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 RRDMTITVLDIIFPTDARLYTKPIKT--ELTREIYSDVLNLDVYGVQQTDLKNKEAA
          280     290     300     310     320

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          300     310     320     330     340
Cry1Ac I-RSPHLMIDILNSITITDAHRGEY-YW---SGHQIMASPVGFSGPEFTFFPLYGTMGNAA
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 FTRSPHLVTRLRGDFDYT---RTKYAYWRYLGHNTYFSFTG-NGTIYSSFNWYDMDM
          330     340     350     360     370     380

```

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          350     360     370     380     390     400
Cry1Ac PQQRIVAQLGQGVYRTLSSTLYR-RPFN--IGINNQLSVLDGTEFAYGTSSNLPSAVYR
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .

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gi|193 TKSTINIPDYANIYKLWTKSYTNISPYTDPVGISQMQLTNNQQLTY-TGTSAPKYVPR
          390     400     410     420     430     440

          410     420     430     440     450     460
Cry1Ac KSGTVDLDEIIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEF
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 -----ETFFEIPPTDEKPLTYENYSHILSYMTSAQH-FGDKKIGY----TFAWMHESVDF
          450     460     470     480     490

          470     480     490     500     510     520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 DNRVDPDKITQIPAVKGDYLYQYGVKQGPQHTGGDLVSMIRT----DR--LGINVYFPQ
          500     510     520     530     540

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          530     540     550     560     570     580
Cry1Ac TSTRYRVRYASVTPHILNVLNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSS
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 P-LDYRIRIRYSTSSNGYLYIYSPNTKIVYLPPTTLVLDGQPTDPMDFSAFRVVEVPASF
          550     560     570     580     590     600

          590     600     610     620     630     640
Cry1Ac LGNIVGVRNFSGTAG---VIIDRFEFIP-VTATLEAE--YNLERAQKAVNALFTSTNQLG
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|193 RASVAGYTNFTIEAGFGPVYIDKIEFIPDNTTLEIEGGDRLEKTKNAVNDLFTN
          610     620     630     640     650     660

```

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          650     660     670     680     690     700
Cry1Ac LKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQ

```

```

>>gi|51998363|emb|CAH33953.1|unnamed protein product [B (561 aa)
  initn: 1125 initl: 328 opt: 807 Z-score: 945.5 bits: 185.9 E(): 9.6e-44
Smith-Waterman score: 1032; 36.411% identity (60.627% similar) in 574 aa overlap
(629-1181:1-483)

```

```

          600     610     620     630     640     650
Cry1Ac TAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVT
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|519                                     MSPMFTSSTKNTLKIETTDYIEDQAAISIE
                                     10      20      30

```

```

          660     670     680     690     700     710
Cry1Ac YLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDD
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|519 CMSDEQNPEIKIMLWDEIKLAKQLSQRNLLQNGDFSGND-----WTFGNDIIGSNNP
          40      50      60      70      80

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          720     730     740     750     760     770
Cry1Ac VFKENYVTLSGTFD---ECYPTYLYQKIDESKLKAFTRYQLRGIYEDSODLEIYSIRYNA
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|519 IFKGFLOMRGARDIYGTLLFPPTYICQKIDESKLKPYTRYRVRFVGGSSKDLKLMVTRYGK
          90     100     110     120     130     140

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          780     790     800     810     820
Cry1Ac KHETV-NVPGTSLWPLSAQSPIGKCGEPNRC-----APHLEWNPDLDLDCSC--
      . . . . . : : : . . . . . : : : . . . . . : : : . . . . . : : : . . . . .
gi|519 EIDAIMNVND----LAYMQPNPSCGD-YRCESSQYVSQGYPTPDGYAPDMY-ACQP
          150     160     170     180     190

```

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      830      840      850      860      870
Cry1Ac ---RDGEKCAHSHHFLSLDIDVGCDDLNEGLGVVWVIFKIKTQDGHARLGNLFFLEEKPLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 NIDRKHVKC-HDRHPDFHIDTGEVDNTNTNVGIDVLLKISNPDGYATVGNLEVIEEGPLT
      200      210      220      230      240      250

      880      890      900      910      920      930
Cry1Ac GEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 GEALAHVKQKEKKKWKQHMKEKRWETQQAYDPAKQAVDALFTNEQ--ELHYHTLDHIQNA
      260      270      280      290      300      310

      940      950      960      970      980      990
Cry1Ac DKRVHSIREAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCNV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 DRLVQSIPIVYVHNWLPNAPGMNYDVYQELNARIMQGYNLDARNVITNGDFTQGLQGWHA
      320      330      340      350      360      370

      1000     1010     1020     1030     1040     1050
Cry1Ac KGHVDVEEQNNQRSVLVPEWEAEVSVQEVVRCPRGRGYILRVYTAYKEGEGCVTIIHEIEN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 TGNAAVQ-QMDGASVVLVLSNWSAGVSNLHAQDHHGYLVRVIAKKEGPGKGYVTMMDCNG
      380      390      400      410      420      430

      1060     1070     1080     1090     1100     1110
Cry1Ac NTDLKFNSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVPADYASVYEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 KQETLKFTSCEE-----
      440

      1120     1130     1140     1150     1160     1170
Cry1Ac KSYTDGRRENPECFNRYRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVEL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 519 -----GYMTKTVEVFPESDRVRIEIGTEGTFYIDSIEL
      450      460      470

      1180
Cry1Ac LLMEE
      : :
gi | 519 LCMQGYDNNNNLHTGNMYEQSYNGNYNQNTSDVYYQGYTNNYNQDSSNMYNQNYTNNDDL
      480      490      500      510      520      530

>>gi|62997562|gb|AA24695.1| Cry [Bacillus thuringiensis (1134 aa)
      initn: 2031 initl: 577 opt: 804 Z-score: 937.4 bits: 185.4 E(): 2.7e-43
      Smith-Waterman score: 2157; 36.871% identity (66.277% similar) in 1112 aa overlap
      (7-1067:8-1090)

      10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNP--EVEVLGGERI-----ETGYTPIDISLSLTQFLL
      : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi | 629 MNSNDSQNHDKLEICSNASLLSTPPYKTEYYEGEVLMDTIPFSSGKSAAQMGTSIVGQIL
      10      20      30      40      50      60

      60      70      80      90      100
Cry1Ac SEFVPGAGFVL-----GLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEAFARNQAI SRL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 G--VLGVFPALQVTNLYSSLLDTLWPD-GKSQWEIFMEQVEEIVDQKIENYARNKALAE L
      70      80      90      100      110

```

```

      110      120      130      140      150      160
Cry1Ac EGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 EGLGNNFVYLEALELNWQSNTRDI---NDVKIRFISLDSLFTQSMPSFRIEGFQLPLLSV
      120      130      140      150      160      170

      170      180      190      200      210      220
Cry1Ac YVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 YAQAANLHLLLRDATTFGKEWGLDSATMDSYKQKALSAEYSDHCVKWYKNGLNKLSK
      180      190      200      210      220      230

      230      240      250      260      270      280
Cry1Ac PDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV---LENF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 STAKDWVKNFQFRREMLTVLDVVALFPNYDAKIYPMQIVTQLTREVVYDTPVGMTNLPNG
      240      250      260      270      280      290

      290      300      310      320      330      340
Cry1Ac DGSFRGSAQG---IEGS-IRSPHLMIDILNSITIIY-----TDAHRGEYYWSGHQIMASVPG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 IGSWYDIAPTFATIENAVIRKPHLDFDIRNLVYVFGDRGASANRSMKFWNGHEIFYANIG
      300      310      320      330      340      350

      340      350      360      370      380      390
Cry1Ac FSGPEFTFPLYGTMG--NAAPQQRIVAQLGQ----GVYRTLSTLYRPFNIGINNQQLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 -SSVFFQVYNYVKLGSNNYPIVVDRIYQTESLAGCIYDIIPGYTYKF-FGAPKVEFH
      360      370      380      390      400      410

      390      400      410      420      430      440
Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 VVDRRN-NTGIFTFNPFGQIIQNVQNSLSQLPLESLDEPAYEAYSHRLCHVTLPVPPG-N
      420      430      440      450      460      470

      450      460      470      480      490      500
Cry1Ac NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK---GNFLFNGSVISGPGFTGGD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 NSNYEGL--PVYSWTHKSASLENNIYDPKITQIPAVKSFPGGQW--GGVEAGPGFTGGD
      480      490      500      510      520

      510      520      530      540      550
Cry1Ac LVRLNSSGNNIQRNGYIEVPIHFPSTSTR--YRVRVRYASVTPI---HLNVNWNQNS-IF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 VTKSVTSEATTILRDVVKLAVTIPQDSIKQYRVRIRYASQTDIPATFFTSDSGNRDFVL
      530      540      550      560      570      580

      560      570      580      590      600      610
Cry1Ac SNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAG---VIIDRFEFIPV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 KSTTTAASNAFENYKFFQYIDIPGTIEFTK-VNEIVTVYLHAYKVNHHVNDIKVEFIPV
      590      600      610      620      630      640

      620      630      640      650      660      670
Cry1Ac TATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi | 629 DNNFARKQLETSEFFAKKLLDTTKE-SLDREVTDYQIDYAKLVCEVSDDELYPMEKQEL
      650      660      670      680      690      700

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      680      690      700      710      720      730
Cry1Ac  SEKVKHAKRLSDERNLLQDSNFKDINRQFERGWGGSTGITIQGGDDVFKENYVTLSGFTSD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  LNIIVTTAKKLSQDRNLLQDIDFSAINR--ENGWIGSRGIEGTEGNINPKSRVRLPGARN
      710      720      730      740      750      760

```

```

      740      750      760      770      780
Cry1Ac  ---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRYNAKHETVNVPGTGLSW
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  IDGKIDSTYFYQKINASKLKPYTRYELRGRIESSKLEIYLIHNNANRIKKNVGNNSL-
      770      780      790      800      810      820

```

```

      790      800      810      820      830      840
Cry1Ac  PLSAQSPIKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHHS--HHFSLDIDVGTDLNEDL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  -LNSYNEIDPC--ISKCSNHI-----LSIEEAELDMNHNTHNPFHFSLCIDTGDLDLNKNI
      830      840      850      860      870

```

```

      850      860      870      880      890      900
Cry1Ac  GVWVFIKIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  GIWVAFKISDLNGYAELRNIECIEVEPLFGEALEKLLKQEQEWTRTENKQYEESSKIRAV
      880      890      900      910      920      930

```

```

      910      920      930      940      950      960
Cry1Ac  AKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPELSVIPGVNAAIPEELEG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  AIKAVEQLFEDSSYQKLRPELDSLNSKAENLVNSIPYVSNDFWFSYVPGINHTVVEELKT
      940      950      960      970      980      990

```

```

      970      980      990      1000      1010      1020
Cry1Ac  RIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNQSRVSVLPVEWAEVQSQEVRV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  KIQLAFALYRHRNSIQNGDFKNGLSWTVTSDVVVEE-NQIDPELVISNWSSQVSQDVVV
      1000      1010      1020      1030      1040      1050

```

```

      1030      1040      1050      1060      1070      1080
Cry1Ac  CPGRGYILRVYAYKEGYGECVTHIEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  EANHRYLLRVYAYKEGYGECVTHIEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQE
      1060      1070      1080      1090      1100      1110

```

```

      1090      1100      1110      1120      1130      1140
Cry1Ac  EYGGAYTSRNRGYNAPSPADYASVYEEKSYTDGRRENPCFENRGYRDYTPPLPVGYVTK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|629  YIKIHETDGIFRIKNIDFTLNKK
      1120      1130

```

>>gi|162767649|emb|CAP58828.1| unnamed protein product [ (648 aa)  
 initn: 1229 initl: 674 opt: 788 Z-score: 922.1 bits: 181.8 E(): 1.9e-42  
 Smith-Waterman score: 1202; 36.677% identity (65.569% similar) in 668 aa overlap  
 (4-624:2-648)

```

      10      20      30      40
Cry1Ac  CMQAMDNPNINCEIPYNCLSN--PEVEVLGGERIETGY----TPID--ISLSLTQF--
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  MATSNRKNENEI--NAVSNHSAQMDLLPDARIEDSLCIAEGNNDIPFVSASTVQTGI
      10      20      30      40      50

```

```

      50      60      70      80      90
Cry1Ac  ----LLSEF-VPGAG---FVLGLVDIIWGFQPSQWDAFLVQIEQLINQRLEEFARNO
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  NIAGRILGLVGVFPFAGQLASFYSFLVGLWLP-RGRDQWEIFLEHVEQLINQQTENARNT
      60      70      80      90      100      110

```

```

      100      110      120      130      140      150
Cry1Ac  AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  ALARLQGLGDSFRAYQOSLEDWLENRDDARTRSVLHTQYIALELDFLNAMPLFAIRNQEV
      120      130      140      150      160      170

```

```

      160      170      180      190      200      210
Cry1Ac  PLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  PLLMVYAQAANLHLLLRDASLFGSEFGLTSQEIQRYYERQVETRDYSDYCVWEYNTGL
      180      190      200      210      220      230

```

```

      220      230      240      250      260      270
Cry1Ac  ERVWGPDSRDWIRYQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLE-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  NSLRGTNAASWVRYNQFRDLTLGLVLDLVALFPYDTRTYPIRTVSQLTREIYTNVPLE-
      240      250      260      270      280      290

```

```

      280      290      300      310      320
Cry1Ac  -----NFDGSRGSAQGIIEGS-IRSPHMDILNSITITDHRGEY----YWSGHQI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  GVMNASMNWYNNNAPSFAIEAAAIRSPHLLDFLEQLTIFSAASSRWSNTRHMTYWRGHTI
      300      310      320      330      340      350

```

```

      330      340      350      360      370
Cry1Ac  MASPVFGSGPEPTFFPLYGTMGNAAPQORIVAQLGQGVYRTLSST-----LYRRPFNIGI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  QSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTESYAGVLLWGIYLEPIH-GV
      360      370      380      390      400      410

```

```

      380      390      400      410      420      430
Cry1Ac  NNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHRLSHV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  PTVRFNFTNPQNIISDRGTANY-SQPYESPGLQKDSLETLPPTERRPNYESYSHRLSHI
      420      430      440      450      460

```

```

      440      450      460      470      480      490
Cry1Ac  SMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  GI----ILQSRVNV---PVYSWTHRSADRNTTIGPNRITQIPMKVASELPQGTTVVRGPG
      470      480      490      500      510      520

```

```

      500      510      520      530      540      550
Cry1Ac  FTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLVNVWNGSSIFS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  FTGGDILLRRTNTGG---FGPIRVTVNGPLTQ-RYRIGFRYASTVDFDFVSRGGTTVNN
      530      540      550      560      570

```

```

      560      570      580      590      600      610
Cry1Ac  NTVPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVRNFSGTAGVIIDRFEFIPVT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  FRFLRMTMNSGDELKYGNFVRRRAFTPFTPTQIQDIIRTSIQGLSGNGEVYIDKIEIIPVT

```

Regulatory Product Characterization Team

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580      590      600      610      620      630
      620      630      640      650      660      670
Cry1Ac ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSEDFCLDEKRELS
      : : : : : : : :
gi|162 ATFEAEYDLER
      640

>>gi|162767647|emb|CAP58827.1| unnamed protein product [ (770 aa)
      initn: 1229 initl: 674 opt: 788 Z-score: 921.0 bits: 181.8 E(): 2.2e-42
      Smith-Waterman score: 1199; 37.667% identity (67.667% similar) in 600 aa overlap
      (55-624:190-770)

      30      40      50      60      70      80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDIIWGFQPSQWDAF
      : : : : : : : :
gi|162 AEGNNIDPFVSASTVQTGINIAGRILGLVLPFAGQLASFYSFLVGLWLP-RGRDQWEIF
      160      170      180      190      200      210

      90      100      110      120      130      140
Cry1Ac LVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFND
      : : : : : : : :
gi|162 LEHVEQLINQKITENARNALTARLQGLGDSFRAYQQSLEDWLENRDDARTRSVLHTQYIA
      220      230      240      250      260      270

      150      160      170      180      190      200
Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDAATINSRYNDL
      . . . . . : : : : : : : : : : : : : :
gi|162 LELDFLNAMPLFAIRNQEVPLLMVYAQAANLHLLLRDASLFGSEFLQTSQEIQRYYERQ
      280      290      300      310      320      330

      210      220      230      240      250      260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYP
      . . . . . : : : : : : : : : : : : : :
gi|162 VERTRDYSDYCVIEWYNTGLNSLRGTNAASWVRYNQFRDLTLGLVLDLVALFPSYDTRTYP
      340      350      360      370      380      390

      270      280      290      300      310
Cry1Ac IRTVSQLTREIYTNPVE-----NFDGSFRGSAQGIEGS-IRSPHMDILNSITITYT
      : : : : : : : : : : : : : : : : : : :
gi|162 INTSAQLTREYVYTDAGATGVNMMASMNWYNNAPSFAIEAAAIRSPHLLDFLEQLTIFS
      400      410      420      430      440      450

      320      330      340      350      360
Cry1Ac DAHRGEY----YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYRTL
      : : : : : : : : : : : : : : : : : : :
gi|162 ASSRSWNRHMTYWRGHTIQSRPIG-GG--LNTSTHGAT-NTSINPVTLRFASRDVYRTE
      460      470      480      490      500      510

      370      380      390      400      410
Cry1Ac SST-----LYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVAYRKSQGTV--DSLDEIP
      : : : : : : : : : : : : : : : : : : :
gi|162 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SQPYESPLQLKDSSETLP
      520      530      540      550      560      570

      420      430      440      450      460      470
Cry1Ac PQNNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQI
      : : : : : : : : : : : : : : : : : : :
gi|162 PETTERPNYESYSHRLSHIGIIL---QSRVNV---PVYSWTHRSADRTNTIGPNRITQI

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580      590      600      610      620
      480      490      500      510      520      530
Cry1Ac PAVKGNFLFNFS-VISGPGFTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRY
      : : : : : : : : : : : : : : : : : : :
gi|162 PMVKASELPQGTTVVRGPGFTGGDILRRNTTGG---FGPIRVTVNGPLTQ-RYRIGFRY
      630      640      650      660      670      680

      540      550      560      570      580      590
Cry1Ac ASVTPIHLLNVNWNSSIFSNTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVR
      : : : : : : : : : : : : : : : : : : :
gi|162 ASTVDFDFVSRGTTVNNFRFLRTMNSGDELKYGNFVRRAFTPPTFTQIQDIIRTSIQ
      690      700      710      720      730      740

      600      610      620      630      640      650
Cry1Ac NFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVS
      : : : : : : : : : : : : : : : : : : :
gi|162 GLSGNGEVYIDKIEIIPVTATFEAEYDLER
      750      760      770

>>gi|25897924|emb|CAD58214.1| unnamed protein product [s (673 aa)
      initn: 821 initl: 591 opt: 786 Z-score: 919.5 bits: 181.3 E(): 2.7e-42
      Smith-Waterman score: 913; 31.981% identity (63.807% similar) in 641 aa overlap
      (22-628:59-673)

      10      20      30      40      50
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLL
      : : : : : : : : : : : : : : : : : : :
gi|258 LASEPNAALQNMNYKEYLQMTTEEYTESYINPSLSISGREALQTALTVI-----RRILG
      30      40      50      60      70      80

      60      70      80      90      100
Cry1Ac SEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGL
      . . . . . : : : : : : : : : : : : : :
gi|258 ALGLPFSGQILSFYQFLNLTFLPLNETAIFEAAMRQLELLNQKITEFARNQALARLQGL
      90      100      110      120      130      140

      110      120      130      140      150      160
Cry1Ac SNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      . . . . . : : : : : : : : : : : : : :
gi|258 GESFNLYQRSLQFLAERNETRNLSLLRAQFIALELEFLNAIPLFALNGQQLPLLSLYAQ
      150      160      170      180      190      200

      170      180      190      200      210      220
Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      : : : : : : : : : : : : : : : : : : :
gi|258 ALNLHLLLLKEASLFGEGFGTQGEISTYYERQLELTAKYTYNCEFYNTGLERLRTNT
      210      220      230      240      250      260

      230      240      250      260      270
Cry1Ac RDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVEN-----
      : : : : : : : : : : : : : : : : : : :
gi|258 ESFLRYHQFRREMTLLLELLALFPYELRLYPTGSNPQLTRELYTEPIFNPPANLGLC
      270      280      290      300      310      320

      280      290      300      310      320      330
Cry1Ac --FDGSFRGSAQGIEGS-IRSPHMDILNSITITYTD---AHRGEYVWSGHQIMASPVGF
      : : : : : : : : : : : : : : : : : : :
gi|258 RRFGTNPYNTFSELENAFIRPPLFERLNSLTISSNRFPLSSNFMEYFSGHTLRRSYLNE

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330      340      350      360      370      380
Cry1Ac  340      350      360      370      380      390
SGPEFTFLPLYGTMGNAAPQQRIVAQLG-QGVYRTLSSSTLYRRPFNIGINN-QQLSVLDGT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  SA--LQEE SYGLITTT---RATINPGLBGTNRIESTALEFRSALIGIYGLNRASFLPGG
390      400      410      420      430
Cry1Ac  400      410      420      430      440      450
EFAYGTSNNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHRSHVSMFRSGFSNSSVS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  LFN-GTTS PANGGCRE---LYETNEELPPEEST---GSSTHRLSHLTF--SFQTNQAGS
440      450      460      470      480
Cry1Ac  460      470      480      490      500
IIRA---PMFSWIHRSAEFNNI IASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  IANAGSLPTYLFTRRELELNNTITPNRITQLPLLKASAPLSGTTLLKGGPFTGGGILRRT
490      500      510      520      530      540
Cry1Ac  510      520      530      540      550      560
SSGNNIQNRGYIEVP IHPFSTSTRYRVRYASVTP IHLNVNWGSSIFSNTVPATATSL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  TNGT---FGTLRLTLNSPLTQ-QYRLRLRFASSTGNF SIRLLRGLSIGELRLGSTMNRG
550      560      570      580      590      600
Cry1Ac  570      580      590      600      610
DNLQSSDF-----GYFESANAFTSSLGNI-VGVRNFGTAVGIIDRFEFIPVTATLE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  QELTYESFFTRFETTTGPFNPPFTTQAEILLTNAEGLSTGGEYIERIEILLPLNPARE
610      620      630      640      650      660
Cry1Ac  620      630      640      650      660      670
AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|258  AEEEELEAAKKA
670

```

>>gi|3410672|gb|AAC31094.1|I90732 Sequence 10 from paten (488 aa)  
 initn: 901 init1: 686 opt: 777 Z-score: 911.0 bits: 179.3 E(): 8e-42  
 Smith-Waterman score: 914; 34.077% identity (65.720% similar) in 493 aa overlap  
 (3-465:10-488)

```

10      20      30      40
Cry1Ac  CMQAMDNNPNINCEPIYCNLSNPEVEV--LGERIE--TGYPIDISLSLTQF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  MKSKNQNMHQSLSNNAVVDKNTGSLNNTTELQNFNHEGIEPFSVSTIQTGIGIVGK
10      20      30      40      50      60
Cry1Ac  50      60      70      80      90      100
LLSEF-VPGAGFVGLVDIIWGFIPG---SQWDAFLVQIEQLINQRIEEFARNQAISRLE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  ILGNLGVFPAGQVASLYSIFLGEWPKGKSQWEIFMEHVEELINQKISTYARNKALADLK
70      80      90      100      110      120
Cry1Ac  110      120      130      140      150      160
GLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  GLGDALAVYHESLESWIENRNNTRRSVVKSQYITLELMFVQSLPSFAVSGBEVPLLPYI

```

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130      140      150      160      170      180
Cry1Ac  170      180      190      200      210      220
VQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  AQAANLHLLLRDASIFGKXWGLSDSEISTFYNRQSGKSKKEYSDHCVKWYNTGLNRLMGN
190      200      210      220      230      240
Cry1Ac  230      240      250      260      270      280
DSRDWIRYNQFRRELTLTVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV-----LENF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  NAESWVRYNQFRDMTLMVLDLVALFPSYDTQMPYIKTTAQLTREYTTDAIGTVHPHPSF
250      260      270      280      290      300
Cry1Ac  290      300      310      320      330
DGS--FRGSAQG---IEGSI-RSPHLMIDLNSITIIYTDHAHRGEYYSWGHQIMASVPGFSG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  TSTTWYNNNAPSFSSTIEAAVVRNPHLLDFLEQVTIYSLLSR---WSNTQYMMN--WGG
310      320      330      340      350
Cry1Ac  340      350      360      370      380      390
PEFTFLPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGIN---NQQLSVLDGTE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  HKLEFRTIGTTLNTSTQGSTNTSINPVTLPFTSRDVRTEESLAGLNLFLTQPVVGVPRVD
360      370      380      390      400      410
Cry1Ac  400      410      420      430      440
FAYG-----TSSNLPSAVYRKSGTV--DSLDEIPPQNNVPPRQGFSHRSHVSMFRSG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  FHWKFVTHPIASDNFYYPGYAGIGTQLQDSENELPPEATGQPNYESYSHRSLHIGLI---
420      430      440      450      460      470
Cry1Ac  450      460      470      480      490      500
FNSSSVSIIRAPMFSWIHRSAEFNNI IASDSITQIPAVKGNFLFNGSVISGPGFTGGDLV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|341  ---SASHVKALVYSWTHRSAD
480

```

>>gi|14537815|gb|AAK66743.1| Cry1-like protein [Bacillus (149 aa)  
 initn: 615 init1: 319 opt: 764 Z-score: 903.3 bits: 176.2 E(): 2.1e-41  
 Smith-Waterman score: 764; 74.675% identity (88.961% similar) in 154 aa overlap  
 (1033-1182:1-149)

```

1010     1020     1030     1040     1050     1060
Cry1Ac  VEEQNQRSVLVVPEWEAEVSQEVRCVGRGYILRVYAYKEGYEGECVTIHEIENNTDEL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|145  GYILRVYAYKEGYEGECVTIHEIENNTDEL
10      20      30
Cry1Ac  1070     1080     1090     1100     1110
KFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEA---PSVPADYASVYEEK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|145  KFSNCEKEQVYPNGTVACNDY--NKNHGANACSSRNRGYDESYESNSSIPADYAPVYEEB
40      50      60      70      80
Cry1Ac  1120     1130     1140     1150     1160     1170
SYTDGRRENPCFNRGRDYTPPLVGVYTKLELYFPETDKVWIEIGETEGTFIVDSVELL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|145  AYTDGQRGNPCFNRGH---TLPAGYVTAELYFPETDTVWVIEIGETEGTFIVDSVELL

```

```

90      100      110      120      130      140
1180
Cry1Ac LMEE
gi|145 LMEE

>>gi|15721993|gb|AAG36711.1| crystal protein [Bacillus t (1236 aa)
  initn: 1792 initl: 370 opt: 773 Z-score: 900.2 bits: 178.6 E(): 3.2e-41
  Smith-Waterman score: 1825; 32.404% identity (58.162% similar) in 1219 aa overlap
  (61-1182:88-1194)

          40      50      60      70      80
Cry1Ac ERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGL-VDIIWGIFGPS--QWDAFLVQIEQ
gi|157 RAALFVANSIIGIMLSKIPVIGPIVSTPFQIMGVALPFLWPPNAPEPQFSWESLMTAAEE
          60      70      80      90      100      110

          90      100      110      120      130      140
Cry1Ac LINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT
gi|157 IADKKIDAQVRANANAEELEGVHNAIRLYQDAVCDWKQDPTNAQLKEQLRIQYIATNTVIF
          120      130      140      150      160      170

          150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGN
gi|157 SRMPSFRVRGFEVPLLSVYVQAANLHLIHLKDGVFGEWGMDSATVDRFYSYLSKSDIEI
          180      190      200      210      220      230

          210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGL-ERVWG-PDSRDWIRYNQFRRELTLTVLIDIVSLFPNYDSRTYPIRTV
gi|157 YTNVICIDWYNGKLSDSIESEPTWNGWNTFNNFRDMTLMVLDLVSISWPTYDPRRYPLPTK
          240      250      260      270      280      290

          270      280      290      300      310
Cry1Ac SQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHLMIDLNSITTYT----DAHRGEYY
gi|157 SQLTRELYTQAI-----GSYKSVEPLLPSPFRWLREIEFFLRDSQDEAEQFAGF
          300      310      320      330      340

          320      330      340      350      360      370
Cry1Ac WSGHQ-----IMASPVGFSGPEFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLY--
gi|157 QQGYQYTLDTTIYRPPVVGTRTSLVDSIAMGLGSDVVYRIKNI SHNGWYPPKCLDFYYTP
          350      360      370      380      390      400

          380      390      400      410      420
Cry1Ac -RRPFNIG-INNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPPQNNVPPRQG
gi|157 SERVESVGEIRTDANNMIDYIGLGCRAKVTEPCDPCTTNTCTIDTVNTTASCDN---PNL-
          410      420      430      440      450      460

          430      440      450      460      470      480
Cry1Ac FSHRLSHV--SMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLF
gi|157 YSHRLSSINSPAPYPG-QNGMLSFC----YGWTHFSVDDNLLIAADSITQIPAVKAYRIG

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          470      480      490      500      510
          490      500      510      520      530      540
Cry1Ac N-GSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLN
gi|157 GYGKVMKGPYTGDDLNVFYGAGE-----INWRLTIPDTPKAYRVARVA-----
          520      530      540      550      560

          550      560      570      580      590      600
Cry1Ac VNWGNSSIFSNVTPATATSLDNLQSSDFGY--FESANAFTSSLGNIVGVNRFSGTAGVII
gi|157 -----TIP-TSQPVDTVRYNQFEYRDIEVISPSTTTVHEYSIGF-DITGDDWGLL
          570      580      590      600      610

          610      620      630      640      650      660
Cry1Ac DRFEFIPVTATLEA--EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVITYLS
gi|157 DKIEFIPIEGPVEAYQADQALEKARKAVNALFTNDAKNALQLKVTDYSDVQAANLIECVS
          620      630      640      650      660      670

          670      680      690      700      710      720
Cry1Ac DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTITIQGGDDVFK
gi|157 DAFHSQEKMILLDQIKYAKRLSQARNLLNYGDFESSDWSGNGWRTSPHVHVASNHPIFK
          680      690      700      710      720      730

          730      740      750      760      770
Cry1Ac ENYVTLSGTF----DECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAK
gi|157 GRYLHMPGATSSQFSNHIYPTYVYQKVDKSLKSYTRYLVRFVGNKSKDELLVRYGKD
          740      750      760      770      780      790

          780      790      800      810      820
Cry1Ac -HETVNVPGTGSWPLSAQSPIGKCGEPNRC-----APHEWNPDL----DCSCR-
gi|157 VHVEMDVPND----IRYALPTNECGSLDRCPASQARTPHTCTCKDTSMTDCQCQN
          800      810      820      830      840

          830
Cry1Ac -----DG---EKC-----AHHS-----HHFSLDI
gi|157 KVNRTSADMYTNGSPSSVMYADGFHAHKS CGCKNNDMPNGTDSHKSCRCKDPHVFSYHI
          850      860      870      880      890      900

          840      850      860      870      880      890
Cry1Ac DVGCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEKPLVGEALARVKRAEKKWRDKREK
gi|157 DTGCVDQEEISLGLWFALKIASENGVANIDNLEIEAQP LTGEALARVKREKQKWKQEMTK
          910      920      930      940      950      960

          900      910      920      930      940      950
Cry1Ac LEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPELS----
gi|157 KRLETEKAVQAQAQSAIQNLFTNAQHNRLKFETLFPQIVHAEKLVQIPYVHHFFPLSGALP
          970      980      990      1000      1010      1020

          960      970      980      990      1000      1010
Cry1Ac VIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVL

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gi|157 TVPGMNFEEIQQLLAVIGNARALYEQRNLVNRNGTFSSGTGSWKVTEGVKVKPLQDT-SVL
1030 1040 1050 1060 1070 1080

Cry1Ac 1020 1030 1040 1050 1060 1070
VPEWAEVSEVVRVCPGRGYILRVAYKEGYGEGCVTIEIENNTDELKFSNCVVEEIIY

gi|157 VLSEWIHEASQQLHIDPNRGVLRVTRARKEGGGKGTVMTSDCADYTETLTFSTSC-----
1090 1100 1110 1120 1130

Cry1Ac 1080 1090 1100 1110 1120 1130
PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCFNRR

gi|157 -----DFNTSGS-----QTMTSGTLS-----
1140 1150

Cry1Ac 1140 1150 1160 1170 1180
GYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|157 -----GFVTKTLEIFPDTDRIRIDIGETEGTFQVESVELICMEQMEEDLYDIAGN
1160 1170 1180 1190 1200

gi|157 VVEEMRYLDSSRSMGGTLDAMCYTKIGEFGC
1210 1220 1230

>>gi|33765725|gb|AAQ52376.1| Sequence 30 from patent US (802 aa)
initn: 899 initl: 264 opt: 769 Z-score: 898.3 bits: 177.7 E(): 4.1e-41
Smith-Waterman score: 1155; 32.342% identity (60.595% similar) in 807 aa overlap
(5-761:26-802)

Cry1Ac 10 20 30
CMQAMDNNP-----NINECIPYNCLSNPEVEVLGGERIE

gi|337 MNQNKHGIIGASNCGCASDDVAKYPLANNPYSSALNLSQNSSILN--WINIIGDAAKE
10 20 30 40 50

Cry1Ac 40 50 60 70 80 90
TGYPIDISLSLTQFLLSEFVPG-AGFVLGLVD-IIWGFGPSQWDAFLVQIEQLINQRI

gi|337 A---VSI GTTIVSLITAPSLTGLISIVYDLIGKVLGGSSQSISDLSICDLLSIIDLRV
60 70 80 90 100 110

Cry1Ac 100 110 120 130 140
EEFARNQALSRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQF---NDMNSALT--

gi|337 SQSVLNDGIADFPVSVLYRNYLEALDSWNKNP-NSASAEELRTRFRIADSEFDRILTRG
120 130 140 150 160 170

Cry1Ac 150 160 170 180 190 200
--TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWG-FDAATINSRYNDLTRL

gi|337 SLTNGGSLARQNAQILLPSFASAAFFHLLLRDATTRYGTNGLYNATPFINYSKLVEL
180 190 200 210 220 230

Cry1Ac 210 220 230 240 250 260
IGNYTDHAVRWYNTGLE--RVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPI

gi|337 IELYTDYCVHWDNRGSTEELRQGPSATAWLEFHRYRREMTLMGLEIVASFSSLDITNYPI
240 250 260 270 280 290

270 280 290 300 310
Cry1Ac RTVSQLTREIYTNPVLNFDGSRFRGSA-----QIEGSIKSPHMLDILNSITIIYT

gi|337 ETDQFLSRVIYTDPIGFVHRSSLRGESWFSFVNANFSDLENAIPNPRPSWFLNMIIST
300 310 320 330 340 350

Cry1Ac 320 330 340 350 360
DA-----HRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV

gi|337 GSLTLPVSPSTDRARV-WYGSRRDISP---ANSQFITELISGQHTTATQ---TILGRNI
360 370 380 390 400

Cry1Ac 370 380 390 400 410
YRTLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSGT---VDSLDE-I

gi|337 FRVDSQACNLNDTTYGVN-RAVFIYHDASE---GSQRSVYEGYIRTTGIDNPRVQNTIYL
410 420 430 440 450 460

Cry1Ac 420 430 440 450 460 470
PPQNNVPPRQGFSHRLSHVSMFRSGF---SNSSVSIIRAPMFSWIHRSAEFNNIIASD

gi|337 PGENS DIPTEPDYTHILSTTINLTGGLRQVASNRRSSLV---MYGWTHKSLARNNTINPD
470 480 490 500 510

Cry1Ac 480 490 500 510 520 530
SITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYR

gi|337 RITQIPLTKVDTRGTGVSVVNDPGFIGGALLQRTDHGSLGVLR--VQFPLHL---RQQYR
520 530 540 550 560 570

Cry1Ac 540 550 560 570 580 590
VRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANAFTSSLGNI

gi|337 IRVRYASTNIRLSVN-GSFGTISQNLPTMRLGEDLRVGSFAIREFNTSIRPTASPDQI
580 590 600 610 620 630

Cry1Ac 600 610 620 630 640
-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH

gi|337 RLTIIEPSFIRQEVYVDRIEFIPVNPTRAEKEDLEAAKAVASLFTTRTD-GLQVNVKDYQ
640 650 660 670 680 690

Cry1Ac 650 660 670 680 690 700
IDQVSNLVITYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGS

gi|337 VDQANLVSCLSDEQYGYDKMMLLEAVRAAKRLSRERNLLQDPDFNTINSTEENGWKAASN
700 710 720 730 740 750

Cry1Ac 710 720 730 740 750 760
GITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKILKAFTRYQLRGYIEDSQLEIY

gi|337 GVTISBGGPFYKGRAIQLASA-RENYPTYIYQKVDASELKPTRYRLDGFVK
760 770 780 790 800

Cry1Ac 770 780 790 800 810 820
SIRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHH

>>gi|112088047|gb|ABI06957.1| Sequence 30 from patent US (802 aa)
initn: 899 initl: 264 opt: 769 Z-score: 898.3 bits: 177.7 E(): 4.1e-41

Smith-Waterman score: 1155; 32.342% identity (60.595% similar) in 807 aa overlap (5-761:26-802)

Sequence alignment for gi|112 showing identity with Cry1Ac. Includes amino acid sequences and position markers (10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 210, 220, 230, 240, 250, 260, 270, 280, 290, 300, 310, 320, 330, 340, 350, 360, 370, 380, 390, 400, 410, 420, 430, 440, 450, 460, 470, 480, 490, 500, 510, 520, 530).

Sequence alignment for gi|404 showing identity with Cry1Ac. Includes amino acid sequences and position markers (520, 530, 540, 550, 560, 570, 580, 590, 600, 610, 620, 630, 640, 650, 660, 670, 680, 690, 700, 710, 720, 730, 740, 750, 760, 770, 780, 790, 800, 810, 820). Includes a synthetic construct reference: >>gi|40457464|gb|AAR86772.1| CRY9C [synthetic construct] (387 aa) with Smith-Waterman score: 802; 40.994% identity (69.255% similar) in 322 aa overlap (22-328:18-337).

```

          250      260      270      280      290
Cry1Ac  TLTVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLENFD---GSRF--GSA-----QG
gi|404  TLVVLDDVVALFPYDVRLYPTGNSNPQLTREVYTDPIVFNPPANVGLCRRWGTNPYNTFSE
          240      250      260      270      280      290

```

```

          300      310      320      330      340
Cry1Ac  IEGS-IRSPHLMILNSITITYTDAH--RGEY--YWSGHQIMASPVGFSGPEFTFPLYGTM
gi|404  LENAFIRPPHLFDRLNSLTISSNRFVSSNFMFYWSGHTLRRSYLNSDAVQEDSYGLITT
          300      310      320      330      340      350

```

```

          350      360      370      380      390      400
Cry1Ac  GNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVY
gi|404  TRATINPGVDGTNRISTAVDFRSALIGIYGVN
          360      370      380

```

>>gi|21685445|emb|CAD30099.1| putative pesticidal cryst (489 aa)  
 initn: 1292 initl: 555 opt: 745 Z-score: 873.2 bits: 172.3 E(): 1e-39  
 Smith-Waterman score: 1122; 43.590% identity (68.590% similar) in 468 aa overlap  
 (632-1078:1-457)

```

          610      620      630      640      650      660
Cry1Ac  VIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|216  MFTSGAKNRLKLETTDYEIDQVANAIECMS
          10      20      30

```

```

          670      680      690      700      710      720
Cry1Ac  DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|216  DEQYSKEKMLLWDQVKHAKYLSQSRNLLQNGDFEDV---FHGWITSDHMYIQSDNSTFK
          40      50      60      70      80

```

```

          730      740      750      760      770
Cry1Ac  ENYVTLSTGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|216  GNYLNLISGARDIYLTIFPTIYQKIDESKLFKPYTRYLVRFVGGSKDVELVVSRYGKEID
          90      100      110      120      130      140

```

```

          780      790      800      810      820
Cry1Ac  TV-----NVPGTGS-----LWPLSAQS-PIGKCGEPNRCAPHLEWNPDLDCS---CRDG
gi|216  TVMNVFDPFIPYVSSRPVCNELYDGEQQPYPNGNVGYYN---PMSAFTPSYTSARQCMGP
          150      160      170      180      190      200

```

```

          830      840      850      860      870      880
Cry1Ac  EK---CAHSHHSLDIDVGCSDLNEDLGVVWVIFKIKTDGSHARLGNLEFLEEKPLVGEA
gi|216  KKQIVC-QDSHQFKFHIDTGEVDYNTNIGIWMVFKISSPDGYALLDNLEVEEGPIDGEA
          210      220      230      240      250      260

```

```

          890      900      910      920      930      940
Cry1Ac  LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKR
gi|216  LSRVKHMEKKWNDQMEAKRSETQQAYDVAKQAIDALFNVQDEALQFDTTLAQIQYABYL
          270      280      290      300      310      320

```

```

          950      960      970      980      990      1000
Cry1Ac  VHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSQWNVKGH
gi|216  VQSIPIVYNDWLSVDVPGMNYDIYVELDARVAQARYLYDTRNIIKNGDFTQGVGMWHVTGN
          330      340      350      360      370      380

```

```

          1010      1020      1030      1040      1050      1060
Cry1Ac  VDVEEQNNQRSVLVPEWEAEVSEQEVRVCPGRGYLLRVYAYKEGYEGCVTTIHEINNTD
gi|216  ADVQ-QIDGVSVLVLSNWSAGVSQNVHLQHNHGYVLRVIAKKEGPGNGYVTLMDCCENQE
          390      400      410      420      430      440

```

```

          1070      1080      1090      1100      1110      1120
Cry1Ac  ELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSY
gi|216  KLTFTSC--EEGYITKTVDFPDTCVRIEIGETEGSFYIESIELICMNE
          450      460      470      480

```

>>gi|46359604|dbj|BAD15305.1| parasporal crystal protein (405 aa)  
 initn: 709 initl: 675 opt: 739 Z-score: 867.4 bits: 170.9 E(): 2.2e-39  
 Smith-Waterman score: 739; 36.232% identity (66.087% similar) in 345 aa overlap  
 (11-347:56-394)

```

          10      20      30      40
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPI
gi|463  SSNALLYSPNKYPYATDPNVIAEGRSYKNWLDMCTGTGDRSPFAAAISKGAUSAIT--
          30      40      50      60      70      80

```

```

          50      60      70      80      90
Cry1Ac  DISLSLTQFLLESEFVPGAG-FVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQ
gi|463  -ISTGLLGLLVFPFASQIGAFYTFLLNTLWPA-SNTQWEQFIAHVEELINAKLTDHVRNS
          90      100      110      120      130      140

```

```

          100      110      120      130      140      150
Cry1Ac  AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
gi|463  ALTKLNLGRNNEIYNEALIVWKQDPNNSKLLKDDVRSKFVGLNSQFEEYIPQFKEEGFEV
          150      160      170      180      190      200

```

```

          160      170      180      190      200      210
Cry1Ac  PLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGL
gi|463  QLLTYIAQSANLHLLLRDSSLYGASWGFQAQATIDNNYRQIRKTAEYANHCTTWTYQTL
          210      220      230      240      250      260

```

```

          220      230      240      250      260      270
Cry1Ac  ERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNVPLEN
gi|463  QRLQGTASSWLSYHRFREMTLTLVDICALFSNYDARSYPLEVRGELTREIYTDVAVAPG
          270      280      290      300      310      320

```

```

          280      290      300      310      320      330
Cry1Ac  FDGSRFG-SAQGIEG-SIRSPHLM-ILNSITITYTDAHRG---EYWSGHQIMASPVGF
gi|463  TNWIDRAPFAELENLIVRAPRTVTWISGDLIVYTGRLYGTGNNYDWAHRL--DFLET
          330      340      350      360      370

```

```

          340      350      360      370      380      390
Cry1Ac  SGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVLDGTGF
      . : . : . : . :
gi|463  NGYRFEGPTYGSTINISRTDSIPMNS
      380      390      400

```

>>gi|118628707|emb|CAL85376.1| unnamed protein product [ (629 aa)  
 initn: 895 initl: 366 opt: 735 Z-score: 859.8 bits: 170.2 E(): 5.7e-39  
 Smith-Waterman score: 946; 33.719% identity (61.488% similar) in 605 aa overlap  
 (40-612:36-628)

```

          10      20      30      40      50      60
Cry1Ac  NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF-VPGAGFVL----GL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  YEIIGASTNGTIELPEDYNTIVSPYDAPASVTTTIEITGTILSDLGVPGASSVSLLNKLNK
      10      20      30      40      50      60

          70      80      90      100     110     120
Cry1Ac  VDIIWGIFGPSQWDAFLVQIEQLINQRI--EEFARNQAI SRLEGLSNLYQIYAESFREWE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  INLLWPNDTNTVWGTFGKETADLLNEVLSPDDPVVKDANTILKGINSLNLYLNALEIWK
      70      80      90      100     110     120

```

```

          130     140     150     160     170     180
Cry1Ac  ADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  KDPNNLTTIENVTDYFRSLNVVFTDHMPSPFAVPGYETKLLTIYAQAANLHLLLRDASRF
      130     140     150     160     170     180

```

```

          190     200     210     220     230     240
Cry1Ac  GQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFREL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  GEGWGLTQEIINTNYNDQLRLTAETDHCVKWYNAGLEKLGKGNLTGENWYTYNRRFREMT
      190     200     210     220     230     240

```

```

          250     260     270     280     290
Cry1Ac  LTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV-LENFDGSGFRGSA---QGIEGS-IR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  LMVLDVVALFPNYDTRMYPIGTSSSELTRMIYTDPIAYTQSDPWYKITSLSFSNLIENSAIP
      250     260     270     280     290     300

```

```

          300     310     320     330     340     350
Cry1Ac  SPHLMIDILNSITITYD---AHRGEYYWSGHQIMASPVGFSGPEFTFPL-YGTMGNAAPQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  SPSFFRWLKSVSINSQWGWGSGPSQTYYWGHVLYSN--SNSNQSLVKVYGDPNFSFIEP
      310     320     330     340     350     360

```

```

          360     370     380     390     400
Cry1Ac  QRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVLDGT---EFAYGTSSNLPASVYRK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  PDSFSSSTDVRTIS-VVRNSVSNYIVSEVRFNSISSTNQISEEIIYKHQSNWSRQETKD
      370     380     390     400     410     420

```

```

          410     420     430     440     450     460
Cry1Ac  SGTVDSLDEIPPQN-NNVPPRQGFSHRLSHVS-MFRSGFSNSSVSIIRAPMFSWIHRSAE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|118  SITELSLAANPPTFGNVAE---YSHRLAYISEAYQS--HNPSKYPTYIPVFGWHTSVR
      430     440     450     460     470

```

```

          470     480     490     500     510     520
Cry1Ac  FNNIIASDSITQIPAVKGNFLFNFS--VISGPGFTGGDLVRLNNSGNNIQRNGYIEVPI
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|118  YDNKIFPDKITQIPAVKSSSAQGGSWKNIVKGPFTGGD-VTTAVSPATVTTDIKIQVTL
      480     490     500     510     520     530

```

```

          530     540     550     560     570
Cry1Ac  HFPSTSTRYRVRYAS--VTPIHLLNVNWNSSIFSNTVPATA--TSLDNLQSSDF-GYF
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|118  DPNSLSQKYRARLRYASNAFVPATLYTNTSSNYNFELKKGTTTEQPTTYSYQYVDIPGSI
      540     550     560     570     580     590

```

```

          580     590     600     610     620     630
Cry1Ac  ESANAFSSLGNLIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTN
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|118  QFNN--TSDTVSVYLHMDSTSNVNVHVDRIEFIPID
      600     610     620

```

```

          640     650     660     670     680     690
Cry1Ac  QLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDI

```

>>gi|142759|gb|AAA22349.1| ORF (381 aa)  
 initn: 728 initl: 677 opt: 714 Z-score: 838.3 bits: 165.5 E(): 9e-38  
 Smith-Waterman score: 784; 37.430% identity (68.436% similar) in 358 aa overlap  
 (8-351:36-379)

```

          10      20      30
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
      . : . : . : . : . : . : . : . : . : . : . : . :
gi|142  PDKHQSFSSNAKVDKISTDSLKNETDIELQNIHEDCLKISEYENVE-PFVSASTIQTG-
      10      20      30      40      50      60

```

```

          40      50      60      70      80      90
Cry1Ac  TPIDISLSLTQFLLESEFVPGAGFVLGLVDIIWGIFGP---SQWDAFLVQIEQLINQRIEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142  ----ISIA-GKILGTLGVPPAQVQVSLYSFILGELWPKGNQWEIFMEHVVEEIIINQKIST
      70      80      90      100     110

```

```

          100     110     120     130     140     150
Cry1Ac  FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142  YARNKALTDLKGGLDALAVYHESLESWVGNRKNTRARSVVKSQYIALELMFVQKLPFAV
      120     130     140     150     160     170

```

```

          160     170     180     190     200     210
Cry1Ac  QNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142  SGEEVPLLPYIAQAANLHLLLRDASIFGKEWGLSSSEISTFYNRQVERAGYSDHCVKW
      180     190     200     210     220     230

```

```

          220     230     240     250     260     270
Cry1Ac  YNTGLERVWGPDSRDWIRYNQFRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142  YSTGLNLRGNTAESWVRYNQFRKDMTLMVLDLVALFSPSYDTLVVPIKTTSQLTREVYTD
      240     250     260     270     280     290

```

```

          280     290     300     310     320
Cry1Ac  PV-LENFDGSGFRGSA-----QGIEGSI-RSPHLMIDILNSITITYDAHRGEYYWSGH

```



Regulatory Product Characterization Team

Cry1Ac PGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVV
gi|160 PGMNYSPTLTLNRLQAWNLVYDLRNLAIPLNGDFRNLSDWNTATSDVNVQ-QLSDTSLVLI

Cry1Ac PEWEAEVSVQEVVPCPRGYILRVTAKEGYGEGCVTIIHEIENNTDELKFSNCVVEEIIYPN
gi|160 PNWNSQVSQQFTVQPNRYVLRVTARKEGVGDGYVIIRDGANQTELTTFN-----

Cry1Ac NIVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFENRGY
gi|160 ---ICDDDT-----GVLS-----ADQTS-----

Cry1Ac RDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|160 -----YITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEEE

>>gi|2624006|emb|CAA68876.1| unknown protein [Bacillus t (526 aa)
initn: 1054 initl: 332 opt: 696 Z-score: 814.9 bits: 161.6 E(): 1.8e-36
Smith-Waterman score: 1075; 37.743% identity (61.376% similar) in 567 aa overlap
(632-1180:1-483)

Cry1Ac VIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|262 MLTSGAKNMLKLETTDYEIDQMAIANENMS

Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|262 GEQYSQEKMMQWHDIKYAKQLSQARNLLQNGDFEDL---FSGWTTSNQMSIQADNATFK

Cry1Ac ENYVTLSGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|262 GNYLHMSGARDIYGTIFPTYIYQKIDESKLPYTRYLRVGFVGGSSKDLMLVMRYGKEID

Cry1Ac TV-----NVPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNP-----DLDCSCRDGEK-
gi|262 TVMNVPNNDIPYVPSM-PVCNELYDQQPPYPNRHVGYNPNPMPVSYTSDTCQCTPGKKH

Cry1Ac --CAHSHHFLSLDIDVGTDLNEDLGVVWIFKIKTDGHARLGNLEFLEEKPLVGEALAR
gi|262 VVC-HDSHQFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVIIEGVPVRGEAVTH

Cry1Ac TVMNVPNNDIPYVPSM-PVCNELYDQQPPYPNRHVGYNPNPMPVSYTSDTCQCTPGKKH
gi|262 VVC-HDSHQFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVIIEGVPVRGEAVTH

Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHS
gi|262 VKQKEKKWNQMEKKRMTKRVYDRAKQAVDALFTG---EELNYDVTLSHIKNADDLVQS

Cry1Ac IREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDV
gi|262 IPYVHNEWLPDFPGMNYDIYQELNARIMQARYLYDARNVITNGDFAQGLQGWHAEGKVEV

Cry1Ac EEQNNQRSVLVVPEWEAEVSVQEVVPCPRGYILRVTAKEGYGEGCVTIIHEIENNTDELK
gi|262 Q-QMNGTSLVVLVSNWSSGVSQLNLHVQHPHGYLLRVSAAKKEGSGKGYVTRMSCNGKQETLT

Cry1Ac FNSCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDG
gi|262 FTSC-----DG

Cry1Ac RRENPCFNRGRDYDTPPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|262 -----GYMTKTVEVPESDRVRIEIGETEGSFYIESIELICMNGY

Cry1Ac TSNNNQNMSNMYDQSYSGNYSQNTSDMYDQGGSVAKFEKE
gi|262 490 500 510 520

>>gi|31745045|dbj|BAC77649.1| hypothetical protein [Baci (533 aa)
initn: 1080 initl: 305 opt: 693 Z-score: 811.3 bits: 161.0 E(): 2.9e-36
Smith-Waterman score: 1051; 37.544% identity (60.526% similar) in 570 aa overlap
(632-1181:1-483)

Cry1Ac VIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|317 MFTSGAKNMLKLETTDYEIDQAAISIECMS

Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|317 DEHSPKEKMMMLWDEVKRAKLLSQRNLLQNGDFEDFSGN---DWTFSNDIIIGSNNSIFK

Cry1Ac ENYVTLSGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|317 GNFLQMRGARDIYGTIFPTYIYQKIDESKLPYTRYLRVGFVGGSSKDLMLVMRYGKEID

Cry1Ac TVMNVPNNDIPYVPSM-PVCNELYDQQPPYPNRHVGYNPNPMPVSYTSDTCQCTPGKKH
gi|317 AIMDVPND-----LSYMQPSPSCGD-YRCESSRYVNGYPTPTDGYASDMYACPSNSGE

```

150      160      170      180      190      200
Cry1Ac 830      840      850      860      870      880
K---CAHSHHFFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLFLEEKPLVGEAL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 KHVKC-HDRHPDFHIDTGELDTNTNVGIDVLFKISNPDGYATLGNLEVIEEGPLTGEAL
210      220      230      240      250      260

890      900      910      920      930      940
Cry1Ac ARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKRV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 THVKQEKKWKQHMEKKRWETQQTYNPAKQAVDTLFTNEQ--ELHYHITLDHIQNADRLV
270      280      290      300      310

950      960      970      980      990      1000
Cry1Ac HSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNWVKGHV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 QSIPIYIHHDWLDPAGMNYDGYQGLNARIMQAYNLYDARNVITNGDFTKGLQGWHAAGKA
320      330      340      350      360      370

1010     1020     1030     1040     1050     1060
Cry1Ac DVEEQNNQRSVLVPEWEAEVSVQEVVCPGRGYILRVTAAYKEGYEGCVTIHEIENNTDE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 AVQ-QIDGASVLVLSNWSAGVSNLHAQDHHGYMLRVIKKEGPKGYVTMMDCNGNET
380      390      400      410      420      430

1070     1080     1090     1100     1110     1120
Cry1Ac LKFSNCVEEIEYNNVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 LKFTSCEE-----
440

1130     1140     1150     1160     1170     1180
Cry1Ac DGRRENPCFNRGRYDTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|317 -----GYMTKTVEVFPESDRVRIEIGETEGTFYVDSIELLCMQ
450      460      470      480

Cry1Ac E
gi|317 GYASNNNPHTGMNYGQSYNGNYTHNDLHSGCTCNQGHNSGCTCNQGYNR
490      500      510      520      530

>>gi|16945770|dbj|BAB72017.1| Cry39ORF2 protein [Bacillu (558 aa)
initn: 1196 initl: 333 opt: 692 Z-score: 809.8 bits: 160.8 E(): 3.5e-36
Smith-Waterman score: 1038; 37.128% identity (60.070% similar) in 571 aa overlap
(632-1181:1-483)

610      620      630      640      650      660
Cry1Ac VIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 MFISNIKNTLKIETTDYEIDQAAISIECMS
10      20      30

670      680      690      700      710      720
Cry1Ac DEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITQGGDDVFK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 NEHSSKEEMMLWDEVKQAKQLSWSRNLLYNGDFEDVSN----GWKTSNTIEIRENSPVFK

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40      50      60      70      80
Cry1Ac 730      740      750      760      770
ENYVTLSTGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNKHE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 GHYLMHFGARDIDGTLFPPTYIYQKIEESKLPYTRYRVRFVGSKDLKLMVTRYGKEID
90      100     110     120     130     140

780      790      800      810      820
Cry1Ac TV-NVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEW-----NPDLD-----CSCRDG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 AMMNVND-----LAYMQPTPSCGD-SRCESSRYVSQGYTPVTDGYASGRYACQSNRG
150     160     170     180     190     200

830      840      850      860      870      880
Cry1Ac EK---CAHSHHFFSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLFLEEKPLVGEA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 TKHVKC-HDRHPDFHIDTGELDTNTNVGIDVLFKISNPDGYATLGNLEVIEEGPLTGEA
210     220     230     240     250

890      900      910      920      930      940
Cry1Ac LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIHAADKR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 LTHVKQEKKWKQHMEKKRWETQQAYDPAKQAVDALFTNEQ--ELHYHITLDHIQNADRL
260     270     280     290     300     310

950      960      970      980      990      1000
Cry1Ac VHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCVNWVKGH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 IQAIPVYHAWLDPAGMNYDGYQGLNARIMQAYNLYDARNVITNGDFTQGLTGWHAAGK
320     330     340     350     360     370

1010     1020     1030     1040     1050     1060
Cry1Ac VDVEEQNNQRSVLVPEWEAEVSVQEVVCPGRGYILRVTAAYKEGYEGCVTIHEIENNTD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 AMVQ-QMDGASVLVLSNWSAGVSNLHVQEHGMYMLRVIKKEGPKGYVTMMDCNGNRE
380     390     400     410     420     430

1070     1080     1090     1100     1110     1120
Cry1Ac ELKFSNCVEEIEYNNVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 TLKFTSCEE-----
440

1130     1140     1150     1160     1170     1180
Cry1Ac TDGRENPCFNRGRYDTPPLVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLM
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 -----GYMTKTVEVFPESDRVRIEIGETEGTFYVDSIELLCM
450     460     470     480

Cry1Ac EE
gi|169 QGYASNNNPHTGMNYGQSYNGNYNQNTSDVYHQGYTNNYNQNSNMYNQNYTHNDLHSG
490     500     510     520     530     540

>>gi|162767644|emb|CAP58825.1| unnamed protein product [ (285 aa)
initn: 673 initl: 673 opt: 686 Z-score: 807.1 bits: 159.3 E(): 4.9e-36

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Smith-Waterman score: 686; 62.658% identity (83.544% similar) in 158 aa overlap (10-167:128-285)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTP
gi|162 KSTASLPVARRSSRSRLGNVSNNGGRIRCEENNQNQCIPYNCLSNPEEVLDDGERISTGNSS
Cry1Ac IDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAPFLVQIEQLINQRIEIEFARNQ
gi|162 IDISLSLVQFLVSNFVPGGFLVGLIDFVWGVGIPQSDAPFLVQIEQLINERIAEAFARNA
Cry1Ac AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQV
gi|162 AIANLEGLGNFNFIYVEAFKEWEEDPNPNPETRTRVIDRFRILDDGLLDRDIPSRISGFVEV
Cry1Ac PLLSVYVQAANLHLSVLRDVSFVGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
gi|162 PLLSVYVQA
280

>>gi|41688284|dbj|BAD08533.1| hypothetical protein [Baci (541 aa)
initn: 1186 initl: 335 opt: 689 Z-score: 806.5 bits: 160.1 E(): 5.3e-36
Smith-Waterman score: 1089; 38.421% identity (61.579% similar) in 570 aa overlap (632-1180:1-484)

Cry1Ac VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|416 MFTSGAKNMLKLETTDYEIDQVANSIENMS
Cry1Ac DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|416 DEQHSQEKMMLWDEVKHKAYLSQSRNLLQNGDFEDL---FSGWTTSNHMSIQADNSTFK
Cry1Ac ENYVTLSTGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|416 GNYLNMMSGARDIYGTIFPTYIYQKIDESKLFKPYTRYLVRFVGSKDLLELVVMRYGKEID
Cry1Ac TV-NVPGTGSWLPL-----SAQSPI--GKCGEPNR---CAPHLEWNPDLDCSCRDG
gi|416 TIMNVNDIPYVPSMPVPCNELYDGEQPPYSKGNVGYNSMPVSAP--SYTSDA-CQCMPG
Cry1Ac EK---CAHSHSHFSLDIDVGTDLNEDLGVVWVIFIKTKQDGHARLGNLEFLEEKPLVGEA

gi|416 KKQVVC-HDSHQKFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVEIEEGPVRGEA
Cry1Ac LARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKDR
gi|416 LAYVKQKEKKNWQMEKKRMETKQAYDRAKQAVDALFTG---EELHYNVTLSQIKNANQL
Cry1Ac VHSIREAYLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGH
gi|416 VQSIPIVHNEWLPDVPGMNYDLYQELNTRIMQARYLYDARNVITNGDFTQGLQGWHAEGK
Cry1Ac VDVEEQNNQRSVLVPEWEAEVSVQEVVRCVPCGRGYILLRVYAYKEGYEGCVTTIHEIENNTD
gi|416 VEVQ-QMNGTAVLVLSNWSGVSQNLHVQHHCYVLRVSAKKEGPGKGVYVMMCGCKQJE
Cry1Ac ELKFSNCVVEEIIYPNNTVTVCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSY
gi|416 TLTFSTSC-----
Cry1Ac EE
gi|416 NGYTSNNSQNMSNMYDQSYSGNYSQNTSNMNYNNYEQHAGCTCNQYNNGGCTCNQG

>>gi|83336130|gb|ABC11712.1| Sequence 1 from patent US 6 (1167 aa)
initn: 1616 initl: 540 opt: 691 Z-score: 803.9 bits: 160.7 E(): 7.4e-36
Smith-Waterman score: 2451; 38.519% identity (66.337% similar) in 1215 aa overlap (8-1182:39-1167)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGY
gi|833 YEILDASSSTVSVDNSVRYPLANDQTTTLQNMNYKDYLRMSEGENPEL--FGNPETFISS
Cry1Ac TPIDISLSLT-QFLLSEFVPGAGFVLGLVDIIWGFGPSQ---WDAFLVQIEQLINQRI
gi|833 STVQTGIGVQVGLGALGVFPAGQIASFYSFIVGQLWPSSTVSVWEMIMKQVEDLIDQKI
Cry1Ac EEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLF

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gi|833 TDSVRKTALAGLQGLDGLDVYQKSLKNWLENRNDTRARSVVVTQYIALELDFVAKIPSF
130 140 150 160 170 180

Cry1Ac 160 170 180 190 200 210
AVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGNYTDHAV
gi|833 AISGQEVPLLSVYAQAANLHLLLRDASIFGAEWGFTPEISTFVDRQVTRTAQYSDYCV
190 200 210 220 230 240

Cry1Ac 220 230 240 250 260 270
RWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIY
gi|833 KWYNTGLDKLKGTTNAASWLKYHQFRREMTLLVLDLVALFPNYDTRTYPIETTAQLTREYV
250 260 270 280 290 300

Cry1Ac 280 290 300 310
TNPVLENFD--GSF--RGSAAQ-----IEGS-IRSPHLMIDLNSITTYTDA----HRG
gi|833 TDPIVFNRETSGGFCRRWSLNSDISFSEVESAVIRSPHLFDLSEIEFYTTTRAGLPLNNT
310 320 330 340 350 360

Cry1Ac 320 330 340 350 360 370
EY--YWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRP
gi|833 EYLEYVWGHSIKIKYKNTNASSALER--NYGTITSNKIKYYDLANKDIFQVRSGLADLANYY
370 380 390 400 410 420

Cry1Ac 380 390 400 410 420
FNI--GINNQQLSVLD---GTEFAYGTSSNLPSAVYRK--SGTVDSLDEIPPQNNVPPRQG
gi|833 AQVYGVVPYASFTLLDKNTGSGSVGGFTYSKPHTTMQVCTQNYNTIDEIPPENE--PLSRG
430 440 450 460 470 480

Cry1Ac 430 440 450 460 470 480
FSHRLSHVSMFRSGFSNSSVSIIRA---PMFSWIHRSAEFNNIIASDSITQIPAVKGNFL
gi|833 YSHRLSHITSY--SFSKNASSPARYGNLVPFAWTHRSADVNTTVYSDKITQIPVVKHAHTL
490 500 510 520 530 540

Cry1Ac 490 500 510 520 530 540
FNGS-VISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFSTSTRYRVRVRYASVTPPIHL
gi|833 VSGTTVIKGPFTGKNILKRTSSGP----LAYTSVSVKSP--LSQRYRARIRYASTTNLRL
550 560 570 580 590

Cry1Ac 550 560 570 580 590 600
NVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT--SSLGN--IVGVRNFSGTAGV
gi|833 FVTISGTRIYSINVNKTMMKGGDLTFNTFDLATIGTAFNFSNYSDSLTVGADSFASGGEV
600 610 620 630 640 650

Cry1Ac 610 620 630 640 650 660
IIDRFEFIPVTATLAEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD
gi|833 YVDFKELIPVNATFAEEDLDVAKKAVNGLFTSKKD--ALQTSVTDYQVNAANLVECLSD
660 670 680 690 700 710

Cry1Ac 670 680 690 700 710 720
EFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFKE

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gi|833 ELYPNKRWLMDAVKEAKRLVQARNLLQDTGFNRIN--GENGWGTSTGIEVAEGDVLFPKD
720 730 740 750 760 770

Cry1Ac 730 740 750 760 770
NVVTLSGTFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAKHET
gi|833 RSLRLTSAREIDTETYPTYLYQQIDESLLKPYTRYKLGFIGSSQDLEKLIHRHRANQIV
780 790 800 810 820 830

Cry1Ac 780 790 800 810 820 830
VNVPGTGSWLPLSAQSPIGKCGEPNRCAP--HLEWNPDLDCSCRDGKCAHSHHFLSLDI
gi|833 KNVPD--NLLP--DVLVNVSCGGIDRCSEQQYVDANLALENGENGENMSSD--SHAFSPHI
840 850 860 870 880

Cry1Ac 840 850 860 870 880 890
DVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREK
gi|833 DTGEIDLNENTGIWVFKIPTTNGYATLGNLELVEEGPLSGETLEAQQEQQWQDKMAR
890 900 910 920 930 940

Cry1Ac 900 910 920 930 940 950
LEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPG
gi|833 KRGASEKAYAAKQAIIDRLFADYDQKQLNSGVEMSDMLAAQNLVQSIPIVYNDALPEIPG
950 960 970 980 990 1000

Cry1Ac 960 970 980 990 1000 1010
VNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCWNVKGVHDVEEQNNQRSLVLPVE
gi|833 MNYTSFTELTLNRLQQAWNLVLDLRLNAPNGDFRNLGSDWNATSDVNVQ--QLDSTSLVLIPI
1010 1020 1030 1040 1050 1060

Cry1Ac 1020 1030 1040 1050 1060 1070
WEAEVSVQEVVCPGRGYILRVTAKEGYGEGCVTIEIENNTDELKFSNCVEEIEYPNNT
gi|833 WNSQVSVQFTVQPNRYVLRVTRARKEGVGDGYVIIRDGANQTETLTFN-----
1070 1080 1090 1100 1110

Cry1Ac 1080 1090 1100 1110 1120 1130
VTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDRRENPCFENRGRYRD
gi|833 -ICDDT-----GVLS-----ADQTS-----
1120

Cry1Ac 1140 1150 1160 1170 1180
YTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|833 -----YITKTVEFTPSTEQVWIDMSETEGVFNIESVELVLEE
1130 1140 1150 1160

>>gi|54695306|dbj|BAD67158.1| hypothetical protein [Baci (486 aa)
initn: 1163 initl: 325 opt: 685 Z-score: 802.5 bits: 159.2 E(): 8.9e-36
Smith-Waterman score: 1058; 37.699% identity (60.885% similar) in 565 aa overlap
(632-1178:1-482)

Cry1Ac 610 620 630 640 650 660
VIIDRFEFIPVTATLAEAYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS

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gi|546          .::: .. :: .....: : :
                MFTSGGKNMLKLETTDYIEDKMANVYKNMS
                10      20      30

        670      680      690      700      710      720
Cry1Ac DEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
      ::  :::  . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|546 DEQYSQEKMMDIKYAKQLSQARNLLQNGDFEDL---FSGWTTSNQMSIQADNATFK
      40      50      60      70      80

        730      740      750      760      770
Cry1Ac ENYVTLSGTDF--ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
      ::  :::  . : : : : : : : : : : : : : : : : : : : : : : :
gi|546 GNYLHMSGARDIYGTIFPTYIYQKIDESKLFKPYTRYLVRFVGSKDLVVMHYGKEID
      90     100     110     120     130     140

        780      790      800      810      820
Cry1Ac TV-NVPGTGSGLWPL-----SAQSPI--GKCGEPNRCAPHLEWNPDLDCSCRDGEK-
      ::  :::  . : : : : : : : : : : : : : : : : : : : : : : :
gi|546 TVMNVNDIPYVPSMPVCNELYDGEQQYPNGNVGYNPMVSTSSYTSDAQCQMPGKKH
      150    160    170    180    190    200

        830      840      850      860      870      880
Cry1Ac --CAHSHHFLSLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|546 VVC-HDSHQFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVIEEGPVRGEALTH
      210    220    230    240    250    260

        890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|546 VKQKEKKWNQOMEKKRMETKQAYDRAKQAVDALFTG---EELNYNVTLSHIKNADDLVQS
      270    280    290    300    310    320

        950      960      970      980      990     1000
Cry1Ac IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDV
      : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|546 IPYVHNEWLRDVPGMNYDIYQELNARIMQASYLYDARNVITNGNFAQGLQGWHAEKGVVEV
      330    340    350    360    370    380

        1010     1020     1030     1040     1050     1060
Cry1Ac EEQNNQRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELK
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|546 Q-QLNGTTVLVLSNWSGISOQLHVQHGHYLLRVSAAKKEGSGKGYVTLMGCKGKKTLLT
      390    400    410    420    430    440

        1070     1080     1090     1100     1110     1120
Cry1Ac FSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDG
      : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|546 FTSC-----DG

        1130     1140     1150     1160     1170     1180
Cry1Ac RRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|546 -----GYITKTVFVPESDRVRIBIGTEGSFYVESIELLCAKG
      450    460    470    480

>>gi|50539656|dbj|BAD32658.1| hypothetical protein [Baci (537 aa)

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initn: 1164 init1: 325 opt: 685 Z-score: 801.8 bits: 159.2 E(): 9.6e-36
Smith-Waterman score: 1059; 37.390% identity (60.847% similar) in 567 aa overlap
(632-1180:1-484)

        610      620      630      640      650      660
Cry1Ac VIIDRFEFIPVTATLBAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|505          MFTSGGKNMLKLETTDYIEDKMANVYKNMS
                10      20      30

        670      680      690      700      710      720
Cry1Ac DEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
      : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi|505 DEQYSQEKMMDIKYAKQLSQARNLLQNGDFEDL---FSGWTTSNQMSIQADNATFK
      40      50      60      70      80

        730      740      750      760      770
Cry1Ac ENYVTLSGTDF--ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
      : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi|505 GNYLHMSGARDIYGTIFPTYIYQKIDESKLFKPYTRYLVRFVGSKDLVVMHYGKEID
      90     100     110     120     130     140

        780      790      800      810      820
Cry1Ac TV-NVPGTGSGLWPL-----SAQSPI--GKCGEPNRCAPHLEWNPDLDCSCRDGEK-
      : : : : . : : : : : : : : : : : : : : : : : : : : : : :
gi|505 TVMNVNDIPYVPSMPVCNELYDGEQQYPNGNVGYNPMVSTSSYTSDAQCQMPGKKH
      150    160    170    180    190    200

        830      840      850      860      870      880
Cry1Ac --CAHSHHFLSLDIDVGCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . :
gi|505 VVC-HDSHQFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVIEEGPVRGEALTH
      210    220    230    240    250    260

        890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . :
gi|505 VVC-HDSHQFKFHIDTGEVDYNTNLGIWVLFKISSPDGYATLDNLEVIEEGPVRGEALTH
      210    220    230    240    250    260

        890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . :
gi|505 VKQKEKKWNQOMEKKRMETKQAYDRAKQAVDALFTG---EELNYNVTLSHIKNADDLVQS
      270    280    290    300    310    320

        950      960      970      980      990     1000
Cry1Ac IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDV
      : . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|505 IPYVHNEWLRDVPGMNYDIYQELNARIMQASYLYDARNVITNGNFAQGLQGWHAEKGVVEV
      330    340    350    360    370    380

        1010     1020     1030     1040     1050     1060
Cry1Ac EEQNNQRSVLVPEWEAEVSEVVRVCPGRGYILRVTAKEGYGEGCVTIHEIENNTDELK
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|505 Q-QLNGTTVLVLSNWSGISOQLHVQHGHYLLRVSAAKKEGSGKGYVTLMGCKGKKTLLT
      390    400    410    420    430    440

        1070     1080     1090     1100     1110     1120
Cry1Ac FSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDG
      : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|505 FTSC-----DG

        1130     1140     1150     1160     1170     1180
Cry1Ac RRENPCFNRYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      : : : : . : : : . : : : . : : : . : : : . : : : . : : : . :
gi|505 -----GYITKTVFVPESDRVRIBIGTEGSFYVESIELLCAKG
      450    460    470    480

1130      1140      1150      1160      1170      1180

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Cry1Ac RRENPCFNRGRDYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLME...
gi|505 -----GYITKTVFVPESDRVRIBIGETEGSFYIESIELICMNGY
450 460 470 480
gi|505 TSNNNQNMSNMYDQGYINNYNQYNTNTYEQHAVCTCNQYNNNGGCTCKQG
490 500 510 520 530

>>gi|592659|gb|AAA54266.1| Sequence 2 from Patent WO 880 (103 aa)
initn: 670 initl: 670 opt: 670 Z-score: 794.8 bits: 155.5 E(): 2.4e-35
Smith-Waterman score: 670; 96.078% identity (100.000% similar) in 102 aa overlap
(150-251:1-102)

120 130 140 150 160 170
Cry1Ac EWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|592 PLLAVQNYQVPLLSVYVQAANLHLSVLRDV
10 20 30

180 190 200 210 220 230
Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
gi|592 SVFGQRWGFDAATINSRYNDLTRLIGNYDYAVRWYNTGLERVWGPDSRDWIRYNQFRRE
40 50 60 70 80 90

240 250 260 270 280 290
Cry1Ac LTLTVLDIVSLFPNYSRTPYRTVQLTREIYTNVPLENFDGSRGSAQGIIEGSIKRSRPH
gi|592 LTLTVLDIVALFS
100

>>gi|3426160|dbj|BAA32397.1| insecticidal protein [Bacil (682 aa)
initn: 333 initl: 172 opt: 679 Z-score: 793.2 bits: 158.0 E(): 2.9e-35
Smith-Waterman score: 685; 27.243% identity (60.465% similar) in 602 aa overlap
(55-633:79-658)

30 40 50 60 70 80
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG-LVDIIWGFGPSQ--WDAFL
gi|342 NMCEEASYASSGPSQLFKVGGSIIVAKILGMIPEVGPLLSWVMSLFWPTIEEKNTVWEDMI
50 60 70 80 90 100

90 100 110 120 130 140
Cry1Ac VQIEQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
gi|342 KYVANLLKQELTNDTLNRATSNLSGLNESLNIYNRALAAWKQKNNFASGELIRSYINDL
110 120 130 140 150 160

150 160 170 180 190 200
Cry1Ac NSALTTAIPL-FAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDL
gi|342 HILFTRDIQSDFLSGYETVLLPSYASAAANLHLLLRDVAIYKGLGYPSTDFVEFYFNEQ
170 180 190 200 210 220

210 220 230 240 250 260
Cry1Ac TRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTPY
gi|342 KYYTEKYSNYCVNTYKSGLE---SKKQIGWSDFNRYRREMTLSVLDIVALFLPYDTGLYP
230 240 250 260 270 280

270 280 290 300 310
Cry1Ac -----IRTVSQTLTREIYTNVPLENFDGSRG--SAQGIIEG-SIRSPHLMILNSITIIYTD
gi|342 SKDGKIHVKAELTREIYSDVINDHVYGLMVPYISFEHAESLYTRRPHAFATWLGKGRFVFN
290 300 310 320 330 340

320 330 340 350 360 370
Cry1Ac AHRGEYVWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRVLSTLYR
gi|342 SINSWTFLLSGGENRYFLTHGEGTIYNGPFLGQDTEYGGTSSYIDISNNSIYNLWTKNYE
350 360 370 380 390 400

380 390 400 410 420
Cry1Ac --RPFN--IGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGVDS-LDEIPPQNNVPPR
gi|342 WIYPWTDPNVITKINFSITDNSN---SSESIYGAERMNKPTVRTDFNFLNRAAGNGPTT
410 420 430 440 450 460

430 440 450 460 470 480
Cry1Ac QG-FSHRLSHVSMRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL
gi|342 YNDYNHILSYMLINGETFGQKR---HGYSFAFTHSSVDRYNTIIVPKIVQIPAVKTN-L
470 480 490 500 510

490 500 510 520 530 540
Cry1Ac FNGSVISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLN
gi|342 VGANIIKGPGHGTGGDLLKL-----EYERFLSLRIKLIASMT-FRIRIRYASNISGQMM
520 530 540 550 560

550 560 570 580 590 600
Cry1Ac VNWG--NSSIFSNTPATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSGTAG
gi|342 INIGYQNPTYF-NIIPPTSRDYTELKFEFQLVDTSYIYSGGSPSSNLTWLDNFSN-GP
570 580 590 600 610 620

610 620 630 640 650 660
Cry1Ac VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|342 VIIDKIEFIPGLITLQNAQGYDQYDQNGMYHQYNSNGSYNYNQYNTYQSYNN
630 640 650 660 670 680

670 680 690 700 710 720
Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK

>>gi|37999235|dbj|BAD00053.1| hypothetical protein [Baci (545 aa)
initn: 1152 initl: 310 opt: 676 Z-score: 791.1 bits: 157.3 E(): 3.8e-35
Smith-Waterman score: 1055; 41.189% identity (70.044% similar) in 454 aa overlap
(632-1067:1-445)

610 620 630 640 650 660
Cry1Ac VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|379 MFTSGTKNMLKIETTDYEIDRVANSIENMS
10 20 30

670 680 690 700 710 720
Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK

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gi|379 DEQHSQEKMLWDEVKHAKQLSQSRNLLQNGDFEDL---FSGWTTSNHMSIQSDNATFK
      40      50      60      70      80
Cry1Ac 730      740      750      760      770
ENYVTLSGTFD--ECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|379 GNYLNMSGARDIYGTIFPTYIYQKIDESKLLKPYTRYLVRFVGVSSKELELVVMRYGKEID
      90      100     110     120     130     140
Cry1Ac 780      790      800      810      820
TV-NVPGTGLWPF-----LSAQSPIGKCGEPNRCAPHLEWNPDL---CSCRDGEK-
gi|379 TIMNVPNDIPYVPSMPFVNCNEVDGEEQLYSNGVNGVYVNPMPVMPVSYTSDACQCPMGKKH
      150     160     170     180     190     200
Cry1Ac 830      840      850      860      870      880
--CAHSHHFFSLDIDVGCITDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALAR
gi|379 VVC-QDSHQFKFHIDTGEVDYKTNLGIWVLLKISSPDGYATLDNLEVEIEEGPVRGEALAH
      210     220     230     240     250     260
Cry1Ac 890      900      910      920      930      940
VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHS
gi|379 VKQKEKKWNQHMKEKRMETKQAYDQAKQAVDALFTG---EALHYDVTLSQIKNANQLVQS
      270     280     290     300     310     320
Cry1Ac 950      960      970      980      990     1000
IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDV
gi|379 IPYVHNEWLPDVPGMNYDLYQELNARIMQARYLYDARNVITNGDFTQGLQGWHAEGKVEV
      330     340     350     360     370     380
Cry1Ac 1010     1020     1030     1040     1050     1060
EQNNQRSVLSVPEWAEVSVQEVVPCGRGYILRVTAKEGYEGCVTIHEIENNTDELK
gi|379 Q-QMNGTSLVLSNWSGVSQNLHVQHHCYVLRVSAKKEGPGKGYVTMMGCNGKQETLT
      390     400     410     420     430     440
Cry1Ac 1070     1080     1090     1100     1110     1120
FSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDG
gi|379 FTSCDGGYMTKTVEVFTESDRVRIEIGETEGSFYIESIELICMNGYTRKNNQNSMYDQ
      450     460     470     480     490     500
>>gi|80975797|gb|ABB54494.1| Cry40 [Bacillus thuringiens (459 aa)
  initn: 1014 initl: 304 opt: 673 Z-score: 788.7 bits: 156.6 E(): 5.2e-35
Smith-Waterman score: 948; 36.648% identity (60.037% similar) in 543 aa overlap
(660-1181:1-456)
Cry1Ac 630      640      650      660      670      680
NALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDEFCLDEKRELSEKVKHAKLSDERNLL
gi|809 MSDEHSPKMKMLWDEVKQAKQLSQSRNLL
      10      20      30
Cry1Ac 690      700      710      720      730      740
QDSNFKDINRQPERGWGGSTGITIQGGDDVFKENVVTLSTGTFD---ECYPTYLYQKIDES

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gi|809 QNGDFGDFSGN---DWTFGNDIIIGSNNPIFKGKFLQMSGARDIYGTIFPTYIYQKIDES
      40      50      60      70      80
Cry1Ac 750      760      770      780      790      800
KLKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGTGLWPLSAQSPIGKCGEPNR
gi|809 KLKPYRRYVRVGFVGVSSKDLKLMVTRYGKEIDAIMVDPN--DLAYMQA-NP--SCGD-YR
      90      100     110     120     130     140
Cry1Ac 810      820      830      840
CAPHLEWN-----PDLDC-----SC---RDGE--KCAHSHHFFSLDIDVGCITDLNEDL
gi|809 CESSSQYVQGQYPIPVTDGYASDRYACQFDRDKKHVKC-HDRHPDFHIDTGEVDANTNV
      150     160     170     180     190     200
Cry1Ac 850      860      870      880      890      900
GVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKE
gi|809 GIDVLFKISNPDGYATLDNLEVEIEEGPLTGEALTHVKQKEKWKQHMEKRWETQAYDYP
      210     220     230     240     250     260
Cry1Ac 910      920      930      940      950      960
AKESVDALFVNSQYDQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEG
gi|809 AKQAVDTLFTNEQ--ELHYLITLDHIQNADRLVQSIPIVYHAWLPDASDMNYDAYQLGNA
      270     280     290     300     310     320
Cry1Ac 970      980      990     1000     1010     1020
RIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQRSVLSVPEWAEVSVQEVV
gi|809 RIMQAYNLYDVRNVTITNGDFAQGLAGWHATGKVDVQ-QMDGTSVLVLSNWSAGVSQNLHA
      320     330     340     350     360     370
Cry1Ac 1030     1040     1050     1060     1070     1080
CPGRGYILRVTAKEGYEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQE
gi|809 QDHHGVVLRVIAKKEGPGKGYVTMMDCNGKQETLKFITSCEE-----
      380     390     400     410
Cry1Ac 1090     1100     1110     1120     1130     1140
EYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTK
gi|809 -----GYMTK
      420
Cry1Ac 1150     1160     1170     1180
ELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|809 TVEVFPESDRVRIEIGETEGTFYIDSIELICMQGYA
      430     440     450
>>gi|89000902|dbj|BAE80089.1| C-terminal half of 130-kDa (559 aa)
  initn: 1199 initl: 486 opt: 664 Z-score: 776.8 bits: 154.6 E(): 2.4e-34
Smith-Waterman score: 1047; 36.713% identity (60.839% similar) in 572 aa overlap
(632-1181:1-484)
Cry1Ac 610      620      630      640      650      660
VIIDRFEPFIVTATLBAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLS

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Cry1Ac FSHRLSHVSMFRSGFSSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNG
gi|262 YNHILSYMLINGETFGQKR---HGYSFAFTHSSVDPNNTIIAANKITQIPVVKASSI-NG
      480          490          500          510          520

      490          500          510          520          530          540
Cry1Ac SVI--SGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNV
gi|262 SISIEKGPFTGGDLVKMRAD--SGLTMRFKAEL-----LDKKYRVRIRYKCNYSKLLIL
      530          540          550          560          570

      550          560          570          580          590          600
Cry1Ac -NW-GNSSIFS--NIVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVI
gi|262 RKWKGEYIQQIHNISPTYGAFSYLESFTITTTENIFDLTMEVTPYQRFVEDIPLSI
      580          590          600          610          620          630

      610          620          630          640          650          660
Cry1Ac IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
gi|262 LDKIEFLPTN
      640

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>>gi|17385646|dbj|BAB78601.1| crystal protein CryE6L [Ba (1270 aa)  
 initn: 1373 initl: 322 opt: 653 Z-score: 758.5 bits: 152.5 E(): 2.5e-33  
 Smith-Waterman score: 1602; 31.721% identity (56.542% similar) in 1261 aa overlap  
 (55-1182:98-1265)

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      30          40          50          60          70
Cry1Ac VEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVGLV-DIIWGIF---GPSQ--WD
gi|173 TKVQSLTISAGLVAAIAGVASVAFPLAIVAGAFAIISMFFDVLWPESENNTNSQVVA
      70          80          90          100          110          120

      80          90          100          110          120          130
Cry1Ac AFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQF
gi|173 DFAAAAEEMMDEKIADEIKAEAVLQLRIVQSRRLRDYQQAACNFQSDPNNESYKALLRDAF
      130          140          150          160          170          180

      140          150          160          170          180          190
Cry1Ac NDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVSFVQGRWGFDAATINSRYN
gi|173 DDADDALKEVMILFSREGYEQLLLPDYVQAANLHLLLLKDVVRFVGVGWGFPGRVEQYYS
      190          200          210          220          230          240

      200          210          220          230          240
Cry1Ac D-----LTRLIGNYTDHAVRWYNTGLE-RVWGPDSR---DWIRYNQFRRELTLTVLD
gi|173 NPTNLGNPQMLLAKYTNYSTSLCWKGIIEERKWMVSEYRSNNEEYAYRSNMMTMMVLD
      250          260          270          280          290          300

      250          260          270          280          290          300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRF--SAQGIEGSIRSP-HLMDI
gi|173 MVALWPTYDPVKYPYATAVELTREIYSL-----IAGGFRDYKGYMPIQYTWKPGSLVTN
      310          320          330          340          350          360

      310          320          330          340          350          360

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Cry1Ac LNSITITYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAOQLGQG--
gi|173 LERFTIYT-----WKNFEYF--P--FAGVETTYQTITGTSSSTKQAGVIPSPEGTA
      370          380          390          400          410

      370          380          390          400
Cry1Ac -----VYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTS-SNLPSAV
gi|173 WTPPGINVEYHLVESFIYGTTLTQLLFYDVYNTPAFKAGSDAVEVPGSIAGTPCKNIPLDA
      420          430          440          450          460          470

      410          420          430          440          450
Cry1Ac YRKSQVDSL-DEIP--PQNNVNP-PRQGFSHRLSHV---SMFRSGFSSSVSIIRAPM
gi|173 NDVNVCVPTLWEEESPANPEGVCYPYNREMQSNLLSEVIPEDPKLLTLPHVPLGYIDAFDA
      480          490          500          510          520          530

      460          470          480          490          500          510
Cry1Ac FSWIHRSAEFN-NIIASDSITQIPAVKGNFL--FNGSVISGPGFTGGDLVRLNSSGNNIQ
gi|173 FAWRSTTCDTRYNLIPANKIGQIPAVKGNWLGQSGSSVVRTSGNTGGDVVRLYEFGN---
      540          550          560          570          580

      520          530          540          550          560          570
Cry1Ac NRGYIEVPIHFPSTSTRYRVRVRYASVTP---IHLNVNWGNSSIFSNTVPATATSLDNLQ
gi|173 ---LGMTVRF--SENRSYIIRLRYATVADDLNIIVRVQRREGELEYESELPLNQTSSNNT
      590          600          610          620          630          640

      580          590          600          610
Cry1Ac S---SDFGYFESANAFTSSLGNIVGVRNFS--GT---AGVIIDRFEFIPVTATLE---AE
gi|173 QWKFEDYGYQE-VGGFYPQVGEYELW--FSPVGTLSHMDIDKIEFIPMETSLEEYLAN
      650          660          670          680          690          700

      620          630          640          650          660          670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
gi|173 QDIEKARKAVNALFTGDVKNALKLNVTDYAIDQAANLVECVSEEFYAQEKMILLDQVKVA
      710          720          730          740          750          760

      680          690          700          710          720          730
Cry1Ac KRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLGSG---TF-DEC
gi|173 KRLSQARNLLNYGDFESPEWSRENGWKTSRHVSVRADNPVFKGRYLHMPGVTSPPSFSNNT
      770          780          790          800          810          820

      740          750          760          770          780          790
Cry1Ac YPTYLYQKIDESKLFKAFTRYQLRGYLEDSDLEIYSIRYNAK-HETVNVPGTSLWPLSA
gi|173 YPTYVYQKVDSEKLSYTRYLVRFVGNKDLLELLVRYGKDVHVEMDVPDHIRY---SL
      830          840          850          860          870

      800          810          820
Cry1Ac QSPIGKCGEPNRCAP-----HLEWNPDL-----DCSCR-----
gi|173 QT--NECGGFDCRCPVSYLARSSHACTCKDTASMHTDCQCQNKANRTVTNMYTNVSPGSA
      880          890          900          910          920          930

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      830      840      850
Cry1Ac ---DG---EKCA-----HHS-----HHFSLDIDVGTDLNEDLGWVVFVK
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 MYTDGFHAQKSCGCKNNDMYQNGTHPHKSCGCKDPHFVFSYHIDTGCVDPEENLGLWFALK
      940      950      960      970      980      990

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      860      870      880      890      900      910
Cry1Ac IKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDA
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 IAGENGVANIDNLEIEAQPLTGEALARVKKREQRWKQERDKKRETEKAVQTAQGAIQN
      1000     1010     1020     1030     1040     1050

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      920      930      940      950      960      970
Cry1Ac LFNVSQYDQLQADTNIAMIHAAADKRVHSIREAYLPELS---VIPGVNAAIFEELEGRIF
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 LFTNTQQNLLKFETLFPQIVNAEMLVQQIPYVYHPFLSGALPAVAGMNFKIVQQLSATIG
      1060     1070     1080     1090     1100     1110

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      980      990      1000     1010     1020     1030
Cry1Ac TAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVEEQNNQRSVLVPEWEAEVSEQEVRVCPG
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 NARSLYNQRNLVQNGTFSSGTGSHVSEGVEVQPLQNT-SVLVLSWSHSASQVSVDPD
      1120     1130     1140     1150     1160     1170

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      1040     1050     1060     1070     1080     1090
Cry1Ac RGYILRVYTAYKEGYGEGCVTIHEIENNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYG
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 RGYVLRVLTARKEGVGKGTVTLSDCADYTETLFTFSC-----
      1180     1190     1200     1210

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      1100     1110     1120     1130     1140     1150
Cry1Ac GAYTSRNRGYNAPSVPADYASVYEEKSYTDGRRENPCFNRGRDYTPLVPGYVTKELE
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 -----DFNTSGS-----QMTSGTLS-----GFVTKTLE
      1220     1230

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      1160     1170     1180
Cry1Ac YFPETDKVWIEIGETEGTFIVDSVELLLMEE
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 IFPDTDRIRIDIGETEGTFKIESVELICMEQMEDDL
      1240     1250     1260     1270

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>>gi|17385650|dbj|BAB78603.1| crystal protein CryE6S [Ba (1280 aa)  
 initn: 1611 initl: 325 opt: 645 Z-score: 749.0 bits: 150.7 E(): 8.4e-33  
 Smith-Waterman score: 1920; 32.392% identity (60.157% similar) in 1275 aa overlap  
 (18-1181:44-1249)

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      10      20      30      40
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLT
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 NNGRGDQSRYPPLTNPASAEQLDMNYIEWLDNCTLKEQVELFR-DTSTTVRDALATTAGII
      20      30      40      50      60      70

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      50      60      70      80      90      100
Cry1Ac QFLLSEFVPGAGFVLGLVDIIWIGIFGPS----QWDAFLVQIEQLINQRIEFARNQAIS
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 TALLSVSNPAAAATAGIITILIPQLWPSGSDVETWEKFMAAAEEILIQQITEAVRNKALT
      80      90      100     110     120     130

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      110      120      130      140      150      160
Cry1Ac RLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLL
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 ELEGVYRTIRLYQLAAERWQNKNDPQAQESIRTQFRATNTIIEFAMPFSFRVAGFEVPLL
      140      150      160      170      180      190

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      170      180      190      200      210      220
Cry1Ac SVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYND-LTRLIGNYTDHAVRWYNTGLER
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 NVYAEAAANLQLALLRDAVKFGRDWGLPQDEVDIYSEQLLPRIAEHTDHCVTYFNRGLEE
      200      210      220      230      240      250

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      230      240      250
Cry1Ac V-----WGP---DSR----DWIRYNQFRRELTTLVLDIVSLFPNYDSRTY
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 AKKLANLNDYARYPWAQYINHSKIQGIENWNLFNDRYRNMTLVLDDLVALWPTYDPRRY
      260      270      280      290      300      310

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      260      270      280      290      300      310
Cry1Ac PIRTVSQLTREIYTN--PVLENFDGSRFGSAQIEGSIRSP-HLMDILNSITTYTDAHRG
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 SMVTKSELTRELYTSVRGAFYGHNNDYDQNFEEIERNIISPPHLVTPINFTVYT---QN
      320      330      340      350      360

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      320      330      340      350      360      370
Cry1Ac EYYW--SG--HQIMASPVGFGSPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYR
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 DYYPMAGLQHKFNYESIVS---LESPVTGVTGTSNLFVFTAD----PFILAVTI--
      370      380      390      400      410

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      380      390      400      410      420      430
Cry1Ac RPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYR-KSGTVDLSLEIPPQNNVPPRQGF
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 ---IGFG-QLGTSLGIYAMSFGRKSGSISHVGDIEIGTDDYLDIV---DRIPVGDSTP
      420      430      440      450      460      470

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      440      450      460      470      480
Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG--
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 NKLWMSA--APTTLGSTTFLQVVS YAWRHPSVDSNNRISIDKITQIPAVKAFFIDDNHV
      480      490      500      510      520

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      490      500      510      520      530      540
Cry1Ac SVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTS--TRYRVRVRYASVTPIHNLNV
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 KVIKPGSTGGDLVAFSREGYGLS-----ISVFI PGSDLVSFYRVRIRIYASSQS AKVTM
      530      540      550      560      570      580

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      550      560      570      580      590      600
Cry1Ac NWNSSIFSNT---VPATATSLDNLQSSDFGYFESANAFTSSLGNIVGV--RNFSGTAGV
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 FGFGGVEESESKEFNFPATYSG-GNLTYSNFGYINTLAIASQSTAQTIEVYFRQYE-EAEF
      590      600      610      620      630      640

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      610      620      630      640      650
Cry1Ac IIDRFEFIPVTATLE---AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
      ::      ::      ::      ::      ::      ::      ::      ::      ::
gi|173 IVDKLEFIPMEMSLEEQADQDLEKARKAVNALFTSDAKSELKVNITDYAVDQAAANLVEC
      650      660      670      680      690      700

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660      670      680      690      700      710
Cry1Ac LSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 VSEDFHAQEKRILLDQVKFAKRLSQARNLLNYGDFESLDWSGENGWRTSPHVHVASDNPI
      710      720      730      740      750      760

720      730      740      750      760      770
Cry1Ac FKENVVTLVSGTF----DECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 FKGRYLHMPGAMSPQYSNNTYPTYAYQKVDSEKLSYTRYLVIRGFGVNSKDLLELLVERYG
      770      780      790      800      810      820

780      790      800      810
Cry1Ac AK-HETVNVPGT-GSLWPLSAQSPIGKCEPNR-----CAPHLEWNPDLDC-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 KEVHVEMDVPNDIRSTLPMNECGGFERCCKVSYQAVSDHTCTCKDTARMNTDCQCKDKIN
      830      840      850      860      870      880

820      830      840
Cry1Ac -----SCRDGEKCAH---HSHH-----FSLDIDVG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 HMTTGVYTSMPVGSAMYPDGYHAHKSCCKGDKTMYGNGKHPKSCGCKDPHFVSYHIDTG
      890      900      910      920      930      940

850      860      870      880      890      900
Cry1Ac CTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 CVDQEENLGLWFALKIASENGVANIDNLEIIIEALPLTGEALARVKKREHKWKQEMEQRKC
      950      960      970      980      990      1000

910      920      930      940      950
Cry1Ac ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIIHAADKRVSIREAYLPEL---SVIP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 KTEEAQAAQTAINTLFTNTQYNRLKFETLFPFILHADELVQRIPVYVHPFLGAYPDVDP
      1010      1020      1030      1040      1050      1060

960      970      980      990      1000      1010
Cry1Ac GVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGVHVDVEEQNNQRSVLVVP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 GMNYDIFQQLSALVNQARGLYDMRNLVRNGTFPSAGIGNWQVTDGVAQTEGNT-SVLILR
      1070      1080      1090      1100      1110

1020      1030      1040      1050      1060      1070
Cry1Ac EWEAEVSEQEVRVCPGRGYILRVYAYKEGYGECVTIHEIENNTDELKFSNCVEEIIYPNN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 EWSDKAIQHLRIHAERGYVLRVTARKEGNGDGYVVIHDCDNQEQEKLTFAC-----
      1120      1130      1140      1150      1160      1170

1080      1090      1100      1110      1120      1130
Cry1Ac TVTCNDYTVNQEEYGGAYTSRNGYNEAPSPADYASVYEEKSYTDGRRENPECFNRGYR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 -----DYTT---MGSSTGTQMMTSPNTNCPNCTTWKEE-----MK
      1180      1190      1200

1140      1150      1160      1170      1180
Cry1Ac DYTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|173 ALVPLSGYVTKTAEIFPDTDRIHIEIGETEGTFKIESVELICMEHMEHAYDMEGDIEA

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1210      1220      1230      1240      1250      1260
gi|173 NIPPIVRPPIMPPTNV
      1270      1280

>>gi|51998374|emb|CAH33958.1| unnamed protein product [B (669 aa)
      initn: 577 initl: 212 opt: 634 Z-score: 740.3 bits: 148.1 E(): 2.6e-32
      Smith-Waterman score: 764; 29.868% identity (58.911% similar) in 606 aa overlap
      (40-617:58-636)

10      20      30      40      50      60
Cry1Ac NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 FAKDPNIFPINLDACQGRPWQDTWESVSDIVTIGTYLIQFLLPEPGIGGIPVIFSIIINKLI
      30      40      50      60      70      80

70      80      90      100      110      120
Cry1Ac GIFGSPQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQ-IYAESFREWEADPTNP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 PSSGQVAALSICDLVSIIRKEVDESVLSDGVADFEEMTAYQDYVYHLYLEDWLTDKSNP
      90      100      110      120      130      140

130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIP-LFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQRWG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 KKLADVVKQFQAREEDFTKLLAGSLSRQKAEILLPTVYVQAANVHLLLRDAVKYKKEWG
      150      160      170      180      190      200

190      200      210      220      230
Cry1Ac FDAATI---NSRYNDLTRL---IGNYTDHAVRWYNTGLERVW--GPDSRDWIRYNQFRRE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 LVCPPLYPGSGRTRDCNERLKAKEYTNYCVGWYKGLDQIRQAGTSAEVWSKFNKFRRE
      210      220      230      240      250      260

240      250      260      270      280      290
Cry1Ac LTLTLVDIVSLFPNYDSRTPYPIRTVSQLTREIYTNVLENFDGSGFRG----SAQGIEGS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 MTLAVLDIIAIFPTYDFEKYPLATSVELTREIYTDVDP--GYSGGNYGWERFFSFNSVEAN
      270      280      290      300      310      320

300      310      320      330      340      350
Cry1Ac -IRSPHMDILNSITITYTDAHRGEY-YWVSGHQIMASPVGFSGPEFTFP-LYGTMGNAAPQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 GTRGPGLVTWLQAIIDYSHSINLQLGYLSGWGTRHYEDFTKGNQAFQRMSTSN-PR
      330      340      350      360      370      380

360      370      380      390      400      410
Cry1Ac QRIVAQLGQGVYRTLSSTLYR-RPFNIGINNQLSVDLGTETAYGTSSNLPASVYRKSQT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 NIIFGNTD--IFKIIISLARYAMQPF-VGYSIPR-HLVSRAEF-FPTTLNFTLYEVNSSGY
      390      400      410      420      430

420      430      440      450      460
Cry1Ac VDSLDEI-PPQNNNVPP-RQGFHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 SQTIESVLPGINKDLPPSRNTNYSRHSNAACVQNETS-----RVNVFGWHTTSMKIDN
      440      450      460      470      480      490

470      480      490      500      510      520

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Cry1Ac IIASDSITQIPAVK-----GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI
gi|519 RIYPDKITQIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVTLPLPYQAS-----LKIRL
500 510 520 530 540

Cry1Ac HFPSTSTRYRVRVRYASVTPPIHLNVN-WGNSSIFSNTVPATATSLDNLQSSDFGYFESAN
gi|519 TSAPTNNKYRVRRLRYASGGPGPFRVERWSPSSVSNANFSRPAATG---GYSSFDYVDTLV
550 560 570 580 590 600

Cry1Ac AFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|519 TTFNQSGVEIIIIQNLSGYH-LIVDKVEFIPIDIQIEKCTKCQFEGDICRCEGVQSLETKK
610 620 630 640 650 660

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
gi|519 EIVNSLFIN

>>gi|51998372|emb|CAH33957.1| unnamed protein product [B (672 aa)
initn: 577 init1: 212 opt: 634 Z-score: 740.2 bits: 148.1 E(): 2.6e-32
Smith-Waterman score: 764; 29.868% identity (58.911% similar) in 606 aa overlap
(40-617:61-639)

Cry1Ac NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIW
gi|519 FAKDPNIFPINDACQGRPWQDTWESVSDIVITIGTYLIQFLLPEPGIGGIPVIFSIINKLI
40 50 60 70 80 90

Cry1Ac GIFGSGQWDAFLVQIEQLINQRIEAFARNQAIISRLLEGLSNLYQ-IYAESFREWEADPTNP
gi|519 PSSGQVAALSICDLVSIIRKEVDESVLSDGVADFEGEMTAYQDYLLHYLEDWLTDKSNP
100 110 120 130 140 150

Cry1Ac ALREEMRIQFNDMNSALTTAIP-LFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWG
gi|519 KKLADVVKQFQAREEDFTKLLAGSLSRQKAEILLLPTYYVQAANVHLLLRDAVKYKKEWG
160 170 180 190 200 210

Cry1Ac FDAATI---NSRYNDLTRL---IGNYTDHAVRWYNTGLERLV--GPDSDRWIRYQFRRE
gi|519 LVCPPLYPGSGRTDCNERLKAKIKEYTNYCVGWYKGLDQIRQAGTSAEVWSKFNKFRRE
220 230 240 250 260 270

Cry1Ac LTLTVDLIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDDGSRG-----SAQIGIEGS
gi|519 MTLAVLDIIAIFPTYDFEKYPLATSVELTREIYTDV--GYSGGNYGWERFFSFSNSVEAN
280 290 300 310 320

300 310 320 330 340 350

Cry1Ac -IRSPHLMIDLNSITTYTDAHRGEY-YWSGHQIMASPVGFSGPEFTFP-LYGTMGNAAPQ
gi|519 GTRGPGLVTLWQAIDYSHSINLQLGYLSGGWGTTRHYEDFTKNGAFQRMSTTSNN-PR
330 340 350 360 370 380

Cry1Ac QRIVAQLGQGVYRTRLSSTLYR-RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQT
gi|519 NIIFGNTD--IPKIIISLARYAMQPF-VGYSIPR-HLVSRAEF-FPTTLNTFLYEYVNSSSGY
390 400 410 420 430 440

Cry1Ac VDSLDEI-PPQNNNVPP-RQGFHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAEFNN
gi|519 SQTIESVLPGINKDLPPSRTNYSHRLSNAACVQNETS-----RVNVFGWTHSTMKKDN
450 460 470 480 490

Cry1Ac IIASDSITQIPAVK-----GNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI
gi|519 RIYPDKITQIPAVKAFALPAGTGYAGGYVTAGPGYTGDDVTLPLPYQAS-----LKIRL
500 510 520 530 540

Cry1Ac HFPSTSTRYRVRVRYASVTPPIHLNVN-WGNSSIFSNTVPATATSLDNLQSSDFGYFESAN
gi|519 TSAPTNNKYRVRRLRYASGGPGPFRVERWSPSSVSNANFSRPAATG---GYSSFDYVDTLV
550 560 570 580 590 600

Cry1Ac AFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|519 TTFNQSGVEIIIIQNLSGYH-LIVDKVEFIPIDIQIEKCTKCQFEGDICRCEGVQSLETKK
610 620 630 640 650 660

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
gi|519 EIVNSLFIN
670

>>gi|16945773|dbj|BAB72019.1| Cry40ORF2 protein [Bacillus (558 aa)
initn: 1087 init1: 328 opt: 632 Z-score: 739.1 bits: 147.7 E(): 3e-32
Smith-Waterman score: 995; 36.316% identity (59.649% similar) in 570 aa overlap
(632-1181:1-483)

Cry1Ac VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|169 MFTNGTKNTLKIETTDYEIDQAAISIECMS
10 20 30

Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|169 DEHSPKEKMMMLWDEVKRAKLLSQSRNLLQNGDFGDFYGN---DWKFGNNIIIGSNNISIFK
40 50 60 70 80

730 740 750 760 770

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Cry1Ac ENYVTLSGTFFD---ECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHE
gi|169 GNFLQMSGARDIYGTIFPTYIYQKIDESKLFKPYTRYRVRGFGSSKDLRLMVTRYGKEID
90 100 110 120 130 140

Cry1Ac TV-NVPGTGSWLPLSAQSPIGKCGEPNRC-----APHLEWNPD-LDCSCRDGE
gi|169 AMNVPND-----LAYMQPNPSCGD-SRCESSSQVYSQGYPTPTDGYAPDRYACPSSSDK
150 160 170 180 190 200

Cry1Ac K---CAHSHHFLSLDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEAL
gi|169 KHVMC-HDRHPFDHIDTGELDTNTNVGIDVLFKISNPDGYATLGNLEVEEGPLTGEAL
210 220 230 240 250 260

Cry1Ac ARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRV
gi|169 THVKQEKKWKQHMEKKRWETQQAYDPAKQAVDTLFTNEQ--ELHYHITLDYIQLTLDWY
270 280 290 300 310

Cry1Ac HSIREAYLPESLVPVGNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVH
gi|169 SRFPIYTMGTGRDAPGMNYDGYQLNARIMQAYNLYDARNVITNGDFTKLGQGWHAAGKA
320 330 340 350 360 370

Cry1Ac DVEEQNNQRSLVLPVEWEAEVSEQEVRVCPGRGYILRVYAYKEGYEGCVTIHEIENNTDE
gi|169 AVQ-QIDGASVLVLSNWSAGVSNLHAQDHHGYMLRVIKKEGPKGYVTMMDCNGNET
380 390 400 410 420 430

Cry1Ac LKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYT
gi|169 LKFTSCEE-----
440

Cry1Ac DGRRENPCFNRGRDYTPPLVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLLME
gi|169 -----GYMTKTVVEVFPESDRVRIEIGETEGTFYVDSIELLCMQ
450 460 470 480

Cry1Ac E
gi|169 GYASNNNPHTGMNYGQSYNGNYQNTSDVYHQYTNNYQNSSNMYNQNYTHNDDLHSGC
490 500 510 520 530 540

>>gi|2815886|gb|AAB97923.1| delta-endotoxin [Bacillus th (645 aa)
initn: 837 init1: 413 opt: 603 Z-score: 703.9 bits: 141.4 E(): 2.7e-30
Smith-Waterman score: 926; 31.613% identity (62.097% similar) in 620 aa overlap
(20-605:42-645)

10 20 30 40

Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
gi|281 YPLTDDPNAGLQNMNYKEYLQTYGGDYTDPLINPNLSVSGKDVIVQGINVGRLLSFFGF
20 30 40 50 60 70

Cry1Ac LLSEFVPGAGFVLGLVDI IWGIFGSPQWDAFLVQIEQLINQRIEFARNQAI SRLEGLS
gi|281 PFSSQWVTYVYTY---LLNSLWPDDENSVWDAFMERVEELIDQKISEAVKGRALDDLTGLQ
80 90 100 110 120

Cry1Ac NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTAIPLFAV---QNYQVPLLSV
gi|281 YNYNLYVEALDEWLNRP-NGARASLVSRFNILDLSLFTQFMPSFGSGPGSQNYATILLPV
130 140 150 160 170 180

Cry1Ac YVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVG
gi|281 YAQAANLHLLLLKADDIYGARWGLNQTQIDQFHSRQSLTQTYTTHCVTAYNDGLAELRG
190 200 210 220 230 240

Cry1Ac PDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV---LEN-
gi|281 TTAESWFKYNQYRREMTLTAMDVLALFPYINLRQYPDGNTPOLTREYVTDPIAFDPLEQP
250 260 270 280 290 300

Cry1Ac -----FDGSFRG--SAQGIEGS-IRSPHMDILNSITIYTDahrgeyywshqima
gi|281 TTQLCRSWYINPAFRNHLNFSVLENSLIRPPLHFERLSNLQILVNYQTNGSAWRGSRVRY
310 320 330 340 350 360

Cry1Ac SPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTLSS-TLYRRP----FNIGINNQ
gi|281 HYLHSSIIQEK--SYGLLSD--PVGANINVQNNDIYQIISQVSNFASPVGSSYSVWDTNF
370 380 390 400 410 420

Cry1Ac QLSVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIIPPQNNVPPRGFSHRLSHVSMFRS
gi|281 YLSSGQVSGISGYTQQGIPAVCLQQRNSTDELPSLNPEGDII---RNYSHRLSHITQYRF
430 440 450 460 470 480

Cry1Ac GFSNS-SVSIIRA--PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFT
gi|281 QATQSGSPSTVSANLPTCVWTHRDVLDNTITANQITQLPLVKAYELSSGATVVKGPGFT
490 500 510 520 530 540

Cry1Ac GGDVLRNLSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNWGNSSII--FS
gi|281 GGDVIRRTMTGG---FGAIRVSVTGPLTQ-RYRIRFRYASTIDFFVTRGGTTINNFR
550 560 570 580 590

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560      570      580      590      600      610
Cry1Ac NTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDRFEPVTTAT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|281 FTRTMNRGQESRYESYRTVEFTTFFNFQTQSQDIIRTSIQGLSGNGEVYLD
      600      610      620      630      640
Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSK

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>>gi|71792192|emb|CAJ21125.1| unnamed protein product [B (696 aa)  
 initn: 858 init1: 405 opt: 599 Z-score: 698.7 bits: 140.5 E(): 5.4e-30  
 Smith-Waterman score: 1083; 35.152% identity (62.727% similar) in 660 aa overlap  
 (20-636:57-693)

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      10      20      30      40
Cry1Ac      CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YPLTDDPNAGLQNMNYKEYLQMYGGDYTDPLINPNLSVSGKDVIVGINIVGRLLSFFGF
      30      40      50      60      70      80
Cry1Ac      LLSEFVPGAGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 PFSSQWVTVYTYLL--NSLWPDDENSVWDAFMKRIEELIDQKISEAVKGRALDELTLGLQ
      90      100     110     120     130     140

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      110     120     130     140     150     160
Cry1Ac NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPLLSV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 DNYNLYVEALDEWLNRN-NGARASLVSRFNILDSLFTQFMPSPGSGPGSQNYSTILLPV
      150     160     170     180     190     200

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      170     180     190     200     210     220
Cry1Ac YVQAANLHLSVLRDVSFVGQRWGFDAATIN---SRYNDLTRLIGNYTDHAVRWYNTGLER
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YAQAANLHLLKLDADYIGARWGLNQTQIDQFHSRQQLTR---TYTNHCVTTYNDGLAE
      210     220     230     240     250

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      230     240     250     260     270     280
Cry1Ac VWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLENF-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 LRGTSVESWLKYHQYRREMTVTAMDVLFPPYNNVRQYPNGANPQLTREVIYDPIVFNPP
      260     270     280     290     300     310

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      290     300     310
Cry1Ac ---DGSFRGSAQGIEGS-----IRSPHLMIDLNSITITYTDAHRGEY-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 EPPSGAFCEFSFYNIRAARERLTFSQLENAIRPPRLFERFQALGIYTGEARLNQNSAPT
      320     330     340     350     360     370

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      320     330     340     350     360     370
Cry1Ac YWSGHQIMASPVFGSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYR--TSSSTLYRRPFF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YWIGHFIRNTRLGDSTTTITN--YGTNNRLTN--FIPPTSDVYQINSISSNLASALST
      380     390     400     410     420     430

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      380     390     400     410     420     430
Cry1Ac I-GINNQQLSVLDGTGFAY-GTSSNLPASAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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gi|717 LFGVTRAQPHYGSGIIWSYVQNNVLPQC---HQNYNSIEELPNQSDE-PTVRSYSYSHRL
      440     450     460     470     480     490

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      440     450     460     470     480     490
Cry1Ac SHVSMFRSG--FSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNFS-V
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 SHITSFNFSVQLNPNVISLGNMPVYVWTHRSVDLNNITSDRITQLPAVKASTLGAGAIV
      500     510     520     530     540     550

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      500     510     520     530     540     550
Cry1Ac ISGPGFTGGDLVRLNNSGNNIQNRGYIEVPIHFPTSTSTRYRVRVRYASVTPIHLLNWNWGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 VKGPGFTGGDVIRRTSVGD---FGTIRVSVT-GSLTQQYRIRFRYASTIDFFDFVIRGG
      560     570     580     590     600

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      560     570     580     590     600
Cry1Ac SSI---FSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVIIDR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 TTINNFRFTHMTSSGEE--RYESYRTVEFSTFFNFQTQSQDIIRTSIQGLSGNGEVYLD
      610     620     630     640     650     660

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      610     620     630     640     650     660
Cry1Ac FEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 IEIIPVNPTRAEEDLEDAKKAVAGLFRTRDQ
      670     680     690

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>>gi|71792202|emb|CAJ21128.1| unnamed protein product [B (780 aa)  
 initn: 1120 init1: 405 opt: 599 Z-score: 698.0 bits: 140.5 E(): 5.9e-30  
 Smith-Waterman score: 1340; 37.047% identity (63.893% similar) in 745 aa overlap  
 (20-721:57-777)

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      10      20      30      40
Cry1Ac      CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YPLTDDPNAGLQNMNYKEYLQMYGGDYTDPLINPNLSVSGKDVIVGINIVGRLLSFFGF
      30      40      50      60      70      80

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      50      60      70      80      90      100
Cry1Ac LLSEFVPGAGFVLGLVDI IWGIFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 PFSSQWVTVYTYLL--NSLWPDDENSVWDAFMKRIEELIDQKISEAVKGRALDELTLGLQ
      90      100     110     120     130     140

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      110     120     130     140     150     160
Cry1Ac NLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAV---QNYQVPLLSV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 DNYNLYVEALDEWLNRN-NGARASLVSRFNILDSLFTQFMPSPGSGPGSQNYSTILLPV
      150     160     170     180     190     200

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      170     180     190     200     210     220
Cry1Ac YVQAANLHLSVLRDVSFVGQRWGFDAATIN---SRYNDLTRLIGNYTDHAVRWYNTGLER
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|717 YAQAANLHLLKLDADYIGARWGLNQTQIDQFHSRQQLTR---TYTNHCVTTYNDGLAE
      210     220     230     240     250

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      230     240     250     260     270     280
Cry1Ac VWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLENF-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

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500      510      520      530      540      550
Cry1Ac  SSGNNIQNRGYIEVPIHFPSTSTRYRVVRYASVTPIHNLVNWGSSIFSNS--TVPATAT
gi|156  ENSQMALTCRYTN-----SSPQEQYKIRIRYASN--RLNMGQLFTTFSHQFVLPPTFN
560      570      580      590      600
Cry1Ac  SLDNLQSS--DFGY--FESANAFTSSLG-NIVGVRNFSGTAGVIIDRFEPVPTATLEAE
gi|156  HFNIEQAKYEDYAYAEFPESMSIRGNLNSDILLILNLAGGELLDDKIEFIPLTKQVKDN
610      620      630      640      650      660
Cry1Ac  YNLERA---QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDEFCLDEKRELSEKV
gi|156  LEKEKIDMLKNLTDLSLNFNSPKDTLKIDSTDYQIDQIAFQIESINEEINPQEKMELLDNI
670      680      690      700      710      720
Cry1Ac  KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGT---FDE
gi|156  KYAKKLNQLRNLLYSR----ESQAQIDWVTSNDVSIYHGKPFNDYTLVMSRTSSSLSE
730      740      750      760      770
Cry1Ac  C----YPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRY-NAKHETVNVPGTG--
gi|156  ITATNYQTYIYKKEIESKLPYTRYLVVRFISNSEDLEIFISRYENEIHTNMNVHGDDDT
780      790      800      810      820      830
Cry1Ac  -----SLWPLSAQSPIGKCGEPNRCAP---HLEWNPDLDCSCRDGKCAHSHS
gi|156  LLNSDIRQNECESKLPPIIFDATSQYSLSPSRTSGISNHSYNNNGHQSSND-----TH
840      850      860      870      880      890
Cry1Ac  HFSLDIDVGCTDLNEDLGVVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
gi|156  IFSFSIDTGEVDFNNYPGIEILFKLSNTNGYASISNLEVIERLLTTEEKQRIIQIENRW
900      910      920      930      940      950
Cry1Ac  RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAADKRVHSIREAYLPE
gi|156  KAKKESQRNETEKITTAQQAINSLFTDTQYSNLKFETTKQNTIENANTILENIPVYVNAL
960      970      980      990      1000     1010
Cry1Ac  LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNNQRS
gi|156  LPTEPGMNFVLFNSPKDQINKAHALYKMRNLIKNGDFINDTKYWSISTDVKLE-KVNET
1020     1030     1040     1050     1060     1070
Cry1Ac  VLVVPEWEAEVSEQEVRVCPGRGYILRVTAAYKEGYGEGCVTIHEIENNTDELKFS--NCVE

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gi|156  ILVSSWEAQASQQILVQKQRYLLRVIKAKEDMGRGNVVISDCLNNAIKIDFTPHDCNM
1080     1090     1100     1110     1120     1130
Cry1Ac  EEIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPC
1070     1080     1090     1100     1110     1120
gi|156  NHIQNSSEFIIKTIHFSNPTEQVRIDIGQSDGVFKVESIELICVNY
1140     1150     1160     1170
>>gi|156711546|emb|CAJ86545.1| Cry48Aa protein [Lysiniba (1177 aa)
initn: 1079 init1: 339 opt: 593 Z-score: 688.2 bits: 139.3 E(): 2.1e-29
Smith-Waterman score: 1291; 28.520% identity (58.394% similar) in 1108 aa overlap
(40-1067:63-1129)
10      20      30      40      50      60
Cry1Ac  NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIW
gi|156  TNYKDWLNLQDFNKDIESYDLVAVSSGTIVVGTMLSAIYAPALIGPIGIIISF
40      50      60      70      80      90
Cry1Ac  GIFGPSQWDA-----FLVQIEQLINQRIEFARNQAI SRLEGLS-NLYQIYAES
gi|156  GTLLPLLWNESENPKTTWIEFIRMGEQLVDKTIISQTVFNILESYLKD LKVNLDV-YEKA
100     110     120     130     140     150
Cry1Ac  FREW-----EADPTNPALREEMRIQFNDMNSALTTAIPL--FAVQNYQVPLLSVYVQ
gi|156  KQDWIELKKQQLPGSPPTKLRNAADIAHQRLDSLHNKFAELNKFVPEYETILLPVYAQ
160     170     180     190     200     210
Cry1Ac  AANLHLVLRDVSFVQGRWGFDA-----TINSRYNDLTRLIGN---YTDHAVRWYNTG
gi|156  AANLHLNLLQQGAMFADQWIEDKYSRNDTFAGNSNDYQNLKSRITITYINHIENTYQNG
220     230     240     250     260     270
Cry1Ac  LERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTY-PIRTV-SQLTREIYTN-P
gi|156  LNYLWNQPEMTWDIYNEYRTKMTITALDLMALFPFYNKELYDPTVGIKSELTREIFINTP
280     290     300     310     320     330
Cry1Ac  VLENFDGSFRGSAQGI EGSIRSPHLM DILNSITITYDAHRGEYYWGHQIMASPVGFSGP
gi|156  VEPHLHRYFKLS-ETEEKLTNNSDLFKWLTSLKFRITLYQPGFPFLIGN--MNSFTNTNGT
340     350     360     370     380
Cry1Ac  EFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQLSVLDGTEFAYG
gi|156  QL-----INN---QQQLWSFPPTTENE---KLFPPSPANIDQVTMYIYYGSGWGPIPE
390     400     410     420     430
Cry1Ac  TSSNLPSAVYRKS GTVDSLDEIPPQNNVPPRQ---GF-SHRLSHVSMFRSGFSNSSVSI

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gi|156 ISTTINKLIFNHDKH-ELISEYDAGNTNAPTRSLSLGSLPNHYLSCLNSYYP-LTATTDGM
    440      450      460      470      480      490
Cry1Ac IRAPM----FSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRLN
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 NKEELKMSYFGWTHNSVDFLNEISKDKITQIPAVKAYRLTNSNRVIKGPSHIGNLVYLS
    500      510      520      530      540      550
Cry1Ac SSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWGSSIFSN--TVPATAT
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 ENSQMALTCRYTN-----SSPQEQYKIRIRYASN--RLNMGQLFTTFSHQFVLPPTFN
    560      570      580      590      600
Cry1Ac SLDNIQSS--DFGY--FESANAFTSSLG-NIVGVRNFSGTAGVIIDRFEFIPVTATLEAE
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 HFNIEQAKYEDYAYAEFPESMSIRGNLNSDILLIILNLAGGELLLDKIEFIPLTKQVKDN
    610      620      630      640      650      660
Cry1Ac YNLERA---QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 LEKEKIDMLKNLTDLSLNFSPSKDTLTKIDSTDYQIDQIAFQIESINEEINPQEKMELLDNI
    670      680      690      700      710      720
Cry1Ac KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLTSGT---FDE
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 KYAKKLNQLRNLQYSR----ESQAQIDWVTSNDVSIYHGKPFNDYTLVMSRTSSSLSE
    730      740      750      760      770
Cry1Ac C----YPTYLYQKIDESKLFKAFTRYQLRGYIEDSDLEIYSIRY-NAKHETVNVPGTG--
    . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|156 ITATNYQTYIYKKEIESKLPYTRYLVRFISNSDLEIFISRYENEIHTNMNVHGDDDT
    780      790      800      810      820      830
Cry1Ac -----SLWPLSAQSPIGKCGEPNRCAP---HLEWNPDLDCSCRDEKCAHSH
    . . . . . : : . . . : : : . : : : : : : : : : : : : : : : : : :
gi|156 LLNSDIRQNECESKLPPIIFDATSQYSLSPSRTSGISNHSYNNNGHQSSCND-----TH
    840      850      860      870      880      890
Cry1Ac HFSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKW
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . . :
gi|156 IFSFSIDTGEVDFNPNYPIELFLKLSNTNGYASISNLEVIEERLLTEBEKRQIIQIENRW
    900      910      920      930      940      950
Cry1Ac RDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSIREAYLPE
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . . :
gi|156 KAKKESQRNETEKITTTAQQAINSLFTDTQYSNLKFFETTKQNITEANTILENIPYVYNAL
    960      970      980      990      1000     1010
Cry1Ac LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSGCWNVKGHVDEEQNNQRS

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    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|156 LPTEPGMNFVLFNSFKDQINKAHALYKMRNLKNGDFINDTKYWSISTDVKLE-KVNKET
    1020     1030     1040     1050     1060     1070
Cry1Ac VLVVPEWEAEVSVQEVRCVPCGRGYILRVYAYKKEGYGEGCVTIHEIENNTDELKFS--NCVE
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|156 ILVLSWEAQASQQLLVQKQRYLLRVIKAKEDMGRGNVVIISDCLNIIAKIDFTPHDCNM
    1080     1090     1100     1110     1120     1130
Cry1Ac EEIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRRENPC
    1070     1080     1090     1100     1110     1120
gi|156 NHIQNSSEFIIKTIHFSPNTEQVRIDIGQSDGVFKVESIELICVNY
    1140     1150     1160     1170
>>gi|632792|gb|AAC60477.1| delta-endotoxin CryIAb7 [Baci (91 aa)
    initn: 578 initl: 578 opt: 578 Z-score: 687.1 bits: 135.4 E(): 2.4e-29
Smith-Waterman score: 578; 92.308% identity (97.802% similar) in 91 aa overlap (5-
95:1-91)
Cry1Ac CMQAMDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|632 MDNPNKINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGF
    10      20      30      40      50
Cry1Ac VLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEIEFARNQAISRLEGLSNLYQIYAESFRE
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|632 VLGLIDLWCFVGPSQWDAFLVQIEQLISQRIEIEF
    60      70      80      90
Cry1Ac WEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
    130     140     150     160     170     180
>>gi|37999234|dbj|BAD00052.1| putative mosquitocidal tox (683 aa)
    initn: 459 initl: 199 opt: 583 Z-score: 680.0 bits: 137.0 E(): 5.9e-29
Smith-Waterman score: 620; 28.058% identity (57.266% similar) in 695 aa overlap
(2-633:13-681)
Cry1Ac CMQAMDNPN-INECIPYNCLSNPEVEVLGG-----ERIEYGYTP
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|379 MNPYQKKTETEYELDALPNYSNMVNAYSRYPLANNPQVPLQNTSYKDWLNMCOQTINPLCTP
    10      20      30      40      50      60
Cry1Ac IDISL-SLTQFL----LSEFVPGAG---FVLGLVDIIWGFGPSQ---WDAFLVQIE
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|379 INIDDSLAAASIAVVGSIILIPGPGEAIGFVLGTFSTILPILWPNGETKIWTDFAEERGL
    70      80      90      100     110     120
Cry1Ac QL----INQRIEIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDM
    . . . . . : : . . . : : . . . . . : : . . . . . : : . . . . .
gi|379 QLFRPELGDAIEILVTGVKSGYNALKNRNMFQEQFTKWKGNRTRSNAEQVIR----DF
    130     140     150     160     170

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150      160      170      180      190
Cry1Ac NSALTTAIPL---FAVQNYQVP-LLSVYVQAANLHLSVLRDVSVFGQRWGFDA-ATIN--
gi|379 DSVRDKVIDLKNNDYMINPENKPAFINLYAQTANIDLILYQRGAVYGDDEKWDINGSISPF
180      190      200      210      220      230

200      210      220      230      240      250
Cry1Ac ----SRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSDRWIRYNQFRRELTLTVLDIVSL
gi|379 WGSKDYYESLTKTIEEYTNCAETYNRSLNLIKKNPNISWDTYNKYRREATLGALDLVAL
240      250      260      270      280      290

260      270      280      290      300
Cry1Ac FPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSI-RSPHLMIDILNSITI
gi|379 FPNYDMHLYPAATKTELTRKIYM-PSFGLQQSNYFQSLEGLLENALTHPPSLFTWLNELNL
300      310      320      330      340      350

310      320      330      340      350      360
Cry1Ac YTDAHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQR--IVAQLGQG---VYR
gi|379 YTVR---ENFNPALQV-SSLSGLQARSRYTQNPTILDNPAQGVNRGTSTQIGLNNLFVYK
360      370      380      390      400      410

370      380      390      400      410      420
Cry1Ac TLSSTLYRRPFN---IGINNQQLSVLDGTEFAYGTSSNLPASVYRKSGETVDSLDEIPPQ
gi|379 -LSMSQYHHPNDCCSIIAGISDMTFYKSDYNGNASATQTY--QAGRNTNNTVTFMNGPQK
420      430      440      450      460

430      440      450      460      470
Cry1Ac ---NNNVPPRQGFSHRLSHVSM--FRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSI
gi|379 ASSSNNISIKQT-KHILSDIKMIYFRTGGMYQVYDFGYS--FAWHTSTVDPDNLIVPNRI
470      480      490      500      510      520

480      490      500      510      520      530
Cry1Ac TQIPAVKG-NFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVR
gi|379 TQIPAVKALGISTDSKVVKGPVFIGDDLKLLK----LQAT----IRIKTDHANTRYKIR
530      540      550      560      570

540      550      560      570      580      590
Cry1Ac VRYASV--TPIHLNVNWGNSSI-FSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNI-
gi|379 VRYASNANTPIVLSLQNTLVTFFPQTI--THSTISELQYKDFQVTFPFGEFIMDKPSID
580      590      600      610      620      630

600      610      620      630      640
Cry1Ac VGVNRFSGTAGVI-IDRFEFIPVTATL---EAEYNLERAQKAVNALFTSTNQLGLKTNVT
gi|379 VAIRGVQNDRNDIWDRIEFLPITQSVLDYTEEQNIEKSQKAVNDLFIN
640      650      660      670      680

650      660      670      680      690      700
Cry1Ac DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG

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>>gi|51090237|dbj|BAD35164.1| C-terminal half of Cry pro (735 aa)
initn: 896 init1: 259 opt: 582 Z-score: 678.3 bits: 136.8 E(): 7.3e-29

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Smith-Waterman score: 963; 36.226% identity (63.396% similar) in 530 aa overlap (620-1121:3-518)

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590      600      610      620      630      640
Cry1Ac IVGVNRFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
gi|510 MNYNVTKAREAVQALFSNPPTTLQLK--VTDHH
10      20      30

650      660      670      680      690      700
Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
gi|510 VNQVARLVECIADQIHPKEKMCLLDQVKLAKRLSRERNLLNYGDFESSDVGWGTGWNVST
40      50      60      70      80      90

710      720      730      740      750      760
Cry1Ac GITIQGGDDVFKENYVTLSTG-----FDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQ
gi|510 NVYTVADNP IFKDHVLMNPSANNPILSDKIFPTYAYQKVEESRLKPYTRYIVRGVFGSSK
100      110      120      130      140      150

770      780      790      800      810      820
Cry1Ac DLEIYSIRYNAK-HETVNVPGTGSWPLSAQS--PIGKCGEPNRCAPHLEWNPDLDCS-C
gi|510 DLEILVARVDEKVKHKNMNP--NDIIPSTPCTGEPVSQ--PTYVPMVSNMTPQDMWCNCP
160      170      180      190      200

830      840      850      860
Cry1Ac RDGEKCA-----HSHHFSLDIDVGCTDLNEDLGWVIFKIKTQDGHARLGNL
gi|510 GNGYQTAAGMMVQSTGMMQDPHEFKFHIDIGELDMERNLGIWIGFKVGTTEGMATLDNI
210      220      230      240      250      260

870      880      890      900      910      920
Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQAD
gi|510 EVVEVGPLTGDALTRMQRKRETKWKQKLTTEKRMKIEKAVQIARDAIQTLFTCPNQSLQSA
270      280      290      300      310      320

930      940      950      960      970      980
Cry1Ac TNIAMIIAADKRVHSIREAY---LPELSVIPGVNAA--IFEELGRIFTAFSLYDARNV
gi|510 ITLQNILRAEKLQKIPYVYNQFLQGVLSAVPGEAYAYDIFQQLSDAVATARALYNQRNV
330      340      350      360      370      380

990      1000      1010      1020      1030      1040
Cry1Ac IKNGDFNGLSCWNVKGVHDVEEQNNQRSVLVVPEWEAEVSVQEVVRCVPGRGYILRVYAYK
gi|510 LNNGDFSAGLSNWNWTEGADVQQIGNA-SVLVISDWSASLSQHVYVVKPEHSLYLLRVYAYK
390      400      410      420      430      440

1050      1060      1070      1080      1090      1100
Cry1Ac EGYGEGCVTIHE-IECNTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGY
gi|510 EGSSEGYVTISDGEENTETLKFV--VGEE---TTGATMSTIRSNIRER---YNERNMAT
450      460      470      480      490

1110      1120      1130      1140      1150      1160
Cry1Ac NEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKELEYFPETDKVWI

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gi|222 SGNQNFSLN-GTSN-LYGYRSDGRITTFNVSNIIDIFRVNMTTHIG-GAFTDDYRGLHRAEF
360 370 380 390 400

Cry1Ac NIGIN---NQQLSVLDGTEFAYGTSSNLPSAVYR-KSGTVDSLDEIPPQNNVPPRQGF
380 390 400 410 420 430

gi|222 -IGANTQNNQRTSLLYSVE-----IPSSHFRFENHTV----FLPGESGLEPNERNYT
410 420 430 440 450

Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSV
440 450 460 470 480 490

gi|222 HRLFQMMNEVSNPNAR---GRVFLHAWTHRSLRRTNGLRSDQILQIPAVKT--ISNGGD
460 470 480 490 500

Cry1Ac ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWN
500 510 520 530 540 550 560

gi|222 RAVVLNYGENIMKLDNLTGLS---YKLTAVDSEASNTRFIVRVRYASMMNNKLNVLNG
510 520 530 540 550 560

Cry1Ac SSIFNTVPATAT---SLDNLQSSDFGYFESANAFTSSLGNIVGVNRFSGTAGVIIDRFE
560 570 580 590 600 610 620

gi|222 AQIASLNVEHTVQRGGLTDLQYGNFKYATFAGNFKMGSQSILGIFKEIPNIDFVLDKIE
570 580 590 600 610 620

Cry1Ac FIPVT--ATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCL
610 620 630 640 650 660

gi|222 LIPSNFMSLEQTQNYNTYNDTIYTHNQGYDTYDQSSGMVHQSYNNYDQNMDDTYQPS
630 640 650 660 670 680

>>gi|51090233|dbj|BAD35161.1| C-terminal half of Cry pro (737 aa)
initn: 896 initl: 259 opt: 578 Z-score: 673.6 bits: 135.9 E(): 1.3e-28
Smith-Waterman score: 961; 35.379% identity (61.733% similar) in 554 aa overlap
(620-1123:3-550)

Cry1Ac IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
590 600 610 620 630 640

gi|510 MNYNVTKAREAVQALFSNPTTLQLK--VTDHH
10 20 30

Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
650 660 670 680 690 700

gi|510 VNQVARLVECIADQHPKEKMCLLDQVKLAKRLSRERNLLNYGDFESSDWWGTDGWNVST
40 50 60 70 80 90

Cry1Ac GITIQGGDDVFKENYVTLSGT----FDECYPTYLYQKIDESKLFKAFTRYQLRGIEDSQ
710 720 730 740 750 760

gi|510 NVYTVADNPIFKDHYLNMPKANNPILSDKIFPTYAYQVVEESRLKPYTRYIVRGFVGS
100 110 120 130 140 150

Cry1Ac DLEIYSIRYNAK-HETVNVPGTGSWPLSAQS--PIGKCGEPNRCAPHEWNPDLDCS-C
770 780 790 800 810 820

gi|510 DLEILVARVDKEVHKRMNVNPN--DIIPTSPCTGEPVSQ-PTYPVPMPSNTMPQDMMCNC
160 170 180 190 200

Cry1Ac RDGEKCA-----HSHHFSLDIDVGCTDLNEDLGWVVIKIKTQDGHARLGNL
830 840 850 860

gi|510 GNGYQTAAGMMVQSTGMMQDPHEFKFHIDIGELDMERNLGIWIGFKVGTTEGMATLDNI
210 220 230 240 250 260

Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQAD
870 880 890 900 910 920

gi|510 EVVEVGPLTGDALTRMQKRETKWKQKLETKRMKIEKAVQIARDAIQTLFTCPNQSCQLQSA
270 280 290 300 310 320

Cry1Ac TNIAMIAADKRVHSIREAY---LPELSVIPGVNAA--IFELEGRIFTAFSLYDARNV
930 940 950 960 970 980

gi|510 ITLQNILRAEKLVQKIPVYVYVQFLQGVLSAVPGEAYAYDIFQQLSDAVATARALYNQRNV
330 340 350 360 370 380

Cry1Ac IKNGDFNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAEVSVQEVRCVPCGRGYILRVYAYK
990 1000 1010 1020 1030 1040

gi|510 LNNGDFSAGLSNWNWTEGADVQQIGNA-SVLVISDWSASLSQHVVYKPEHSYLLRVYAYK
390 400 410 420 430 440

Cry1Ac EGYGEGCVTIHE-IENNTDELKFSNCEVEEIIYPNNTVTCN---DY-----TVNQEEYGG
1050 1060 1070 1080 1090

gi|510 EGSSEGYVTISDTEENTETLKFVMEETTGATMSTIRSNIRERYERNMATPDPDAYGG
450 460 470 480 490 500

Cry1Ac A-----YTSRNRGYN-EAPSVPADYAS-VYEEKSYTDGRRENCEFNRYRDRYT
1100 1110 1120 1130

gi|510 TNGYASNQNMVNYSSSENYGMSAHSNNMNYQSESFSGSKPYDGDGNSMINGSNNYEANGY
510 520 530 540 550 560

Cry1Ac PLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170 1180

gi|510 PGNNNINDQSENYGANAYSSNNMNYQSESSGFTPYGDENNMTNYPNNYEMNPYSDDMMN
570 580 590 600 610 620

>>gi|51090229|dbj|BAD35158.1| C-terminal half of Cry pro (737 aa)
initn: 896 initl: 259 opt: 578 Z-score: 673.6 bits: 135.9 E(): 1.3e-28
Smith-Waterman score: 961; 35.379% identity (61.733% similar) in 554 aa overlap
(620-1123:3-550)

Cry1Ac IVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYH
590 600 610 620 630 640

gi|510 MNYNVTKAREAVQALFSNPTTLQLK--VTDHH
10 20 30

Cry1Ac IDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGST
650 660 670 680 690 700



Cry1Ac VRLNSSGNNIQNGYIEVPIHFPSTSTR-YRVRVRYASVTPIHLLNVNWNSSIFSNTVPA  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 VYLS-----DKSQLSLACRYTNSSPQDFLIRIRYASNKRNMVQL-PTPFSTHQFVLPQ  
 550 560 570 580 590 600

Cry1Ac 570 580 590 600 610  
 TATSLDNLQSS--DFGYFESANAFTSSLGNI---VGVRFNSGTAGVIIDRFEFIPVTAT  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 TFNHLNIEQTKYEDYEYQLPGSLTIN-GNVNIDLLFLLNVLDGGELLDDKIEFIPLTQK  
 610 620 630 640 650

Cry1Ac 620 630 640 650 660 670  
 LEAEYNLERA---QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 VKDNLEKPKIDMLKNTLSLNFSPAKDTLKNINSTDYQIDQIAFAQIESINEEINTQEKMKL  
 660 670 680 690 700 710

Cry1Ac 680 690 700 710 720 730  
 SEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGT--  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 LDNIKYAKKLNLRLNLYSRE----SQAQIDWVTSNDVSIYHGKPKFNEYTLVMSSGSL  
 720 730 740 750 760 770

Cry1Ac 740 750 760 770 780  
 ---FDECYPTYLYQKIDESKLFKAFTRYQLRGIYIEDSQDLEIYSIRY-NAKHETVNVPGTG  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 SKITSSNYPTIYKKEESKLPYTRYLVRGFISNSDNLEIFISRYENEIHTNMNVHVD  
 780 790 800 810 820 830

Cry1Ac 790 800 810 820  
 -----SLWPL---SAQSPIGKCGEPNRCAP---HLEWNPDLDCSCRDGEK  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 DTLNLSYKRNCESEKLPVFDETSQYPLS---PSRTSGISNHSYNGAQSSC-----  
 840 850 860 870 880

Cry1Ac 830 840 850 860 870 880  
 CAHSHHPSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARLGNLEFLEEKPLVGEALARVK  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 --HDTQIFSFSDIDTGDVDFNEYPGIEILFKLSNSNGYASISNLEVIERLLTEEEKRHII  
 890 900 910 920 930 940

Cry1Ac 890 900 910 920 930 940  
 RAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMHAADKRVHSIR  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 EIENRWAKKEIQRNETEKETTQAQQAINNLFDTQYSKLFETTKQSIISKANAILENIP  
 950 960 970 980 990 1000

Cry1Ac 950 960 970 980 990 1000  
 EAYLELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEE  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 VVYNSLLPTEPGMNFELFNSFKDQINKAHTLYKMRNSIKNGDFINGTEYWSISTDVKLE-  
 1010 1020 1030 1040 1050 1060

Cry1Ac 1010 1020 1030 1040 1050 1060  
 QNNQRSVLVPWEAEVSVQEVRCVPRGYILRVYAYKEGYGEGCVTIHEIENNTDELKFS  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .  
 gi|156 KTNIEITILVMSSWSAQSSQQLVQKQNRYLRLVIAKEDMGSGNVITISDCLNIIAKIEFI  
 1070 1080 1090 1100 1110 1120

1070 1080 1090 1100 1110 1120  
 Cry1Ac NCVEEEIYPNNTVTVCNDYTVNQEEYGGAYTSRNRNGYNEAPSPADYASVYEEKSYTDGRR

gi|156 PHDCNMN

>>gi|156711552|emb|CAJ86549.1| Cry48Aa protein [Lysiniba (1129 aa)  
 initn: 1075 init1: 370 opt: 570 Z-score: 661.4 bits: 134.3 E(): 6.4e-28  
 Smith-Waterman score: 1249; 28.584% identity (56.988% similar) in 1109 aa overlap  
 (40-1064:63-1121)

10 20 30 40 50 60  
 Cry1Ac NINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVGLVDIIW  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 TNYKDWLNLQCFDNKDIESYDLVAVSSGTIVVGTMLSAIYAPAIAGPIGVIGALIIISF  
 40 50 60 70 80 90

70 80 90 100 110  
 Cry1Ac GIFGPSQWDA-----FLVQIEQLINQRIEEFARNQAIISRLLEGLS-NLYQIYAES  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 GTLLPLLWSEDENNPKTWVIEFIRMGERLVDKTISQTVLNILESYLKDGLKVNLIID-YEKA  
 100 110 120 130 140 150

120 130 140 150 160  
 Cry1Ac FREW----EADPTNPA---LREEMRIQFNDMNSALT--TAIPLFAVQNYQVPLLSVYVQ  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 KQDWIELKKQQLPGSPPSINLRNAADIAHQRLDSLHNKFAELNVFKVASYETILLPVYQA  
 160 170 180 190 200 210

170 180 190 200 210  
 Cry1Ac AANLHLSVLRDVSFVFGQRWGFDA-----ATINSRYNDL--TRLIGNYTDHAVRWYNT  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 AANLHLNLLQQGAMFADQWIEDKYSRPNDTFAGNSNDYQDLLKSRIT-TYINHIENTYKD  
 220 230 240 250 260 270

220 230 240 250 260 270  
 Cry1Ac GLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRT--VSQLTREIYTN-  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 GLNYLWNQPEMTWDIYNEYRTNMTLALDPLPFPFNKELYDPRVGIKSELTRVYIINT  
 280 290 300 310 320 330

280 290 300 310 320 330  
 Cry1Ac PVLENFDGSFR-GSAQGIEGSIRSPHLMIDLNSITIIYTDahrgeyywsgHQIMASPVGFS  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 PVDPHLHRFYKLGETE--DKLTNNSLFPKWLTSKLFRTFNQPGFPFLIGN--MNYFKKTN  
 340 350 360 370 380

340 350 360 370 380 390  
 Cry1Ac GPFTFPPLYGTMGNAAPQORIVAQLGQGVYRTLSSSTLYRRPFNIGINNQLSVLDGTEFA  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 GTQL-----INN---QQQLWSFPG---TTEIEKLFPSPANIDKVTMYIYGGSWVEVP  
 390 400 410 420 430

400 410 420 430 440  
 Cry1Ac YGTSSNLPsAVY--RKSgtVDSLDEIPPQNNVPPRQGF---SHRLSHVSMFRSGFSNS  
 : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|156 EPISITINKLIFNHHKHLITEYDA---GNTNAPTMGIIYVNLPHKYLSCLSNYSYP-LTAT  
 440 450 460 470 480

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450          460          470          480          490          500
Cry1Ac SVSIIIRAPM---FSWIHRSAEFNIIASDSITQIPAVKGNFLFNQSVISGPGTGGDL
gi|156 TNGMGKEELKMSYFGWTHESVDFLNEISNDKITQIPAVKAYLNLSNSRVIKGPGHIGGNL
490          500          510          520          530          540

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510          520          530          540          550          560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTR-YRVRVRYASVTPIHLLNVNWNSSIFNTVPA
gi|156 VYLS-----DKSQLSLACRYTNSSPQDFLIRIRYASNKRNMVQL-FTPFSTHQFVLPQ
550          560          570          580          590          600

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570          580          590          600          610
Cry1Ac TATSLDNLQSS--DFGYFESANAFTSSSLGNI---VGVNRFSGTAGVIIDRFEPVPTAT
gi|156 TFNHLNIEQTKYEDYEYAQLPGLSLTIN-GNVNIDLFLNVLDDGGELLDDKIEFIPLTQK
610          620          630          640          650

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620          630          640          650          660          670
Cry1Ac LEAEYNLERA---QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKREL
gi|156 VKDNLEKEKIDMLKNLTDLSLNFSPAKDTLTKIDSTDYQIDQIAFAQIESINEEINTQEKMKL
660          670          680          690          700          710

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680          690          700          710          720          730
Cry1Ac SEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTG--
gi|156 LDNIYAKKLNQLRNLLYSRE----SQAQIDWVTSNDVSIYHGKPKFNEYTLVMSSGSSL
720          730          740          750          760          770

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```

740          750          760          770          780
Cry1Ac ---FDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRY-NAKHETVNVPGTG
gi|156 SKITSSNYPTYIYKKEESKLPYTRYLVRFISNSDNLEIFISRYENEIHTNMNVHVD
780          790          800          810          820          830

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```

790          800          810          820
Cry1Ac -----SLWPL---SAQSPIGKCGEPNRCAP---HLEWNPDLDCSCRDGEK
gi|156 DTLNLSYKRQNECESKLPVDFDTSQFPLS----PSRTSGISNHSYNGAQQSSC-----
840          850          860          870          880

```

```

830          840          850          860          870          880
Cry1Ac CAHSHHFLSLDIDVCGTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVK
gi|156 --HDTQIFSFSDTGDVDFNEYPGIEILFKLSNSNGYASISNLEVEERLLTEEEKRHII
890          900          910          920          930          940

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890          900          910          920          930          940
Cry1Ac RAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIR
gi|156 EIENRWAKKEIQRNETEKETTQAQQAINNLFDTQYSKLFKFTTKQSIKANAILENIP
950          960          970          980          990          1000

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```

950          960          970          980          990          1000
Cry1Ac EAYLPBELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEE
gi|156 VYNSLLPTEPGMNFELNSFKDQINKAHTLYKMRNSKNGDFINGTYKWSISTDVKLE-
1010         1020         1030         1040         1050         1060

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```

1010         1020         1030         1040         1050         1060
Cry1Ac QNNQRSVLVPEWEAEVVSQEVRCVPCGRGYILRVVTAYKEGYGECVTHIEIENNTDELKFS
gi|156 KTNIEITILVMSWSAQSSQQLVQKQNRVLLRVIKAKEDMGSQNVITISDCLNNAKIEFI
1070         1080         1090         1100         1110         1120

```

```

1070         1080         1090         1100         1110         1120
Cry1Ac NCVEEIYPNNVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRR
gi|156 PHDCNMN

```

>>gi|51998369|emb|CAH33956.1| unnamed protein product [B (661 aa)  
initn: 712 initl: 415 opt: 566 Z-score: 660.1 bits: 133.3 E(): 7.6e-28  
Smith-Waterman score: 909; 31.530% identity (59.969% similar) in 647 aa overlap  
(21-633:44-659)

```

10          20          30          40          50
Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQLP
gi|519 PQMTMRNTNYKEWLNMCDSNTQFIGDISTYSSPEAALSVRDAVLGTGINSVGTILSNLQVP
20          30          40          50          60          70

```

```

60          70          80          90          100          110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEFAFNQAISRLEGLSNL
gi|519 LAS--QSFGIISRLIGILWA--GPDPEALMVLVEELIKKSIDQRVRENALRELEGLQGI
80          90          100          110          120

```

```

120         130         140         150         160         170
Cry1Ac YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
gi|519 MRLYQTRLQAWLVNKNDDN--RRALVTQYAIVDNFFEKNNMPKFKERNFEILLPVYAQAAN
130         140         150         160         170         180

```

```

180         190         200         210         220         230
Cry1Ac LHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
gi|519 LHLILLRDADYFGAQWQLGDDEIRDNYIRLQGLIREYKDKHCITFYNOQLNQFNRSNAQDW
190         200         210         220         230         240

```

```

240         250         260         270         280
Cry1Ac IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNPVENFDGSGFRGSAQ-
gi|519 VSFNFRFTDMTTLVLDLAILFPNYDPRRYPLAVKTELTREYVTDVP--GFTGVLESGGRT
250         260         270         280         290         300

```

```

290         300         310         320         330
Cry1Ac -----GIEGSIRS-PHLMIDILNSITIYT---DAHRGEYYWGHQIMASPVGF
gi|519 YPWYNPNNTFTTAMENNARRRPSYTTWLNRIFFVYTRTLGNMSDVRNIWGGHTLVEN--GN
310         320         330         340         350         360

```

```

340         350         360         370         380
Cry1Ac SGPEFTFPYLGTMGNAAPQORI-VAQLGQGVYRTLSSSTLYRRPFNIGI--NNQQLSVLDG
gi|519 DGSEITHN-FGKTDSITPIQYFNANLSVFSIESLA----RIYLGTEANNYITSQYGV
370         380         390         400         410

```

```

390      400      410      420      430      440
Cry1Ac  TEFAYGTSS--NLPSAV-YRKSGTVDS---LDEIPPQNNVPPRQGFSHRSLSHVSMFRSG
..  . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  SRVIFNTSNINNVPGSLRYEVPANLPSQTILSELPGKDKPRNAGDFSHRSLYSISNFDAR
420      430      440      450      460      470

```

```

450      460      470      480      490      500
Cry1Ac  FSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLV
: : : . . . : : : : . . . : : : : . . . : : : : . . . : : : : . . . :
gi|519  RS-SSGGIVSLLTFGWAHTSMDRNNRLEPDKITQIDAVKGGWGNIGFVIGP--TGGNLV
480      490      500      510      520      530

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```

510      520      530      540      550
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW---GNSSI--FSN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  KVSDSWHSLK-----VQAPQRQTSYRIRLRYACLVT-HGDAIFVEHSGSSSHVSVFFD
540      550      560      570      580

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560      570      580      590      600      610
Cry1Ac  TVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFS-GTAGVIIDRFEFIPVTATL
. . . . . : : : . . . : : : . . . : : : . . . : : : . . . : : : . . .
gi|519  CSNSSGRPSNTLLESDFRYIDVPGIFTPSINPLIRYRTQSPGTHA--IDKFEFIPLNTF-
590      600      610      620      630      640

```

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620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
. : : . . . : : : . . . : : : . . . : : : . . . : : : . . . : : :
gi|519  -PNQSLEKREQEVNDLFIN
650      660

```

>>gi|51998367|emb|CAH33955.1| unnamed protein product [B (671 aa)  
 initn: 712 initl: 415 opt: 566 Z-score: 660.0 bits: 133.3 E(): 7.6e-28  
 Smith-Waterman score: 909; 31.530% identity (59.969% similar) in 647 aa overlap  
 (21-633:54-669)

```

10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
: : : . . . : : : . . . : : : . . . : : : . . . : : : . . . :
gi|519  PQMTMRNTNYKEWLNMCDSNTQFIGDISTYSSPEAALSVRDAVLTGINSVGTILSNLQVP
30      40      50      60      70      80

```

```

60      70      80      90      100      110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGFQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
. : . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|519  LAS--QSPGIIIRLIGILWA--GPDPEALMVLVEELIKKSIDQVRRENALRELEGLQGI
90      100      110      120      130

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```

120      130      140      150      160      170
Cry1Ac  YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAAN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  MRLYQTRLQAWLVNKNDDN--RRALVTQYAIVDNFFEKNNPKFKERNFELLPLVYAQAAN
140      150      160      170      180      190

```

```

180      190      200      210      220      230
Cry1Ac  LHLVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
: : : . . . : : : . . . : : : . . . : : : . . . : : : . . . :
gi|519  LHLILLRDADYFGAQWQLGDDEIRDNYIRLQGLIREYKDHCIITFYNQGLNQFNRSNAQDW
200      210      220      230      240      250

```

```

240      250      260      270      280
Cry1Ac  IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVENFDGSGFRGSAQ-
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  VSFNRFRTDMTLTLVLDLAILFPNYDPRRYPLAVKTELTRREYVTDVP--GFTGVLESGGRT
260      270      280      290      300      310

```

```

290      300      310      320      330
Cry1Ac  -----GIEGSIRS-PHLMIDILNSITITYT----DAHRGEYVWSGHQIMASPVGF
. . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|519  YPWYNPNNTTTFAMENNARRRPSYTTWLNRIFFVYTRTLGNMSDVRNIWGGHTLVEN--GN
320      330      340      350      360      370

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340      350      360      370      380
Cry1Ac  SGPEFTFPLYGTMGNAAPQORI-VAQLGQGVYRTLSTLYRRFPNIGI--NNQQLSVLDG
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  DGSEITHN-FGKTDSITPIQYFNANLSVFSIESLA----RIYLLGGTEANNYITSQYGV
380      390      400      410      420

```

```

390      400      410      420      430      440
Cry1Ac  TEFAYGTSS--NLPSAV-YRKSGTVDS---LDEIPPQNNVPPRQGFSHRSLSHVSMFRSG
..  . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  SRVIFNTSNINNVPGSLRYEVPANLPSQTILSELPGKDKPRNAGDFSHRSLYSISNFDAR
430      440      450      460      470      480

```

```

450      460      470      480      490      500
Cry1Ac  FSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLV
: : : . . . : : : : . . . : : : : . . . : : : : . . . : : : : . . . :
gi|519  RS-SSGGIVSLLTFGWAHTSMDRNNRLEPDKITQIDAVKGGWGNIGFVIGP--TGGNLV
490      500      510      520      530      540

```

```

510      520      530      540      550
Cry1Ac  RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW---GNSSI--FSN
. . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519  KVSDSWHSLK-----VQAPQRQTSYRIRLRYACLVT-HGDAIFVEHSGSSSHVSVFFD
550      560      570      580      590

```

```

560      570      580      590      600      610
Cry1Ac  TVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFS-GTAGVIIDRFEFIPVTATL
. . . . . : : : . . . : : : . . . : : : . . . : : : . . . : : : . . .
gi|519  CSNSSGRPSNTLLESDFRYIDVPGIFTPSINPLIRYRTQSPGTHA--IDKFEFIPLNTF-
600      610      620      630      640      650

```

```

620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
. : : . . . : : : . . . : : : . . . : : : . . . : : : . . . : : :
gi|519  -PNQSLEKREQEVNDLFIN
660      670

```

>>gi|51998365|emb|CAH33954.1| unnamed protein product [B (682 aa)  
 initn: 712 initl: 415 opt: 566 Z-score: 659.9 bits: 133.3 E(): 7.7e-28  
 Smith-Waterman score: 909; 31.530% identity (59.969% similar) in 647 aa overlap  
 (21-633:65-680)

```

10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFL
: : : . . . : : : . . . : : : . . . : : : . . . : : : . . . :
gi|519  PQMTMRNTNYKEWLNMCDSNTQFIGDISTYSSPEAALSVRDAVLTGINSVGTILSNLQVP
40      50      60      70      80      90

```

```

          60      70      80      90     100     110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLNQRIEEFARNQAIISRLEGLSNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 LAS--QSPGIIISRLIGILWA--GPDPEALMVLVEELIKKSIDQVRRENALRELEGLQGI
          100     110     120     130     140     150

```

```

          120     130     140     150     160     170
Cry1Ac YQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAAN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 MRLYQTRLQAWLVNKNDDN--RRALVTQYAIVDNFFEKNMMPKFKERNFEILLPVAQAAN
          160     170     180     190     200

```

```

          180     190     200     210     220     230
Cry1Ac LHLVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 LHLILLRDADYFGAQWQLGDDEIRDNYIRLQGLIREYKDHCIITFYNQGLNQFNRSAQDW
          210     220     230     240     250     260

```

```

          240     250     260     270     280
Cry1Ac IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGFSFRGSAQ-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 VSFNFRFRTDMLTTLVLDLAILFPNYDPRRYPLAVKTELREYVYTDPV--GFTGVLESGGRT
          270     280     290     300     310     320

```

```

          290     300     310     320     330
Cry1Ac -----GIEGSIRS-PHLM DILNSIT IYT---DAHRGEYYWSGHQIMASPVGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 YPWYNPNNTTFTAMENNARRRPSYTTWLNRIFFVYTRTLGNMSDVRNIWGGHTLVEN--GN
          330     340     350     360     370     380

```

```

          340     350     360     370     380
Cry1Ac SGPEFTFLYGTMGNAAPQORI-VAQLGGQVYRTLSSTLYRRPFNIGI--NNQQLSVLDG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 DGSEITHN-FGKTDSITPIQYFNANLVSFVSIESLA----RIYLGGETEANNYITSQYGV
          390     400     410     420     430

```

```

          390     400     410     420     430     440
Cry1Ac TEFAYGTSS--NLPSAV-YRKSQTVDS---LDEIPPQNNVPPRQGFSHRLSHVSMFRSG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 SRVIFNTSNINNVPGSLRYEVPANLPSQITLSELPGKDKPRNAGDFSHRLSYISNFDAR
          440     450     460     470     480     490

```

```

          450     460     470     480     490     500
Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 RS-SSGGIVSLTLFGWAHTSMDRNRNLEPKITQIDAVKGGWGNIGFVIPGP--TGGNLV
          500     510     520     530     540     550

```

```

          510     520     530     540     550
Cry1Ac RLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVN---GNSSI--FSN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 KVSDSWHSLSK-----VQAPQRQTSYRIRLRYACLVT-HGDAlFVEHSGSSHIVSFFD
          560     570     580     590     600

```

```

          560     570     580     590     600     610
Cry1Ac TVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFS--GTAGVIIDRFEFIPVTATL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 CSNSSGRPSNTLLESDFRYIDVPGIFTPSINPLIRYRQTSFGTHA--IDKFEPILNLF-

```

```

          610     620     630     640     650     660
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|519 -PNQSLKREQEVDLFIN
          670     680

```

>>gi|33765722|gb|AAQ52373.1| Sequence 24 from patent US (116 aa)  
 initn: 543 initl: 543 opt: 543 Z-score: 644.2 bits: 127.9 E(): 5.8e-27  
 Smith-Waterman score: 543; 72.174% identity (92.174% similar) in 115 aa overlap  
 (514-628:2-116)

```

          490     500     510     520     530     540
Cry1Ac NFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 NNRGHLPIPIQFSSRSTRYRVRVRYASATPI
          10     20     30

```

```

          550     560     570     580     590     600
Cry1Ac HLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 QNVVHWENSSFFSGTVPATAQSLDNLQSNNGFYFETANTISSSLDGIVGIRNFSANADLI
          40     50     60     70     80     90

```

```

          610     620     630     640     650     660
Cry1Ac IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 IDRFEFIPVDATSEAEHDLERAQKA
          100     110

```

>>gi|112088041|gb|ABI06954.1| Sequence 24 from patent US (116 aa)  
 initn: 543 initl: 543 opt: 543 Z-score: 644.2 bits: 127.9 E(): 5.8e-27  
 Smith-Waterman score: 543; 72.174% identity (92.174% similar) in 115 aa overlap  
 (514-628:2-116)

```

          490     500     510     520     530     540
Cry1Ac NFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 NNRGHLPIPIQFSSRSTRYRVRVRYASATPI
          10     20     30

```

```

          550     560     570     580     590     600
Cry1Ac HLNVNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 QNVVHWENSSFFSGTVPATAQSLDNLQSNNGFYFETANTISSSLDGIVGIRNFSANADLI
          40     50     60     70     80     90

```

```

          610     620     630     640     650     660
Cry1Ac IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 IDRFEFIPVDATSEAEHDLERAQKA
          100     110

```

>>gi|6010670|gb|AAF01213.1| endotoxin [Bacillus thuringi (140 aa)  
 initn: 517 initl: 426 opt: 511 Z-score: 605.3 bits: 120.9 E(): 8.6e-25  
 Smith-Waterman score: 511; 54.015% identity (81.752% similar) in 137 aa overlap  
 (13-147:1-137)



Regulatory Product Characterization Team

```

gi|898 NLMGLYGALNVNRFADWKKSGMVFNGLADELRKQMSLTLHLMFTQTIIRDFSQPGYQA
      140      150      160      170      180      190
      160      170      180      190      200      210
Cry1Ac PLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGL
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|898 ILLPSYTSAAANLHLLLRDIEIYGKELGFSQQVLDSSYRELILFTKEYTTHCVDYNAAL
      200      210      220      230      240      250
      220      230      240      250      260      270
Cry1Ac ERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYP-----IRTVSQ--LTREIY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 N---AQKQKQGWIAFNHYRRNMTLTVLDVITLFPSPYDARKYPADKKDKVKKLSKTELTREIY
      260      270      280      290      300      310
      280      290      300      310      320      330
Cry1Ac TNPVLENFDGSRGSAQGIIEGSI-RSPHLMIDLNSITTYTDAHRGEYYWSGHQIMASPVG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 TA-FLET---SPNQVTEIMEASLTRDPHIFTWIKRLDFWTD---LYPDNKFLSANRNG
      320      330      340      350      360
      340      350      360      370      380
Cry1Ac FSGPEFTFP---LYGTMGNAAPQQRIVAQLGQGVYRTLSSLYRRPFNIGINNQLSVL
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|898 FSYTNSSTVQESIVYDGSFGSTLTHAIP-INSNIYKV--SITDTRSIPNRIPOVDFHKM
      370      380      390      400      410
      390      400      410      420      430      440
Cry1Ac DGTEFAYGTSSNLPASVYRKSQVDSLDEIPPQNNVPPRQGFSHRLSHVSM-FRSGFSN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 DGTLSYSSGKLPPEELRTTFFGFSTNENTP---NQPNSSDYTHILTYMKTGIIISGGAP
      420      430      440      450      460      470
      450      460      470      480      490      500
Cry1Ac SSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 KRVSL-----AWAHKSVNPNQIFTDITQVPAVKSSLLNVQAKVIKPGHGTGGDLVAL
      480      490      500      510      520      530
      510      520      530      540      550
Cry1Ac NSSGNNIQNRGYIEVPI--HFPSTSTRYRVRVRYASVTPHILNVNWNWGS--SI--FSNT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 IN--NNLQA-GRMDITCKTSNFNESERRYGLRIRYAANNSFSIYVSYVSSSEGSIRQTSRI
      540      550      560      570      580
      560      570      580      590      600
Cry1Ac VPATATSLDNLQSSDFGY--FESANAFTSSL-----GNIVGVRNFSGTAG--VIIDR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 IESTFSRPNNIIPDLKYDEPKYNEAFDAILPVRLSPNQSTTISISYQNALPANQLIIDR
      590      600      610      620      630      640
      610      620      630      640      650      660
Cry1Ac FEFIPVTATL---EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|898 IEFIPITQSVLDYTEKQNLKESQKTVNNLFVS
      650      660      670
      670      680      690      700      710      720
Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKEN

```

```

>>gi|41688283|dbj|BAD08532.1| putative mosquitocidal tox (686 aa)
  initn: 576 initl: 223 opt: 511 Z-score: 595.0 bits: 121.3 E(): 3.2e-24
Smith-Waterman score: 916; 30.804% identity (59.970% similar) in 672 aa overlap
(4-612:34-686)

```

```

      10      20      30
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERI
      :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
gi|416 YQNKNEYEILNAPSNNNTNMPNRYPFANDPNAMMKNGNYKDWLDI-C--NPEYRYSNPEAY
      10      20      30      40      50      60
      40      50      60      70      80
Cry1Ac ETGYTPIDISLSLTQFLLSEFVPGAGFVLG-LVDIIWGI--FGPSQ-----WDAFLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 RNTKAAMSPVGLVSTILGVLGGPISVTLGAIIGVVTAVLEFIPADEYDNTKETGWGLIA
      70      80      90      100      110      120
      90      100      110      120      130      140
Cry1Ac QIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 AIKELIYEEIKGEAMNAAKAKLDGLYKVMKNYDNKLNWVKNGDKSPVEQNEIQRVFADTN
      130      140      150      160      170      180
      150      160      170      180      190      200
Cry1Ac SALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 NSFLLLSIQFQQLGHEVSLPLFAVAANFHLLLRDVSYKGEWGTNNIIIEGYHSDQLD
      190      200      210      220      230      240
      210      220      230      240      250
Cry1Ac LIGNYTDHAVRWYNTGLE---RVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 MTQDYTNVAVDTYKNGLEAKKIKNSDKLDWDFYNQYRRDMLTVLDVIALFPYTVDRKY
      250      260      270      280      290      300
      260      270      280      290      300
Cry1Ac PIRTVSQLTREIYT-----NPVLEN-----FDGSFRGSAQGIIEGSI-RSPHLMIDLN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 PISTKVELTREIYTDMINYINNPFMTNPVEGQRFAGYTVAQFNSIENALTREPHEFTWLK
      310      320      330      340      350      360
      310      320      330      340      350      360
Cry1Ac SITIYTDHRGEY-YWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 EVTGYFYAQYGGQSFMTGIQNTSYRTNYEDYPPFSGPLHGVR-YAGDTARSVDNNGKDVY-
      370      380      390      400      410
      370      380      390      400      410
Cry1Ac TLSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPASVYRKSQVTV-----DS----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 ---SIYSTMPLETFNNHVHELTPGTAYYFVKGHRHDATDRRTGNSSQKILGEDSKTGR
      420      430      440      450      460      470
      420      430      440      450      460      470
Cry1Ac -----LDEIP---PQNNVPPR-QGFSHRLSHVSMFRSGFSN-SSV---SIIRAP-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 IATGPSYFISEIPYDKETNETIRPTPEKYNHRLSYISAYATDCGRISGVRGDGCFRTPQ
      480      490      500      510      520      530

```

```

          460      470      480      490      500      510
Cry1Ac MFSWIHRSAEFNIIASDSITQIPAVKGNFLFN--GSVISGPGFTGGDLVRLNSSGNNI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 MCAWTHVSADPYNTIHPDKITQISAVKAFYIWDTGEGQVVSQPGFTGGDLVKLPYNA---
          540      550      560      570      580      590

```

```

          520      530      540      550      560      570
Cry1Ac QNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNVN-WGN-SSIFSNVTPATATSLDNLQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 ----RLKIRLKPSTSTSKYRVRVRYASMGAGTLRAEKWSPYGSVFSNF--AYEYTGDSNK
          600      610      620      630      640

```

```

          580      590      600      610      620      630
Cry1Ac SSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|416 FNNFKYLETLSEFNSIIVGVEIIIQNLS-SSQLIVDKLEFIPI
          650      660      670      680

```

```

          640      650      660      670      680      690
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQ

```

>>gi|46852037|gb|AAT02712.1| Cry1Ab [Bacillus thuringien (167 aa)  
 initn: 492 initl: 392 opt: 492 Z-score: 581.7 bits: 116.8 E(): 1.8e-23  
 Smith-Waterman score: 492; 54.601% identity (76.687% similar) in 163 aa overlap  
 (518-677:6-167)

```

          490      500      510      520      530      540
Cry1Ac NGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|468          GQISTLRVNITAP-LSQRYRVRIRYASTTNLQFHT
          10      20      30

```

```

          550      560      570      580      590      600
Cry1Ac NWNSSIFSNTVTPATATSLDNLQSSDFGYFESANAFTSSLGNIV---GVRNFSGTAGVII
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|468 SIDGRPINQGNFSAATSSGSLQSGSFRIVGFTTPFNFSNGPVSFTLSAHVFNSENGEVYI
          40      50      60      70      80      90

```

```

          610      620      630      640      650      660
Cry1Ac DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|468 DRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTVDVTDYHIDQVSNLVECLSDEF
          100      110      120      130      140      150

```

```

          670      680      690      700      710      720
Cry1Ac CLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|468 CLDEKQELSEKVK
          160

```

>>gi|145843784|gb|ABP96899.1| cry4A [Bacillus thuringien (255 aa)  
 initn: 581 initl: 293 opt: 493 Z-score: 580.2 bits: 117.1 E(): 2.1e-23  
 Smith-Waterman score: 592; 42.636% identity (67.829% similar) in 258 aa overlap  
 (668-910:8-255)

```

          640      650      660      670      680      690
Cry1Ac QLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi|145          KSCGMYYKKKMLLLDEVKNAKQLSQRNVLQNGDFESA
          10      20      30

```

```

          700      710      720      730      740      750
Cry1Ac NRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFD---ECYPTYLYQKIDESKLLKAFTRY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : :
gi|145 TL---GWTTSDNITIQEDDPIFKGHYLMHMSGARDIDGTIFPTIYFQKIDESKLLKPYTRY
          40      50      60      70      80      90

```

```

          760      770      780      790      800
Cry1Ac QLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPNRC----AP
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|145 LVRGFVGSKDELVELVVSRYGEEIDAIMNVPADLNYLPSTFD----CEGSNRCETSAPV
          100      110      120      130      140

```

```

          810      820      830      840      850      860
Cry1Ac -HLEWNPDLDCSCR--DGEK---CAHSHHFFSLDIDVGCTDLNEDLGVWVIFKIKTQDGH
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|145 ANIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSFTIDTGALDTNENIGVWVMFKISSPDGY
          150      160      170      180      190      200

```

```

          870      880      890      900      910      920
Cry1Ac ARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQY
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|145 ASLDNLEVIIEGPIEDGEALSRVKHMEKKWNDQMEAKRSETQQAYDVAK
          210      220      230      240      250

```

```

          930      940      950      960      970      980
Cry1Ac DQLQADTNIAMIIHAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNV

```

>>gi|31745044|dbj|BAC77648.1| putative mosquitocidal tox (666 aa)  
 initn: 485 initl: 207 opt: 495 Z-score: 576.3 bits: 117.8 E(): 3.5e-23  
 Smith-Waterman score: 602; 26.301% identity (55.780% similar) in 692 aa overlap  
 (2-635:13-666)

```

          10      20      30
Cry1Ac CMQAMDNNPNINECIPY-----NCLSNPEVEVLGGERIETGY
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|317 MNSYQNKNEYEILKSSPNNTNIPNRYPFANDRDMSPMSWNDCCQGSFWDVWESTASFTG-
          10      20      30      40      50

```

```

          40      50      60      70      80      90
Cry1Ac TPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQL---INQRIEE
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|317 ----IGIDLITFLGEPSTIGINLLFSVI----GKLLPSGQNVASLSICDLSIRKEVDE
          60      70      80      90      100      110

```

```

          100      110      120      130      140
Cry1Ac FARNQAIISRLGSLNLYQIYA-ESFREW--EADPTPALREEMRIQFN---DMNSALTT
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|317 SVLSDAYGDFNGVNNYQTYIYLTSLKKWLDAGKPTTGQLLTDVTKHFEFSEFEFNALLKG
          120      130      140      150      160      170

```

```

          150      160      170      180      190
Cry1Ac AIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRW-----GFDAATINSRYN--
      . . . . . : : . . . . : : . . . . : : . . . . : : . . . . : :
gi|317 SL---SRPKGEILLPTIYQGANLHLLLRDFVQYKAVWEKELRTENVESELI SPSFDYE
          180      190      200      210      220

```

Regulatory Product Characterization Team

200 210 220 230 240 250
Cry1Ac -DLTRLIGNYTDHAVRWYNTGLERVW--GPDSDRWIRYNQFRRELTTLTVLDDIVSLFPNYD
gi|317 GHFKEQLAEHINHCHITWYQAGLNQIKESGTSTENWLKFNKFRREMTLSVLDIIAIFPTYD

260 270 280 290 300 310
Cry1Ac SRTYPIRTVSQLTREIYTNPVLEN-FDGSFRGSAQGIIEGS-IRSPHLMIDILNSITITYTDA
gi|317 FENYKSETHIELSREVYTDVPVGYNGWEQNLNGFNTLEANGTRGPGLVTWKKIDIFTDE

320 330 340 350 360 370
Cry1Ac HRGEYIWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAVLQGGVYRTLSSTLYRR
gi|317 VTEYSGWSPVALLR---GWAGTRH-YEII--TGSSNTLQRISGTTSDVSNI--DFINSR

380 390 400 410
Cry1Ac PFNIGINNQQLSVLDGTEFAYGTSSNLPSAV-YRKSQTVDLDEI--P-----P
gi|317 IFII-TSLARYALAGAAGNPGSPRYRVSVEFRSTGRYTFLYEVNSPGISSMTIESKLP

420 430 440 450 460 470
Cry1Ac QNNNVPPRQGFQSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNMIASDSITQIP
gi|317 GVKNATGFTDYFNRLSNAACVQFGTS-----RVNVVYGWTHISMEGEYVYPNKITQIP

480 490 500 510 520 530
Cry1Ac AVKG-NFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHFPSTST-RYRVRVRY
gi|317 AVKAWIIRGTSSVAVGPGHTGGNLVKM--SYHSVWS-----IKFTCQQLKRYRVRIRY

540 550 560 570 580 590
Cry1Ac ASVTPIHLMNVN-W-GNSSIFSNTVPATATSLDNLQSSD-FGYFESANAFTSSLGNIVGVR
gi|317 ASDGNCQLAMRRWRGGPGYVQEARHTVQRTFSGSMTYDSFKYLDIFTMPAEDYTFDLTID

600 610 620 630 640 650
Cry1Ac NFSGTAGVIIDRFEFIP---VTATLEAEYNLERAQAVNALFTSTNQLGLKTNVTDYHID
gi|317 LESGGA-LYIDKIEFIPDDLTTLEYEERNLEKTKNAVNDLFTN

660 670 680 690 700 710
Cry1Ac QVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGGWGSGTI

>>gi|111927191|gb|ABH71843.1| Sequence 8 from patent US (265 aa)
initn: 432 init1: 432 opt: 486 Z-score: 571.7 bits: 115.6 E(): 6.4e-23
Smith-Waterman score: 486; 36.842% identity (65.351% similar) in 228 aa overlap
(8-228:40-265)

10 20 30
Cry1Ac CMQAMDNNPN-INECIPYNCLSNPEVEVLGGERIETG

gi|111 SYNQSGNDMQIIQPSSNALLYSPNKYPYATDPNVIAEGRSYNNWLDTCVGVGDGTRSPEA
10 20 30 40 50 60

40 50 60 70 80 90
Cry1Ac YTPIDISLSLTQFLLSEFVPGAGFVLG-----LVDIIWGIFGPSQWDAFLVQIEQLINQ
gi|111 YATAEEAVGLSIDLLAETIYFLGFPIASPITRALSALLGGLF--SSGDTLMQHVQQLINQ

100 110 120 130 140 150
Cry1Ac RIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIP
gi|111 KIEIYARNTALAEALLGLRNLAEVYSVALEYWQQNRNSAQAESVRSRFRSLETIFIQRMP

160 170 180 190 200 210
Cry1Ac LFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAAATINSRYNDLTRLIGNYTDH
gi|111 LFAIQGYEVPLLSVYAAAANLHLLLRDSSIHGLDWGFDQGEVNSNYDRQIRLSAEYANH

220 230 240 250 260 270
Cry1Ac AVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDDIVSLFPNYDSRTYPIRTVSQLTRE
gi|111 CITWYQAGLQGLQGTGR
250 260

>>gi|29329421|emb|CAD83753.1| unnamed protein product [P (265 aa)
initn: 432 init1: 432 opt: 486 Z-score: 571.7 bits: 115.6 E(): 6.4e-23
Smith-Waterman score: 486; 36.842% identity (65.351% similar) in 228 aa overlap
(8-228:40-265)

10 20 30
Cry1Ac CMQAMDNNPN-INECIPYNCLSNPEVEVLGGERIETG
gi|293 SYNQSGNDMQIIQPSSNALLYSPNKYPYATDPNVIAEGRSYNNWLDTCVGVGDGTRSPEA

40 50 60 70 80 90
Cry1Ac YTPIDISLSLTQFLLSEFVPGAGFVLG-----LVDIIWGIFGPSQWDAFLVQIEQLINQ
gi|293 YATAEEAVGLSIDLLAETIYFLGFPIASPITRALSALLGGLF--SSGDTLMQHVQQLINQ

100 110 120 130 140 150
Cry1Ac RIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIP
gi|293 KIEIYARNTALAEALLGLRNLAEVYSVALEYWQQNRNSAQAESVRSRFRSLETIFIQRMP

160 170 180 190 200 210
Cry1Ac LFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQRWGFDAAATINSRYNDLTRLIGNYTDH
gi|293 LFAIQGYEVPLLSVYAAAANLHLLLRDSSIHGLDWGFDQGEVNSNYDRQIRLSAEYANH

220 230 240 250 260 270
Cry1Ac AVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDDIVSLFPNYDSRTYPIRTVSQLTRE



```

                10      20
Cry1Ac      550      560      570      580      590
TPIHLNVNWGSSIFSNVTPATATSLDNLQSSDFGYFESANAFT--SSLGNIV--GVRNFS
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|468      VDFDFVSRGGTTVNNFRFLRTMNSGDELKYGNFVRRRAFTTPTFTQIQDIIRTSIQGLS
30          40          50          60          70          80

        600      610      620      630      640      650
Cry1Ac      GTAGVIIDRFEFIPVATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLV
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|468      GNGEVYIDKIEIIPVATFEAEYDLERAQEAVALFTNTNPRRLKTDVTDYHIDQVSNLV
90          100         110         120         130         140

        660      670      680      690      700      710
Cry1Ac      TYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|468      ACLSDEFCLDEKRELEKVKYAEAT
150         160         170

>>gi|29329423|emb|CAD83754.1| unnamed protein product [P (153 aa)
  initn: 443 init1: 443 opt: 464 Z-score: 549.3 bits: 110.7 E(): 1.1e-21
Smith-Waterman score: 464; 49.673% identity (72.549% similar) in 153 aa overlap
(157-304:1-153)

```

```

        130      140      150      160      170      180
Cry1Ac      NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRW
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|293      YEVPLLSVYADAANLHLLILRDSYIYGAFW
                10      20      30

```

```

        190      200      210      220      230      240
Cry1Ac      GFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLD
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|293      GFDEDEYYRNYARQIRLSAEYANHCTTWYQTGLRRLQGRATRDWINYNRFRRELTTLTVLD
40          50          60          70          80          90

```

```

        250      260      270      280      290      300
Cry1Ac      IVSLFPNYDSRTYPIRTVSQLTREIYTNVPLEN--FDGSPFRG--SAQGIEG-SIRSPHLM
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|293      ICALFSSYDIPSYPMGTQIQLTREIYTDVPHVSDWLQSTSPGLISFSSLENLVVRAPHLF
100         110         120         130         140         150

```

```

        310      320      330      340      350      360
Cry1Ac      DILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|293      TWL

```

```

>>gi|111927192|gb|ABH71844.1| Sequence 10 from patent US (153 aa)
  initn: 443 init1: 443 opt: 464 Z-score: 549.3 bits: 110.7 E(): 1.1e-21
Smith-Waterman score: 464; 49.673% identity (72.549% similar) in 153 aa overlap
(157-304:1-153)

```

```

        130      140      150      160      170      180
Cry1Ac      NPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRW
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|111      YEVPLLSVYADAANLHLLILRDSYIYGAFW
                10      20      30

```

```

        190      200      210      220      230      240
Cry1Ac      GFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLD
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|111      GFDEDEYYRNYARQIRLSAEYANHCTTWYQTGLRRLQGRATRDWINYNRFRRELTTLTVLD
40          50          60          70          80          90

```

```

        250      260      270      280      290      300
Cry1Ac      IVSLFPNYDSRTYPIRTVSQLTREIYTNVPLEN--FDGSPFRG--SAQGIEG-SIRSPHLM
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|111      ICALFSSYDIPSYPMGTQIQLTREIYTDVPHVSDWLQSTSPGLISFSSLENLVVRAPHLF
100         110         120         130         140         150

```

```

        310      320      330      340      350      360
Cry1Ac      DILNSITIIYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|111      TWL

```

```

>>gi|51998361|emb|CAH33952.1| unnamed protein product [B (690 aa)
  initn: 433 init1: 198 opt: 471 Z-score: 547.8 bits: 112.6 E(): 1.4e-21
Smith-Waterman score: 636; 28.068% identity (57.828% similar) in 709 aa overlap
(2-635:13-690)

```

```

                10      20      30      40
Cry1Ac      CMQAMDNPNINECIPY-----NCLSNPEVEVLGGERI-ETGYTPIDI
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      MSPYQNKNEYEILESSNNTNTPNRYPFANNRDMSTMWNCQGISWDEIWEVETITSI
10          20          30          40          50          60

```

```

        50      60      70      80      90
Cry1Ac      SLSLTQFLLSEFVPGAGFVGLVDIIWGFGPSQWDAF---LVQIEQLINQRIEFARN
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      GINLIEFVIE---PSLGGINTLLSII-GKLIPTNRQTVSALSICDLLSIRKEVADSVLS
70          80          90          100         110

```

```

        100      110      120      130      140
Cry1Ac      QAISRLEG-LSNLYQIYAESFREWEAD--P---TNPA---LREEMRIQFNDMNSALTTA
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      DAIADFDGKLNKYREYLLSYLGAWLKDQKPLQKTNNSDIGQLVYVYFKLSERDFNEILGGS
120         130         140         150         160         170

```

```

        150      160      170      180      190      200
Cry1Ac      IPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWG--FDAATINSRY-----NDL
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      L---SRNNAQVLLLPFAQAANVQLLLLRDAVQYKAQWFFFLSAENVRSELISPSNGCDF
180         190         200         210         220         230

```

```

        210      220      230      240      250
Cry1Ac      T-----RL---IGNYTDHAVRWYNTGLERVW--GPDSRDWIRYNQFRRELTTLTVLDIVSL
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      TGDYYERLCKCKTAEYITNYCLYQVGLNQIKQGGTGADTWSKFNKFRREMTLAVLDIIAI
240         250         260         270         280         290

```

```

        260      270      280      290      300
Cry1Ac      FPNYDSRTYPIRTVSQLTREIYTNVPLEN-----LENFDGSPFRG--SAQIEGSIRSPHL
. . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519      FPTYDFEKYPLPTHVELTREIYTDVAGYSSGTYSWLRNWPNTFNGLANGTRG---PGL
300         310         320         330         340

```

```

          310          320          330          340          350
Cry1Ac MDILNSITIIYTDahrgeyy--WSGHQIMASpVGFSG--PEFTFPLYGTMGNAAPQQRIVA
          . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519 VTWLSKIGIYNE-YVSRyFAGWVGTRHYEDYTKGNgIFQRMStTNSDLrNIDFQnADVY
          350          360          370          380          390          400

```

```

          360          370          380          390          400          410
Cry1Ac QLQGVYRtLSStLYRRPFNIGInNQQLSVLDGTEfAYGTSSnLPSAVYRkSGTVDsLDE
          . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519 KITSLAIMNLVGETTARp-EYRVSkADFRrVGGPDLNyDAGNGLSRM-----TIESTFP
          410          420          430          440          450          460

```

```

          420          430          440          450          460          470
Cry1Ac IPPQNNVpPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEfNNIIASDSIT
          . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|519 LVLHsNGV---RGPShRLSNAACVvYg---NSRVNV----YGWtHTSLKRENIIEANQIT
          470          480          490          500          510

```

```

          480          490          500          510          520
Cry1Ac QIPAVKg----NFLFNgs--VISGPGfTGdDLVRL---NSSGNnIQNRGyIEVPIHfPSt
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 QIPAVKsYyLQnYLANAYTYVikGT-HTGdLIRfLrTKSEYNAVYAGGgIRLIInNKtA
          520          530          540          550          560          570

```

```

          530          540          550          560          570          580
Cry1Ac STRYRVRrVRYASVtPIHLNV----NWGNSSIFsNTVPATATSLDNLQSSDFGyFESANA
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 GQSYRIRfRYAAdKAaFFSVyLYPGGwG-SNRFVSLekSYSGNyDDLkYSDFKFAEIItp
          580          590          600          610          620          630

```

```

          590          600          610          620          630
Cry1Ac FTSSLgNI----VgVRNFsGTAGVIIDRFefIPV-TATLe--AEYNLERAQKAVNALfT
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 PLPS-SNIQMDVEMQANSfQSDVNVVLDKIEFLPSnTtTLEyEGERdLEKTKNAVNDLfT
          640          650          660          670          680

```

```

          640          650          660          670          680          690
Cry1Ac STNQLGLKtNVTdYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDErNLLQDSNF
          .
gi|519 N
          690

```

>>gi|51998359|emb|CAH33951.1| unnamed protein product [B (693 aa)  
 initn: 433 init1: 198 opt: 471 Z-score: 547.8 bits: 112.6 E(): 1.4e-21  
 Smith-Waterman score: 636; 28.068% identity (57.828% similar) in 709 aa overlap  
 (2-635:16-693)

```

          10          20          30
Cry1Ac CMQAMDNPNINeCIPY-----NCLSNPEVEVLGGERI-ETGYTP
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 MKKMSpYQNKNEYeILESSNNtNTPNRYPFANrDMStMSWnDcQGISWDEIWESVETI
          10          20          30          40          50          60

```

```

          40          50          60          70          80          90
Cry1Ac IDISLSLQtQLLSEfVPGAGfVLGLVDIIWGIFGPSQWDAf----LVQIEQLINRIEFf
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 TSIGINLIEfVIE---PSLGGINTLLSII-GKLIPtNRQtVSALSIcDLLSIIRKEVADs
          70          80          90          100          110

```

```

          100          110          120          130          140
Cry1Ac ARNQAIrSRLEG-LSNLyQIYAESfREWEAD--P---TNPA----LREEMRIQfNDMSNAL
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 VLSDAIADfDGKLKNyREYyLSYLGAwLkDGKPLQKTnNSDIGQLVvYyFKLSERDFNEIL
          120          130          140          150          160          170

```

```

          150          160          170          180          190
Cry1Ac TTAIPLfAVQNYQVPLLSVYVQAANLHLsVLRDVsVFGQRWg--FDAATINSRY-----
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 GGSL---SRNNAQVLLLPtFAQAANVQLLLLRDAVQYKAQWfPFLSAENVRSELIspNSG
          180          190          200          210          220          230

```

```

          200          210          220          230          240
Cry1Ac NDLT-----RL---IGNyTDHAvRWYNTGLERVW--GPDSRDWIRYNQfRRELTtLVLDI
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 CDfTGdYyERLkCKTAEYtNYCLYwYQVGLNqIKQGGTgADtWSKfNKfRREMTLAVLDI
          240          250          260          270          280          290

```

```

          250          260          270          280          290
Cry1Ac VSLFPNyDSRTYPIrTVSQtLREIYtNPV-----LENFDGSGFRG-SAQIEGSIRs
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 IAIFPTyDFEKYPLPHtVELTREIYtDAVGYSSGTYSWLRNWPntFNGLeANGTRG----
          300          310          320          330          340

```

```

          300          310          320          330          340          350
Cry1Ac PHLMDILNSITIIYTDahrgeyy--WSGHQIMASpVGFSG--PEFTFPLYGTMGNAAPQQR
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 PGLVtWLSKIGIYNE-YVSRyFAGWVGTRHYEDYTKGNgIFQRMStTNSDLrNIDFQnA
          350          360          370          380          390          400

```

```

          360          370          380          390          400          410
Cry1Ac IVAQLGQGVYRtLSStLYRRPFNIGInNQQLSVLDGTEfAYGTSSnLPSAVYRkSGTVDs
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 DVYKITSLAIMNLVGETTARp-EYRVSkADFRrVGGPDLNyDAGNGLSRM-----TIES
          410          420          430          440          450          460

```

```

          420          430          440          450          460          470
Cry1Ac LDEIPPQNNVpPRQGFShRLSHVSMFRSGfSNSSVSIIRAPMfSWIHRSAEfNNIIASD
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 TFPLVLHsNGV---RGPShRLSNAACVvYg---NSRVNV----YGWtHTSLKRENIIEAN
          470          480          490          500          510

```

```

          480          490          500          510          520
Cry1Ac SITQIPAVKg----NFLFNgs--VISGPGfTGdDLVRL---NSSGNnIQNRGyIEVPIHf
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 QITQIPAVKsYyLQnYLANAYTYVikGT-HTGdLIRfLrTKSEYNAVYAGGgIRLIInN
          520          530          540          550          560          570

```

```

          530          540          550          560          570
Cry1Ac PSTSTRYRVRrVRYASVtPIHLNV----NWGNSSIFsNTVPATATSLDNLQSSDFGyFES
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 KTAGQSYRIRfRYAAdKAaFFSVyLYPGGwG-SNRFVSLekSYSGNyDDLkYSDFKFAEI
          580          590          600          610          620          630

```

```

          580          590          600          610          620          630
Cry1Ac ANAFTSSLgNI----VgVRNFsGTAGVIIDRFefIPV-TATLe--AEYNLERAQKAVNA
          . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|519 ITPPLPS-SNIQMDVEMQANSfQSDVNVVLDKIEFLPSnTtTLEyEGERdLEKTKNAVND

```

```

        640      650      660      670      680
Cry1Ac LFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQD
      ....
gi|519 LFTN
      690

```

```

>>gi|89000901|dbj|BAE80088.1| delta-endotoxin [Bacillus (684 aa)
  initn: 464 initl: 210 opt: 469 Z-score: 545.5 bits: 112.1 E(): 1.8e-21
Smith-Waterman score: 530; 26.299% identity (55.682% similar) in 616 aa overlap
(54-618:81-680)

```

```

        30      40      50      60      70
Cry1Ac EVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVLGLV-----DIIWGI FGPS
      .....
gi|890 CQTITPLCTPIDPDINSVAAAIGVIGSIIIGLIPGPEAIGLILGTFSIIIPFLWPENKTI
      60      70      80      90      100      110

```

```

        80      90      100      110      120      130
Cry1Ac QWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE---WEADPTNPALR
      .....
gi|890 IWEEFTHRGLHLIRPELTPTEIEIIVNPLKGYYNALREQLNFSEFAIW-ARNKNAATT
      120      130      140      150      160

```

```

        140      150      160      170      180      190
Cry1Ac EEMRIQFNDMNSALTAIPLFAVQNYQVP-LLSVYVQAANLHLSVLRDVSVFGQRWGFDA
      .....
gi|890 GDVLRFRFNIDADIIRLKHQLTVDVVRNKPALLSLYAQTANIDLILFQRGAKYGDWEARYA
      170      180      190      200      210      220

```

```

        200      210      220      230      240
Cry1Ac -----ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLT
      .....
gi|890 RNQPIPFKTSQEYYDSLKEKIENYTNDAIATYRNLNIIKNIKISWDFVFNLYRREMTLS
      230      240      250      260      270      280

```

```

        250      260      270      280      290      300
Cry1Ac VLDIVSLFPNYDSRTYPIRTVSQLTREIYTNFV-LENFDGSGFRGSAQGIIEGSI-RSPHLM
      .....
gi|890 ALDLVALFPNYDICRYPISKTELTRKVMSSFYLALE--LNESLESLENLTHPPSLF
      290      300      310      320      330      340

```

```

        310      320      330      340      350
Cry1Ac DILNSITIIYT--DAHRGEYY---WSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVA
      .....
gi|890 TWLKRNLNLYTISENYSPLRVSSLSGLSAVYSHTHQQQALYVGGPQGITGGS-PQE---I
      350      360      370      380      390      400

```

```

        360      370      380      390      400      410
Cry1Ac QLGQGVYRTRLSSTLYR---RPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVD
      .....
gi|890 RFDGFVYKLFMSQNI SPNGCYPIG-GIPQMSFYISD----Y-SGSPRPNKDYYSASAIQ
      410      420      430      440      450

```

```

        420      430      440      450      460
Cry1Ac --SLDEI--PPQN---NNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSA
      .....
gi|890 YISINSYMNQPNATKSNNISIRET-KHILSDIKMNSYQTGGFYFPFHSFGYSFAWHTHTSV

```

```

        460      470      480      490      500      510
Cry1Ac EFNIIASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPI-
      .....
gi|890 DPNLIVPNRITQIPAVKAHILSTTAKVIAGPGHTGGDLVALLNDDPRIGTMS-IECKTG
      520      530      540      550      560      570

```

```

        530      540      550      560      570      580
Cry1Ac HFPSTSTRYRVRYASVTPIHNLVNWGNSSIFSNTVPATATSLDNLQSSDFGYFE-SAN
      .....
gi|890 SFTQPSRRYGLRMRYAANNQFSVSI SRNDQGVASFVTERTFRTNNIIPTDLKYNFKYN
      580      590      600      610      620      630

```

```

        590      600      610      620      630
Cry1Ac AFTSSLGNI-----VGVRFNSGTA--GVIIDRFEFIPVTATLEAEYNLERAQKAVNAL
      .....
gi|890 NYDQIIMDLPPNTIINIGIRQTNALSINQFIIIDRIEFYPMDQGVACKMQ
      640      650      660      670      680

```

```

        640      650      660      670      680      690
Cry1Ac FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS

```

```

>>gi|22121135|gb|AAM92282.1| CryIA(b) protein [Zea mays] (68 aa)
  initn: 451 initl: 451 opt: 451 Z-score: 539.2 bits: 107.6 E(): 4.1e-21
Smith-Waterman score: 451; 98.529% identity (98.529% similar) in 68 aa overlap (5-
72:1-68)

```

```

        10      20      30      40      50      60
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      .....
gi|221 MDNHNHINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGF
      10      20      30      40      50

```

```

        70      80      90      100      110      120
Cry1Ac VLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEAFARNQAIISRLEGLSNLYQIYAESFRE
      .....
gi|221 VLGLVDIIWGIF
      60

```

```

>>gi|50539655|dbj|BAD32657.1| delta-endotoxin [Bacillus (675 aa)
  initn: 597 initl: 247 opt: 462 Z-score: 537.3 bits: 110.6 E(): 5.2e-21
Smith-Waterman score: 841; 31.571% identity (61.329% similar) in 662 aa overlap
(11-633:46-673)

```

```

        10      20      30      40
Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPI
      .....
gi|505 HSNNQKDIPNRYPFNTNPNVAMKNGYKDWVNECEGSNVSPSPAAVTSA-----II
      20      30      40      50      60

```

```

        50      60      70      80      90
Cry1Ac DISL-SLTQFLLESEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEAFARNQ
      .....
gi|505 SIVLKTAKALVSSLVDAIKSSLGISEVITKN-NVSQLSMELV--NQLINRRIQETIMDL
      70      80      90      100      110      120

```

```

        100      110      120      130      140      150
Cry1Ac AISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIP-LFAVQNYQ

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. . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 GSASLNGLMISYKRYLNALEAWDKDKSNITLQENVIEEFKYVESFFENLKGIIYRTSSSQ
      130      140      150      160      170      180

      160      170      180      190      200      210
Cry1Ac VPLLSSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 ITLLPTFAQAANLHLSMLRDAVMYQEGWNLQSH-LDYKM-ELDIALKDYTNVCEVYVNRG
      190      200      210      220      230      240

      220      230      240      250      260      270
Cry1Ac LERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 LNALRGSTALDWLEFNSFRDMTMLVLDLVAIFPNYDPVQYPLPTKIGLSRKIYTDVPGT
      250      260      270      280      290      300

      280      290      300      310
Cry1Ac NFDGSF-----RGSQAQ--GIEGSIR--SPHLMILNSITTYTDA-----HRGEYY-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 TRDTEFGNWTLTDRTLANFNLERDVTDSPLVKWLVDMNIYTGAIIDSYPIGSGPGERIG
      310      320      330      340      350      360

      320      330      340      350      360      370
Cry1Ac -WSGHQIMASPVGFGSPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 VVYGN--MNSFVLTGSRLESYNMYGEIAHEDP---ITNIRDNDIYKV---DLRAAYVAT
      370      380      390      400      410

      380      390      400      410      420
Cry1Ac INNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIP--PQNNVPPRQG-----
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 IRN---ALDST---FGVSSSHFFNVMGKNELYQSKQPYSPYITITFPGEESLEGVND
      420      430      440      450      460

      430      440      450      460      470      480
Cry1Ac FSHRLSHVSMFRSGFSNSSVSIIRAPMFS--WIHRSAEFNIIASDSITQIPAVKGNFL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 YSHLLCNVKNITGGRLRQTSARG-RSSLLSHAWTHKSLNPKNIIAADKITHIPAVKGSNLS
      470      480      490      500      510      520

      490      500      510      520      530      540
Cry1Ac FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 ASSAVIKGPGFTGGDLRL---GPN-QFVDYILTPDNPQVSQIYFDVRLRYACMGGANIL
      530      540      550      560      570      580

      550      560      570      580      590      600
Cry1Ac VN-WGNSSIFSNTPATATSLDNLQSSDFGYFESANAFTSSLGNI-VGVRNFGTAGVII
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 IQFWNKWEIGVLVSTTSSLENLKYENFAYITTRLSTFGQGGYNNMSIYNPTSNPNVII
      590      600      610      620      630      640

      610      620      630      640      650      660
Cry1Ac DRFEFIPVTAT---LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|505 DKIEFIPVSGTPPEYEGKHKLNQADVNNLFLN
      650      660      670

      670      680      690      700      710      720

```

```

Cry1Ac DEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK

>>gi|17977981|emb|CAC80986.1| Cry30Aa protein [Bacillus (688 aa)
  initn: 421 initl: 176 opt: 453 Z-score: 526.6 bits: 108.6 E(): 2.1e-20
Smith-Waterman score: 519; 26.562% identity (54.688% similar) in 640 aa overlap
(38-612:59-678)

      10      20      30      40      50      60
Cry1Ac NPNINCEIPYNCLSNPEVEVLGGERIETGYTPIIDISLSLTQFLLS-----EFVPGAGFV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 YPLTNNPKVPLQNTNYKDWLNMCOQTITPLCTPIDTDSKLVATAIKVIGAIKFSMPGPGAA
      30      40      50      60      70      80

      70      80      90      100
Cry1Ac LGLV-----DIIWGFQPSQWDAFLVQIEQLINQRIE---EFARNQAIISRLEGLSN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 VGLVLKSFSTIIPILWPNDKTPIWKEFTKQGLQFRPELGRDAIEIIGNDVQAEYNSLEI
      90      100      110      120      130      140

      110      120      130      140      150      160
Cry1Ac LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP-LLSVYVQA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 MMRDFENKFNWESNRTR-ANAIAVTAFSTVNTQIIRLKERFLIAPENRPAFLNLYAQT
      150      160      170      180      190      200

      170      180      190      200      210
Cry1Ac ANLHLSVLRDVSVFGQRWGFDAATINSR-----YNDLTRLIGNYTDHAVRWYNTG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 ANIDLILYQRGSVYGDKW---VADINNRSTSPFSSKDYQSLKGGKIKDYTNCAETRN
      210      220      230      240      250      260

      220      230      240      250      260      270
Cry1Ac LERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 LTLLKPKPHIQWDIYNRYRREALGALDLVALFPNYDICIYPTQTRTELTRKVVYV-PSFY
      270      280      290      300      310      320

      280      290      300      310      320      330
Cry1Ac NFDGSFRGSAQIEGSI-RSPHLMILNSITTYTDAHRGEYYW-----SGHQIMASPVGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 -LQALQORDIETVENQLTHPPSLFTWLNELNLYTIRERFNPVQLVASLSGLQA-TSRYTQ
      330      340      350      360      370      380

      340      350      360      370      380
Cry1Ac SGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNI----GINNQLSVLD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 NTTTTISNPVQGPVREGTPTK--ISLANYYIYKLFMSQ-YRHPNDCLPISGINEMSFYRSD
      390      400      410      420      430

      390      400      410      420      430      440
Cry1Ac GTEFAYGTSSNLPSAVYRKS-----TVDSLDEIPPQN---NNVPPRQGFSSHRLSHVSMF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 ---YAGAG--PAPVHYSAGESPTNVIKTYMNGPQNALISINET-SHILSDIKMN
      440      450      460      470      480      490

      450      460      470      480      490
Cry1Ac RSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNLFGNS-VISGPGFTG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179 YSRITGGVYPLYDFGYSFAWHTSVDPDNLIVPNRITQIPAVKAYSLTSPARVIVGPGHTG

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      500      510      520      530      540      550
Cry1Ac  GDLVRLNSSGNNIQNRGYIEVPIH---FPSTSTRYRVRVRYASVTPIHNLNVN-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|179  GDLVALLNSGT---QSGTMQIQCKTGSFTGPSRQYGLRMRYAANSAFTVSLSYTLGQTR
      560      570      580      590      600
Cry1Ac  GNSSIFSNTVPATATSLD-NLQSSDFGYFESANAFTSSL-GNIVGVRNFSGTAGV-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|179  GTSFVTENTFRSNNIIPDLDKYEEFKYKDYLIITMTLPANTIITISMQQATGLLNQL
      610      620      630      640      650      660
Cry1Ac  IIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|179  IIDRIEFYPMDQGVVACTVN
      670      680

```

>>gi|51090240|dbj|BAD35166.1| Cry protein [Bacillus thur (810 aa)  
 initn: 783 initl: 440 opt: 451 Z-score: 523.2 bits: 108.3 E(): 3.2e-20  
 Smith-Waterman score: 843; 30.925% identity (58.237% similar) in 692 aa overlap  
 (2-636:33-685)

```

      10      20      30
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  QNYNNGLEILDSSGGVCSPPRYPLANAPGSELQNMGYKEWLEMCSIKGAETFADKSTLSAQ
      10      20      30      40      50      60
Cry1Ac  RIETGYTPIDISLSLTQFLLSEFVPGAGFVGLGLVDI IWGIFGPSQWDAFLVQIEQLINQR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  SQEGLRTAITIALSLLSNLPGFPYPAKLLSIIFPFLWPTNTQAQWEAFMKVVEELVDQK
      70      80      90      100      110      120
Cry1Ac  IEEFARNQAIISRLGLESLNYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  IETFARDQAIQRLRGIQDVISLYQRDAKNFNNDYPTSEPIQRQLSQFTATNTFIVGSM
      130      140      150      160      170      180
Cry1Ac  FAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  FRVGRHEVPLLTTFVQAANLHLLLRDAIMFGESWGMCPVTVAGYQDNDFNNRIADYTDYS
      190      200      210      220      230      240
Cry1Ac  VRWYNTGLERV-----W-----GP-----DSRDWIRYNQFRRELTTLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  VSIYNQGLQKAKTLKANLRDYEKYPWARYYNSVSGPEFAYGDMENWNLYNRYRDMTLMV
      250      260      270      280      290      300
Cry1Ac  LDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGS-IRSPHLM
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  LDLVALWPTYNPQQYPIAPKIQLTREIYTE-LRGNAGNTKRPMSDAIDAELIPPRFLFTW

```

```

      310      320      330      340      350      360
Cry1Ac  LNSITITYT-DAHRGEYYWSGHQIMAS---PVGFSGPEFTFPLYGTMGNA---APQQ----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  LESVDMHRWPTSAGYYYTQFNAGIKHRYKYTLDSQTLTSSLRGASGNNFNLPVPAEETIN
      370      380      390      400      410      420
Cry1Ac  RIVAQLGQGVYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRKSQTV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  RVQNQHGEGLY-TFS--FYRS---GQSDPFLNI-----GTTADKPY-----VS
      430      440      450
Cry1Ac  SLDEIPPQNNVPPRQGFSHRSLSHVS-----MFRSGFSNSSVSIIRAPMFSWIHRSAEF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  TMNRIPVEGDQTA---NHRLSWITGMVIPELSIPAFGHYNTYISCAAEGWTHLSVER
      460      470      480      490      500      510

```

>>gi|51090236|dbj|BAD35163.1| cancer cell-killing Cry pr (829 aa)  
 initn: 686 initl: 360 opt: 449 Z-score: 520.6 bits: 107.8 E(): 4.4e-20  
 Smith-Waterman score: 767; 29.412% identity (57.102% similar) in 697 aa overlap  
 (2-630:34-698)

```

      470      480      490      500      510      520
Cry1Ac  NNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLN--SSGNNIQNRGYIEVPIH
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  SNEIKSDKITQIPAVKAFQLSNNASVVRGPGSTGGDLVQFSATSSGNK---QLWIKVKPT
      520      530      540      550      560      570
Cry1Ac  FPSTSTRYRVRVRYASVTPIHNLNVN---GNSSIFSNTVPATATSLDNLQSSDFGY---F
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  TIALGRRFKVIRYAAANVTFTVQKCVTVGVACWETATKSVTTTYSGLTLTYNAFYVDIF
      580      590      600      610      620      630
Cry1Ac  E-SANAFTSSLGNIVGVRNFSGTAG--VIDRFEFIPVTATLEAEYNLERAQKAVNALFT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  EIPANESEFSL-----EFLSTSGGPIYIDKIEFIPVNPPEPPVP-EGIYQIVTALNN
      640      650      660      670      680
Cry1Ac  STNQLGLKTNVTDYHIDQVSNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  SSVVMDPPTGWTRHNHVLWQNNNTNNQKRFVYNSQAGYQIRNLADENLVLTREGANV
      690      700      710      720      730      740
Cry1Ac  VRWYNTGLERV-----W-----GP-----DSRDWIRYNQFRRELTTLV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  VSIYNQGLQKAKTLKANLRDYEKYPWARYYNSVSGPEFAYGDMENWNLYNRYRDMTLMV
      250      260      270      280      290      300
Cry1Ac  LDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQGIIEGS-IRSPHLM
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510  LDLVALWPTYNPQQYPIAPKIQLTREIYTE-LRGNAGNTKRPMSDAIDAELIPPRFLFTW

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60      70      80      90      100     110
Cry1Ac INQRIIEFARNQAIISREGLSNLYQIYAESFREWEADPTNPALREEMRI--QFNDMNSAL
      . . . . .
gi|510 INQKLEDEYARSKAISSELNGLKNVLELYQDAADDWNNENPGD--LRNKNRVLTFERNVNGHF
      120     130     140     150     160     170

150     160     170     180     190     200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQGRWFDAATINSRYNDLTRLIG
      . . . . .
gi|510 ENSMPSFAVRNFEVNLFPVYAEANLHLLLRDAVKFGEWGMSTDPGAER--DDMYRRLR
      180     190     200     210     220     230

210     220                                     230
Cry1Ac N----YTDHAVRWYNTGLERV-----W-----GPDSRD-----W
      . . . . .
gi|510 SRTEIYTDHCVNTYNQGLQAKSLQANVSDYSRYPTQYNQSGGFSYREAKEGEYRGTENW
      240     250     260     270     280     290

240     250     260     270     280
Cry1Ac IRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENF--DGSFRGSA
      . . . . .
gi|510 NLYNAFRDMTILVLDIIAQFPTYDPGLYSRPFVKSSELTREVYTDIRGTTWRSDANL--NTII
      300     310     320     330     340     350

290     300     310     320     330
Cry1Ac QGIEGSI---RSPHLMIDLNSITIIYTDHRGEYYWSGHQIMASPVGF-----SGPEFT
      . . . . .
gi|510 DAIENRMVGSRLQLFTWLTEMKFYIRNTGSITSYTHGDLM---VGLEKKIRKRTNDNQW
      360     370     380     390     400     410

340     350     360     370     380     390
Cry1Ac FPLYGTMGNAAPQQRIVAQLGQGV--YRTLSSTLYRRPFNIGINNQQLSVLDGTEFAYGT
      . . . . .
gi|510 LPLEGQNTSYTRIDRPGIELGKNYWYARTQQWFETRLLQLVWNTDVLVSLNAGTVGNEFW
      420     430     440     450     460     470

400     410     420     430     440     450
Cry1Ac SSNLPSSAVYRKSGETVDSLDEIPPQNNVPPRQGFSHRSLSHVSM--FRSG--FSNSSVSII
      . . . . .
gi|510 ARDVPD--YR-----NIYARSTRNHFI-----NHRLSWIKFEPVRDNCPPAWPGYKQL
      480     490     500     510

460     470     480     490     500     510
Cry1Ac RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLNG--SVISGPGFTGGDLVRLNSSGNN
      . . . . .
gi|510 SALLFGWTHNSVDPFNTIASDRITQIPAVKGYLVDNGATVVRGPGNTGGDLVRLPAYN--
      520     530     540     550     560     570

520     530     540     550     560
Cry1Ac IQNRGYIEVPIHFPSTSTR---YRVRVRYASVTPIHL----NVNWNSSIFSNTPATAT
      . . . . .
gi|510 -QQWTQLRVKVR--PSTTARTRGYNVRIYASEGNANLFGVKYVDTANRFYETGNYAVNQ
      580     590     600     610     620     630

570     580     590     600     610     620
Cry1Ac SLDNLQSSDFGYFESANAFTSSLGNI--VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLE
      . . . . .

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gi|510 FSGSMTYNSFKYLD-AIGFAANEEEFRIELRCNSG-GPIYIDKIEFIPVNPPIPEPEGIY
      640     650     660     670     680     690

630     640     650     660     670     680
Cry1Ac RAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLS
      . . . . .
gi|510 QIVTALNNSVVTSEEFMIGLITTRCGVNLWSNNGNTLQKWRVFNQDQNAFQIKSTPN
      700     710     720     730     740     750

>>gi|87887911|dbj|BAE79727.1| cry4A [Bacillus thuringien (696 aa)
      initn: 345 initl: 189 opt: 445 Z-score: 517.1 bits: 106.9 E(): 7e-20
      Smith-Waterman score: 583; 28.505% identity (56.857% similar) in 649 aa overlap
      (44-627:70-695)

20      30      40      50      60      70
Cry1Ac CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFV--LGLVDIIWG-
      . . . . .
gi|878 QSTNYKDWLNMCCQONQYGGDFETFIDSGELSAITIVVGTVLTGFGFTPLGLALIGFT
      40      50      60      70      80      90

80      90      100     110     120
Cry1Ac ---IFGPSQ----WDAFLVQIEQLINQRIIEEFARNQAIISREGLSNLYQIYAESFREWE
      . . . . .
gi|878 LIPVLFPAQDQSNQSDFTITQTKNIIKKEIASTYISNANKILNRSFNVISTYHNHLKTWE
      100     110     120     130     140     150

130     140     150     160     170
Cry1Ac ADPTNPALREEMRIQFNDMNSALTTAIPLFA-----VQNYQVPLLSVYVQAANLHL
      . . . . .
gi|878 NNP-NPQNTQDVRTQIQLVHYHFQNVIPVPELVNSCPNPSDCDYNNLVLSSYAQAANLHL
      160     170     180     190     200     210

180     190     200     210     220
Cry1Ac SVLRDVSVF---GQRWGFDA---ATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWG-
      . . . . .
gi|878 TVLNQAVKFEAYLKNRQFDYLEPLPTAIDYYPVLTKAIEDYTNVYCVTTYKAGLNLIKTT
      220     230     240     250     260     270

230     240     250     260     270
Cry1Ac PDSR----DWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN
      . . . . .
gi|878 PDSNLDGNINWNTYNTYRTKMTTAVLDLVALFPNYDVGVQYPIGVQSELTREIYQ--VL-N
      280     290     300     310     320     330

280     290     300     310     320     330
Cry1Ac FDGS-FRG-SAQGIEGSI-RSPHLMIDLNSITIIYTDHRG-EYYWSGHQIMASPVGSGP
      . . . . .
gi|878 FEESPXYDFQYQEDSLTRPHLFTWLDLNFYEKAQTTNNFFTSYHNMFFHYT-LDNI
      340     350     360     370     380     390

340     350     360     370     380     390
Cry1Ac EPTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL----YRRPFNIGINNQQLSVLDGT
      . . . . .
gi|878 SQKSSVFGNH-NVTDKLLSLG-LATNIYIFLLNVIISLDNKYLNDYN-NISKMDFITNGT
      400     410     420     430     440     450

400     410     420     430     440
Cry1Ac ----EFAYGTSSNLPSSAVYRKSGETVDSLDEIPPQNNV--PPRQGFSHRSLSHVSMFRSG
      . . . . .

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gi|878 RLLEKELTAG-SGQITYDVNKNIFGLPILKRENNQGNPTLFPTYDNYSHILS----FIKS
      460      470      480      490      500
Cry1Ac FSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGLS-VISGPGFTGGDL
      450      460      470      480      490      500
gi|878 LSIPATYKTQVYTFAWHTSSVDPKNTIYTHLTTQIPAVKANS LGTAS KVVQGP GHTGGDL
      510      520      530      540      550      560
Cry1Ac VRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTP-----IHLNVNWGNSSIFS
      510      520      530      540      550
gi|878 IDF-----KDHFKITCQHSNFQSSYFIRIRYASNGSANTRAVINLSIP-GVAELGM
      570      580      590      600      610
Cry1Ac NTVPA-TATSLDNLQSSDFGYFESANAFTSSLG-NIVGVRNFSGT---AGVIIDRFEFIP
      560      570      580      590      600      610
gi|878 ALNPTFSGTDYTNLKYKDFQYLEFSNEVKFAPNQNISLVFNRSVYVYVNTVTLIDKIEFLP
      620      630      640      650      660      670
Cry1Ac VTATLEAEYN---LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDE
      620      630      640      650      660
gi|878 ITRSIREDRKQKLETVQQL
      680      690

>>gi|23268634|gb|AAN16462.1| insecticidal protein Cry1C (181 aa)
  initn: 327 init1: 173 opt: 431 Z-score: 509.3 bits: 103.5 E(): 1.9e-19
Smith-Waterman score: 431; 43.750% identity (70.833% similar) in 192 aa overlap
(242-422:1-181)

      220      230      240      250      260      270
Cry1Ac VRWYNTGLERWVGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREI
      220      230      240      250      260      270
gi|232 LTVLDIAAFFPNYDNRYPYIQPVGQLTREV
      10      20      30
Cry1Ac YTNPVLENFDGSAQG----IEGS-IRSPHMDILNSITTYDAHR-GE-YYWSGH
      280      290      300      310      320
gi|232 YTDPLI-NFNPLQSVLQPLTFNVMESSAIRNPHLFDILNLTIFTDWFSVGRNFWYGGH
      40      50      60      70      80
Cry1Ac QIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLTLYR---RPFNIGIN
      330      340      350      360      370      380
gi|232 RVISSLIG--GNNITSPIYGREANQEPFRSFT--FNGPVFRTLSPNTLRLQLQPWPAPPF
      90      100      110      120      130      140
Cry1Ac NQQLSVLDGTEFAYGTSSNLPYSAVYRKSQTVDSLDEIPPQNNVPPRQGFHRLSHVSMF
      390      400      410      420      430      440
gi|232 N--LRGVEGVEFS--TPTN--SFTYRGRGTVDLSLTELPPEDN
      150      160      170      180
Cry1Ac RSGFSSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGLS-VISGPGFTGG
      450      460      470      480      490      500

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>>gi|51090228|dbj|BAD35157.1| cancer cell-killing Cry pr (825 aa)
  initn: 799 init1: 360 opt: 439 Z-score: 508.9 bits: 105.6 E(): 2e-19
Smith-Waterman score: 733; 28.846% identity (57.840% similar) in 676 aa overlap
(2-613:34-675)

      10      20      30
Cry1Ac CMQAMDNNPNINCEIPYNCLSNPEVEVLGGE
      10      20      30      40      50
gi|510 NCNNGGYEVLNSGKGYCQPRYPFAQAPGSELQNMGYKEWMNMC-----TSGDPTVLGEG
      10      20      30      40      50
Cry1Ac RIETGYTPIDISLSLTLQFLLSEFVPGAGFVGLGLVDI IWGIFGPSQ---WDAFLVQIEQL
      40      50      60      70      80
gi|510 YSADVRDAVITSIINIASYLLSVFPFPAAGVAAGLIGALLGLLWPTNTQAVWEAFMNTVEAL
      60      70      80      90      100      110
Cry1Ac INQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRI--QFNDMNSAL
      90      100      110      120      130      140
gi|510 INQKLDEYARSKAISELNGKLVLELYQDAADDWNEPNPGD--LRNKNRVLTFEFRNVNGHF
      120      130      140      150      160      170
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIG
      150      160      170      180      190      200
gi|510 ENSMPSFAVRNFEVNLPLVYAEANLHLLLRDAVKFGEWGMSTDPGAER--DDMYRRLR
      180      190      200      210      220      230
Cry1Ac N----YTDHAVRWYNTGLERV-----W-----GPDSRD-----W
      210      220      230
gi|510 SRTEIYTDHCVNTYNGQLQAKSLQANVSDYSRYPWTQYNQSGGFSYREAKGEYRGTENW
      240      250      260      270      280      290
Cry1Ac IRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENF--DGSFRGSA
      240      250      260      270      280
gi|510 NLYNAFRDMTILVLDIIAQFPYDPLYSRVPKSELTRVYTDIRGTTWRSANL-NTI
      300      310      320      330      340      350
Cry1Ac QGIEGSI---RSPHMDILNSITTYDAHRGEYYWSGHQIMASPVGF-----SGPEFT
      290      300      310      320      330
gi|510 DAIENRMVGSRLQLFTWLTEMKFYIRNTGSITSYTHGDLM--VGLEKKIRKTDNDNDQW
      360      370      380      390      400      410
Cry1Ac FPLYGTMGNAAPQQRIVAQLGQGV--YRSLTLYRPFNIGINNQQLSVLDGTEFAYGT
      340      350      360      370      380      390
gi|510 LPLEGQNTSYTRIDRPGIELGKNYWYARTQQWFETRLLQLWANTDVLNSL NAGTVGNEFW
      420      430      440      450      460      470
Cry1Ac SSNLPYSAVYRKSQTVDSLDEIPPQNNVPPRQGFHRLSHVSM--FRSG--FNSNSVSI
      400      410      420      430      440      450
gi|510 VRDVPD--YRNIYARST-----RNHFIE----NHRLSWIKFEPVRDNCPPAWGKQL
      480      490      500      510

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```

          460      470      480      490      500      510
Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 SALLFGWTHNSVDLNNIISQYRITQIPAVKAYWNRGAFSVIRGPGSTGGNLVQLGTGGE-
      520      530      540      550      560      570

```

```

          520      530      540      550      560      570
Cry1Ac IQNRGYIEVPIHFPST-STRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 -----VSVKVRPEQTGSDWYRVRIRYAAGSRGRLNVKKYVSSIHASVTYDYNMTMSSST
      580      590      600      610      620      630

```

```

          580      590      600      610      620
Cry1Ac SSDFGYFESANAFTSSLGNI---VGVNRFSGTAGVIDRFEFIPVTATLEAEYNLERAQK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 QGTYNFQYLDVYNFRLAEPFVWLTNESG-GPIWIDKIEFIPLSPIPELVPVPGTYQI
      640      650      660      670      680

```

```

          630      640      650      660      670      680
Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 VTALNNSVVTSEEFQCMGIGLTTTRCGVNLWSNNGNTLQKWRVYNGDQNAFQIKSTPNED
      690      700      710      720      730      740

```

>>gi|51090232|dbj|BAD35160.1| cancer cell-killing Cry pr (825 aa)  
 initn: 799 initl: 360 opt: 439 Z-score: 508.9 bits: 105.6 E(): 2e-19  
 Smith-Waterman score: 733; 28.846% identity (57.840% similar) in 676 aa overlap  
 (2-613:34-675)

```

          10      20      30
Cry1Ac          CMQAMDNNPNINECIPYNCLSNPEVEVLGGE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 NNNNGYEVLSNGKGYCQPRYPFAQAPGSELQNMGYKEWMNMC-----TSGDPTVLGEG
      10      20      30      40      50

```

```

          40      50      60      70      80
Cry1Ac RIETGYTPIDISLSLTQFLLSEFVPGAGFVGLGLVDIIWGFGPSQ---WDAFLVQIEQL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 YSADVRDAVITSINIASYLLSVPFPAGVAAGILGALLGLLWPTNTQAVWEAFMNTVEAL
      60      70      80      90      100      110

```

```

          90      100      110      120      130      140
Cry1Ac INQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRI--QFNDMNSAL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 INQKLDEYARSKAISELNGLNKLVLELYQDAADDWNNENPGD--LRNKNRVLTEFRNVNGHF
      120      130      140      150      160      170

```

```

          150      160      170      180      190      200
Cry1Ac TTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGWGFDAAATINSRYNDLTRLIG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 ENSMPSFAVRNFEVNLPPVYAEAAANLHLLLRDAVKFGEGWGMSTDPGAER--DDMYRRLR
      180      190      200      210      220      230

```

```

          210      220      230
Cry1Ac N----YTDHAVRWYNTGLERV-----W-----GPDSRD-----W
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 SRTEIYTDHCVNTYNOGLQQAKSLQANVSDYSRYPWTQYNQSGGFSYREAKGEYRGTENW
      240      250      260      270      280      290

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          240      250      260      270      280
Cry1Ac IRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLENF--DGSFRGSA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 NLYNAFRDMTILVLDIIAQFPPTYDPLYSRPVKSELTRVYTDIRGTTWRSANL-NTI
      300      310      320      330      340      350

```

```

          290      300      310      320      330
Cry1Ac QGIEGSI---RSPHLMIDILNSITIYTDahrgeyywsgHQIMASPVGF-----SGPEFT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 DAIENRMVGSRQLQFLTWLTWKFYIRNTGSITSYTHGDLM--VGLEKKIRKTDNDNDQW
      360      370      380      390      400      410

```

```

          340      350      360      370      380      390
Cry1Ac FPLYGTMGNAAPQQRIVAQLGQGV--YRTLSTLYRRPFNIGINNQLSVLDGTEFAYGT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 LPLEGQNTSYTRIDRPGIELGKNYWYARTQQWFETRLLQLWANTDVLNAGTVGNEFW
      420      430      440      450      460      470

```

```

          400      410      420      430      440      450
Cry1Ac SSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSM--FRSG--FSNSVSI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 VRDVPD--YRNIYARST-----RNHFIE-----NHRLSWIKFEPVRDNCPPAWPGYKQL
      480      490      500      510

```

```

          460      470      480      490      500      510
Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNG-SVISGPGFTGGDLVRLNSSGNN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 SALLFGWTHNSVDLNNIISQYRITQIPAVKAYWNRGAFSVIRGPGSTGGNLVQLGTGGE-
      520      530      540      550      560      570

```

```

          520      530      540      550      560      570
Cry1Ac IQNRGYIEVPIHFPST-STRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 -----VSVKVRPEQTGSDWYRVRIRYAAGSRGRLNVKKYVSSIHASVTYDYNMTMSSST
      580      590      600      610      620      630

```

```

          580      590      600      610      620
Cry1Ac SSDFGYFESANAFTSSLGNI---VGVNRFSGTAGVIDRFEFIPVTATLEAEYNLERAQK
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 QGTYNFQYLDVYNFRLAEPFVWLTNESG-GPIWIDKIEFIPLSPIPELVPVPGTYQI
      640      650      660      670      680

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          630      640      650      660      670      680
Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|510 VTALNNSVVTSEEFQCMGIGLTTTRCGVNLWSNNGNTLQKWRVYNGDQNAFQIKSTPNED
      690      700      710      720      730      740

```

>>gi|16945772|dbj|BAB72018.1| putative mosquitocidal tox (666 aa)  
 initn: 482 initl: 208 opt: 437 Z-score: 507.9 bits: 105.1 E(): 2.3e-19  
 Smith-Waterman score: 627; 27.890% identity (58.237% similar) in 692 aa overlap  
 (2-633:12-664)

```

          10      20      30      40
Cry1Ac          CMQAMDNNPNINECIPY-----NCLSNPEVEVLGGERI-ETGYTPIDIS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|169 NSYENKNEYEILESSNNTNMPNRYPFANDRDMSTMSFNCQGISWDEIWESAETITSIG
      10      20      30      40      50      60

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50      60      70      80      90
Cry1Ac LSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDAF----LVQIEQLINQRIEEFARNQ
gi|169 IDLIEFLME---PSLGGINTLFSII-GKLIPTNHQSVSALSICDLLSIIIRKEVADSVLSD
70      80      90      100     110

100     110     120     130     140
Cry1Ac AISR-LEG-LSNLYQIYAESFREWEAD--P---TNPA----LREEMRIQFNDMNSALTTA
gi|169 AICRFLDGKLNKYREYYLPYLEAWLKDGKPLQKTNNSDIGQLVKVYFELSERDFNEILGGS
120     130     140     150     160     170

150     160     170     180     190     200
Cry1Ac IPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWG--FDAATINSRY-----NDL
gi|169 L---ARNNAQILLLPYFCASCKCQLLLLRDAVQYEEQWFFPLSAENVRSELISPNSGCDF
180     190     200     210     220     230

210     220     230     240     250
Cry1Ac T-----RL---IGNYTDHAVRWYNTGLERVW--GPDSDWIRYNQFRRELTTLTVLDIVSL
gi|169 TGDYERLKCKIAEYTDYCEYWYQAGLNQIKQAGTGADTWAKFNKFRREMTTLTVLDIIAI
240     250     260     270     280     290

260     270     280     290     300
Cry1Ac FPNYSRRTYPIRTVSQLTREIYTNPVLNFDGSGFR-----GSAQGIIEGS-IRSPHLMDI
gi|169 FQTYDFKKYPLPHTVELTREIYTDVPGYS-SGTYSWLKYWTGAFNTLEANGTRGPGLVTW
300     310     320     330     340     350

310     320     330     340     350     360
Cry1Ac LNSITIYDHAHRGEYY--WSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
gi|169 LRSIGIYNE-YVSRYSFGWVGTRHYEDYTTGNG-NFQR-MSGTTSN---DLRDISFPNSD
360     370     380     390     400

370     380     390     400     410
Cry1Ac VYRTLSSSTLYRRPFNIG-INNQQLSVLDGTEFAYGTSS-NLPSAVYRKSGTVDSLDEIPP
gi|169 IFKIESKAIMNL---VGEINARPEYRVSRAEFSESTAFIYLYDAGNSGLSSMTITSKLPG
410     420     430     440     450     460

420     430     440     450     460     470
Cry1Ac QNNVPPRQGFQSHRSLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIP
gi|169 IKNPEPSYRDYSHRSLSNAACVGAG--NSRINV----YGWHTMSKYNLYPDKITQIP
470     480     490     500     510

480     490     500     510     520     530
Cry1Ac AVKGNFLFN---GSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVVR
gi|169 AVKAFDISDTGPGQVIAGPGHTGGNVVSL-----PYYSRLKIRLIPASTNKNYLVRVR
520     530     540     550     560

540     550     560     570     580     590
Cry1Ac YASVTPIHNLVN-WGNSSIFSNT--VPATATSLDNLQSSDFGYFESANAFTSSSLGNIVGV
gi|169 YTSTSNRLLVERWSPSSIINSYFFLPSTGPG-----DSFGYVDTLVTTFNQPGVEIIII
570     580     590     600     610     620

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600     610     620     630     640     650
Cry1Ac RNFSGTAGVIIDRFEFIPVTAT--LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|169 QNLD--TPINVDKVEFIPVNSTALEYEGKQSLEKAQDVVNDLFFVK
630     640     650     660

660     670     680     690     700     710
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTG

>>gi|17977979|emb|CAC80985.1| Cry29Aa protein [Bacillus (650 aa)
initn: 432 initl: 114 opt: 425 Z-score: 493.9 bits: 102.5 E(): 1.4e-18
Smith-Waterman score: 656; 27.341% identity (58.610% similar) in 662 aa overlap
(2-633:50-648)

10      20      30
Cry1Ac CMQAMDNN-PNINECIPYNCLSNPEVEVLGG
gi|179 SNIPNNYSKYPIANTLNQTMQNTNYKDWNTMCAIDNNLKSIN---PFE--ANLQNSLVGL
20     30     40     50     60     70

40      50      60      70      80
Cry1Ac ERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQW---DAFLVQIEQ
gi|179 FAITAAIASL-LSAPITG--GTSIAAGTAIAAAIIPILW---PSQENNLPKLLAISEA
80     90     100    110    120

90      100     110     120     130     140
Cry1Ac LINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT
gi|179 TLYSFQDQRVREDALTRLESCLKDSVKYFENAFTFWINNP-NSNTTTTTRERFQEVNGRFV
130    140    150    160    170    180

150     160     170     180     190     200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF---DAATINSRYNDLRL
gi|179 GSMAFFRAKNYEPILLSTYAQAARLHLLHLDGITYAEKWNLRSRQDDMPGLDLYKEFNK
190    200    210    220    230    240

210     220     230     240     250     260
Cry1Ac LIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVLDIVSLFPNYSRTPYPIR
gi|179 YCNEYIEHCIKWYNESLSLLKSVGA-NWLEYNQYRTFLTASVLDVLSLFSYDPRLYKER
250    260    270    280    290    300

270     280     290     300     310     320
Cry1Ac -TVSQLTREIYTNPVLNFDGSGFRGSAQGIIEGSIRSPHLMIDLNSITIYDHAHRGEYYWS
gi|179 LSVEILLTRKLYTDPI--NYHRGISLEADESKYTLLE-PTLFTQLYTLTTFYSNIF---YNYM
310    320    330    340    350

330     340     350     360     370     380
Cry1Ac GHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINN
gi|179 GH---TNTYRYSPLD-----KIFAERSFG---KQSSYIDKVPV---IPN
360    370    380    390

390     400     410     420     430
Cry1Ac QQLSVLDGTEFAYGTSSNLPSAVYRK--SGTVDSLDEIPPQNNVPPRQGFQSHRSLSHVSM

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gi|179 DK-SIIYKIR-AYDNHNGLFNVMYFGFWDGKEDQIQKIIIGSSSTEIYIKNCTRHLADVIS
400 410 420 430 440 450

Cry1Ac FRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL-FNGSVISGPGFT
440 450 460 470 480 490

gi|179 HDLDEKNKCYSD----FAWTSTTISLENEIKNDIITQIPAVKAYQLGVQSQVIKPGPHT
460 470 480 490 500

Cry1Ac GGDLVRLNSSGNNIQNRGYIEVPI-HFPSTSTRYRVRVRYAS----VTPHILNVNWGNS
500 510 520 530 540 550

gi|179 GGDLI-----NLKSNLYLRISCOHLSNVTKKYFVRIRYATNGSLNTRPI-INITIPGM
510 520 530 540 550

Cry1Ac S----IFSNTPVATATSLDNLQSSDFGYFESANAFT---SSLGNIVGVRNFSGTAGVII
560 570 580 590 600 610

gi|179 TPQGMVLDNTFSGTGYSD--NLEYQNFYKFEFLKEVTLNPNQSIISLTLNRSQNSNSILL
560 570 580 590 600 610

Cry1Ac DRFEFIPVTATL---EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
610 620 630 640 650 660

gi|179 DRIEFLPITPSIRKSKEQQNLEKNQKTVNKLFFN
620 630 640 650

Cry1Ac DEFCLDEKRELESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
670 680 690 700 710 720

>>gi|3668333|gb|AAC61891.1| insecticidal protein Jeg72 [ (674 aa)
initn: 677 init1: 239 opt: 419 Z-score: 486.6 bits: 101.2 E(): 3.5e-18
Smith-Waterman score: 678; 29.511% identity (58.010% similar) in 593 aa overlap
(81-633:105-672)

Cry1Ac LSEFVPGAGFVGLVDIIWGFVGFQWDAFLVQIEQLINQRIEEFARNQAIKSRLEGLSNL
60 70 80 90 100 110

gi|366 KAVASSLADSIKSSSLGISTTITENNVSQVSMVQVHQIINRRIQETILDGESSLNLGLVAI
80 90 100 110 120 130

Cry1Ac Y-QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIP-LFVQNYQVPLLSVYVQA
120 130 140 150 160

gi|366 YNRDYLGALEAWNNKSNINYNQTNVAEAFKTVEREFFTKLKGIIYRTSSSQITLLPTFTQA
140 150 160 170 180 190

Cry1Ac ANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR
170 180 190 200 210 220

gi|366 ANLHLSMLRDAVMYQEGWNLQSHINYSK--ELDDALEDYTNVCEVYTKGLNALRGSTAI
200 210 220 230 240 250

Cry1Ac DWIRYNQFRRELTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGF----
230 240 250 260 270 280

gi|366 DWLEFNSFRDMLTMLVLDLVAIFPNYNPVRYPLSKISLSRKIYTDVGRGTRDPSFGDWT
260 270 280 290 300 310

Cry1Ac ---RGSAQ--GIEGSIR-SPHLMIDLNSITIYT---DAHR---GEYY--WSGHQIMASP
290 300 310 320

gi|366 NTGRTLANFNDLEREVTDSPSLVKWLGDMTIYTGAIKSYRPTSPGDRIGVWYGNINAFYH
320 330 340 350 360 370

Cry1Ac VGFSGPEFTFPLYGTMGNAAPQQRIVAQQLGQGVYR-----TLSSSTLYRRPFNIGINNQQ
330 340 350 360 370 380

gi|366 TGRTDV-VMFRQTGDYEDPSTFISNIIYDDIYKLLDLRAAAVSTIQGAMDTTFVGSSSR
380 390 400 410 420 430

Cry1Ac LSVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPQNNVPPRQGFSHRLSHVSMFRSG
390 400 410 420 430 440

gi|366 FFDIRGRNQLYQSNKPYPSLPITIT-----FPGEESSEGNANDYSHLLCDVKILQED
440 450 460 470 480

Cry1Ac FSNSSVSIIRAPMFS--WIHRSAEFNIIASDSITQIPAVKGNFLF-NGSVISGPGFTGG
450 460 470 480 490 500

gi|366 SSN--ICEGRSLLSHAWTHASLDRNNTILPDEITQIPAVTAYELRGNSSVAVGPGSTGG
490 500 510 520 530 540

Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPHILNVNWGNSIFSNTPV
510 520 530 540 550 560

gi|366 DLVKM--SYHSVWS---FKV---YCSELKNYRVRIRYAS---HGNCQFLMKRWPSTGVA
550 560 570 580

Cry1Ac ATATSLDNLQ---SSDFGY--FESANAFTSS--LGNIVGVRNFSGTAGVIDRFEFIPVT
570 580 590 600 610

gi|366 PRQWARHNVQGTFSNSMRYEAFKYLDIFTITPEENNAFTIDLESGDGLFIDKIEFIPVS
590 600 610 620 630 640

Cry1Ac AT---LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|366 GSAFYEYEGKQNIIEKTKQKAVNDLFIN
650 660 670

>>gi|3668335|gb|AAC61892.1| insecticidal protein Jeg74 [ (675 aa)
initn: 528 init1: 204 opt: 419 Z-score: 486.6 bits: 101.2 E(): 3.5e-18
Smith-Waterman score: 645; 28.871% identity (58.871% similar) in 620 aa overlap
(56-633:76-673)

Cry1Ac EVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVGLVDIIWGFVGFQWDAF---LV
30 40 50 60 70 80

gi|366 NECDGITPSIFGTLGLVASIVISTINLATSPSIGDAFALVSSI-GEYWPETKTSFPLSVA
50 60 70 80 90 100

Cry1Ac QIEQLINQRIEEFARNQAIKSRLEGLSNLYQ-IYAESFREWEAD--PTNPA---LREEMR
90 100 110 120 130

gi|366 DVNRLIREALDQNAINRATGKFNGLMDTYNTVYLKLNLDQWYDTRIPANPQGSQDLREAAR
110 120 130 140 150 160







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Cry1Ac NSALTTAIPLFAVQ-NYQVPLLSVYVQAANLHLSVLRDVSVFQQRW---GFDAATINSR
gi|268 EPIIDKDLMLKNNASYRIPTLPAYAQIATWHLNLLKHAATYNIWLQNGINPSTFNSS
190 200 210 220 230 240
200 210 220 230 240 250
Cry1Ac --YND-LTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTTLVLDIVSLFPN
gi|268 NYYQGYLKRKIQEYTDYCIQTYNAGLTMIRTNATWNNMYNTYRLEMTLTVLDLIAIFPN
250 260 270 280 290 300
260 270 280 290 300 310
Cry1Ac YDSRTYPIRTVSQLTREIYTNVLENFDGSRFGSAQGIEGSIIRPHLMDILNSITIYTDA
gi|268 YDPEKYPIGVKSELIREVYTN--VNSD-TFRTITELENGLYRNP-----TLFTWI
310 320 330 340 350
320 330 340 350 360
Cry1Ac HRGEYYWGHQIMASPV---GFSGPEFTFPLYGTMGN---AAPQQRIVAQLGQGVYRTLS
gi|268 NQGRFYTRNSRDILDYDIFSGFTGNQMAFTHTNDNRNIWGAHVHGNIIISQDTSKVF----
360 370 380 390 400
370 380 390 400 410 420
Cry1Ac STLYR-RFPN-IGINNQLSVLDGTEFAYGTSSNLPASVYRKSQVSDSLDEIPPQNNVNP
gi|268 -PFYRNKPIDKVEIVRHREYSIIYEMIFFSNS---SEVFRYSSNSTIENNYKRTDSYMI
410 420 430 440 450 460
430 440 450 460 470 480
Cry1Ac PRQG-----FSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNNLIASDSITQIPA
gi|268 PKQTKWNEEYGHSTLSYIK--TDNYIFSVVRERRRVAFSWHTTSVDFQNTIDLDNITQIHA
470 480 490 500 510 520
490 500 510 520 530
Cry1Ac VKG-NFLPNSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYAS
gi|268 LKTLKVVSSNSKIVKGLGHTSENVLKDS-MNFRVR-----FLKNVQQYQVRIRYAT
530 540 550 560 570
540 550 560 570 580 590
Cry1Ac VPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFTSSSLGNIVGVRNFSGT
gi|268 NAPKTTVFLTGIDTI-SVELPST-TSRQNPATDLTYA
580 590 600
600 610 620 630 640 650
Cry1Ac AGVIIIDRFEPFVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY
>>gi|29329415|emb|CAD83750.1| unnamed protein product [P (134 aa)
initn: 342 init1: 342 opt: 361 Z-score: 428.6 bits: 88.2 E(): 5.9e-15
Smith-Waterman score: 361; 46.667% identity (71.111% similar) in 135 aa overlap
(821-952:1-134)
800 810 820 830 840 850
Cry1Ac LSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGCSDLNEDLGV
gi|293 RKHRKC-HQAHQFEPFHIDTGTIDLVEDLGI

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10 20
Cry1Ac WVIFKIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAK
gi|293 WVIFKICATDGYASLDDLEVEEGALGVEALELVKKREKKWRHQEHCQSQTCHKYDAAK
30 40 50 60 70 80
920 930 940 950 960
Cry1Ac ESDVALFVNSQYDQLQADTNIAMIAHADKRVHSI---REAYLPELSVIPGVNAIFEELE
gi|293 HAVMALFTNTRYEKLFETTISNILYADHLVQSIPVYVNYKYPVEV
90 100 110 120 130
970 980 990 1000 1010 1020
Cry1Ac GRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQRSLVLPVEWAEVQSEVR
>>gi|111927188|gb|ABH71840.1| Sequence 2 from patent US (134 aa)
initn: 342 init1: 342 opt: 361 Z-score: 428.6 bits: 88.2 E(): 5.9e-15
Smith-Waterman score: 361; 46.667% identity (71.111% similar) in 135 aa overlap
(821-952:1-134)
800 810 820 830 840 850
Cry1Ac LSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGCSDLNEDLGV
gi|111 RKHRKC-HQAHQFEPFHIDTGTIDLVEDLGI
10 20
860 870 880 890 900 910
Cry1Ac WVIFKIKTDQGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAK
gi|111 WVIFKICATDGYASLDDLEVEEGALGVEALELVKKREKKWRHQEHCQSQTCHKYDAAK
30 40 50 60 70 80
920 930 940 950 960
Cry1Ac ESDVALFVNSQYDQLQADTNIAMIAHADKRVHSI---REAYLPELSVIPGVNAIFEELE
gi|111 HAVMALFTNTRYEKLFETTISNILYADHLVQSIPVYVNYKYPVEV
90 100 110 120 130
970 980 990 1000 1010 1020
Cry1Ac GRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQRSLVLPVEWAEVQSEVR
>>gi|152013905|gb|ABS20059.1| dipterans toxic crystal pr (126 aa)
initn: 347 init1: 235 opt: 349 Z-score: 414.9 bits: 85.5 E(): 3.5e-14
Smith-Waterman score: 349; 47.619% identity (73.810% similar) in 126 aa overlap
(923-1048:2-126)
900 910 920 930 940 950
Cry1Ac DKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVHSI REAYLPEL
gi|152 DEALQFDTTLAQIQAAYLVQSIPVYVNDWL
10 20 30
960 970 980 990 1000 1010
Cry1Ac SVIPGVNAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWVKGHVVDVEEQNNQRSV
gi|152 SDVPGMNYDIYVELDARVAQARYLYDTRNIKNGDFTQGVMGVHWVGNADVQ-QIDGVSV
40 50 60 70 80 90

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```

1020      1030      1040      1050      1060      1070
Cry1Ac LVVPEWEAEVSVQEVRCVCPGRGYILRVVAYKEGYGECVCTIHEIENNTDELKFSNCVVEEBI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|152  LVLSNWSAGVSNVHLQHNNHGYVLRVIAKKEGPGNG
      100      110      120

```

```

1080      1090      1100      1110      1120      1130
Cry1Ac YPNNTVTCTNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRRENPCFEN

```

>>gi|2725272|gb|AAB92954.1|I67292 Sequence 9 from patent (1168 aa)  
 initn: 734 initl: 192 opt: 361 Z-score: 414.6 bits: 88.7 E(): 3.6e-14  
 Smith-Waterman score: 869; 24.664% identity (55.426% similar) in 1115 aa overlap  
 (42-1065:70-1125)

```

20      30      40      50      60
Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG----FVLGLVDI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  EEFGKTGYMDPLKQHLQIAWDTSQNGTVDYLALTKASISLIGLIPGADAVVPPINMFVDF
      40      50      60      70      80      90

```

```

70      80      90      100      110
Cry1Ac IWG-IFG-PSQWDA-----FLVQIEQLINQRIIEEFARNQAISRLEGLS-----NLY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  IFPKLFGRGSQQNAQAQFELIEKVKELVDEDFRNFTLNLLNLYDGMQTALSHFQNDV
      100      110      120      130      140      150

```

```

120      130      140      150
Cry1Ac QIYAESFRE---WEADPT--NPALREEMRIQ--FNDMNSALTTAIPLFA----VQNYQV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  QIAICQGEQPLMLDQTPACTPTTDHLLSVRESFKDARTTIETALPHFKNPMLSTNDNT
      160      170      180      190      200      210

```

```

160      170      180      190      200
Cry1Ac P-----LLSVYVQAANLHLSVLRDVSFVGRW---GFDAATINSRYNDLTRLIGNY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  PDFNSDTVLLTLPMTTAAATLNLILHQGYIQFAERWKSVDYDFINQTKVDLQRRIQDY
      220      230      240      250      260      270

```

```

210      220      230      240      250      260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWI-RYNQFRELTLTVLDIVSLFPNYSRTPYPIRTVSO
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  STTVSTTFEK-FKPTLNPSNKESVKNYRVRSMTLQSLDIAATWPTLDNVNYPNSVDIQ
      280      290      300      310      320      330

```

```

270      280      290      300      310      320
Cry1Ac LTREIYTNPVLENFDGSRGSAQGIIEGSIIRSPHMLDILNSITIIYTDHRGEYYWSGHQIM
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  LDQ---TRLVFSVAVAGPWEGN-----DNITS-NIIDVLTPI-----NTG---IGFQES
      340      350      360      370

```

```

330      340      350      360      370      380
Cry1Ac ASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLSV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  SDLRKFTYPRIELQSMQPHGQYVNSKSVHEHCYSDG---LKLNYKNKTIITAGVSNIDESN
      380      390      400      410      420      430

```

```

390      400      410      420      430      440
Cry1Ac LDGTEFAYGTSSNLP-SAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFS

```

```

. . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  QNN-KHNYGPVINSPIITDINVNSQNSQYLLDLNSVMVNGGQKAVGCCPLSSNGNSNNAALP
      440      450      460      470      480      490

```

```

450      460      470      480      490
Cry1Ac NSSVSII-----RAPMF-SWIHRSAEFN-NIIASDSITQI-PAVKGNFLFNGSV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  NQKINVIYSVQSNDKPEKHADTYRKGWYMSHSHPYDLVPEVNIIGDIDPDTKQPSLLKGF
      500      510      520      530      540      550

```

```

500      510      520      530      540
Cry1Ac ISGPGFTGGDLVRLNS---SGNNIQNRGYIEVPIHFPSTST-RYRVRVRYASVTPIHNL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  PAEKGY--GDSIAYVSEPLNGANAVKLTYSYQVLKMEVNTQTTQKYRIRIRYATGGDTAAS
      560      570      580      590      600      610

```

```

550      560      570      580      590
Cry1Ac VNWGNSISFNTVTPATATSLDNLQSSDFGYFESANA-----FTSSL---GN-IVGVRN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  IWFHIIGPSGNDLTNEGHNFSVSSRNKMFVQGNNGKYVLNILLTDSIELPSGQQTILIQN
      620      630      640      650      660      670

```

```

600      610      620      630      640
Cry1Ac FSGTAGVIIDRFEFI--PVTAT-----LEAEYNLERAQKAVNALFTSTNQLGLKTNVTD
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  -TNSQDLFLDRIEFISLPSTSTPTSTNFVEPE-SLEKIINQVNLQFSSSSQTELAHTVSD
      680      690      700      710      720      730

```

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650      660      670      680      690      700
Cry1Ac YHLDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG--W
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  YKIDQVVLKVNALSDVDFVGEKKALRKLVNQAKQLSKARNVLVGGNF-----EKGHEW
      740      750      760      770      780

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710      720      730      740      750      760
Cry1Ac GGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFTRYLQRYIEDSQD
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  ALSREATMVANHELFGDHLPPP--TLYPSYAYQKIDESKLSNRYTVSGFIAQSEH
      790      800      810      820      830      840

```

```

770      780      790      800      810      820
Cry1Ac LEIYSIRYNAK-HETVNVPGTGLWPLSA-QSPIGKCGEPNRCAPHLEWNPDLDCSCRDG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  LEVVVSRYGKEVHMDLIDIPYEEAL-PISSESP--NCCKPAAC-----QCSSCDG
      850      860      870      880

```

```

830      840      850      860      870      880
Cry1Ac EKCAHSHHFLSDIDVGGCTDLNEDLGVVWIFKIKTQDGHARLGNLFLEEKPLVGEALAR
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  SQ--SDSHFFSYSIDVGLSQSDVNLGIEFGLRIAKPNGFAKISNLEIKEDRPLTEKEIKK
      890      900      910      920      930      940

```

```

890      900      910      920      930      940
Cry1Ac VKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|272  VQRKEQKWKAFNQEAEVATTLQPTLDQINALYQNEWDWNG-SVHPHVTYQHL SAVVVPT
      950      960      970      980      990      1000

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950      960      970      980      990      1000

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Cry1Ac IREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDV
gi|272 LPKQRHWFMEDREGEHVLTQQFQQALDRAFFQIEEQNLIHNGFNANGLTDWTVTGDQAL
1010 1020 1030 1040 1050 1060

1010 1020 1030 1040 1050 1060
Cry1Ac EEQNNQRSVLVVPEWEAEVSVQEVVRCV---GRGYILRVTAAYKEGYEGCVTIHEIENNTD
gi|272 T-IFDEDVLELAHWDAISQITIEIMDFEEDTEYKLRV---RGKGGKVTVTVQHGEEELE
1070 1080 1090 1100 1110 1120

1070 1080 1090 1100 1110 1120
Cry1Ac ELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSY
gi|272 TMTFNNTSFTTQEQTFYFEGDITVDVHVQSENNTFLIDSVELIEIIEEM
1130 1140 1150 1160

>>gi|152013909|gb|ABS20061.1| dipterans toxic crystal pr (126 aa)
initn: 339 initl: 235 opt: 345 Z-score: 410.2 bits: 84.7 E(): 6.3e-14
Smith-Waterman score: 345; 47.619% identity (73.016% similar) in 126 aa overlap
(921-1046:2-126)

900 910 920 930 940 950
Cry1Ac WRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAAMIHAADKRVSIREAYLP
gi|152 VQDEALQFDTTLAQIYAAYLVQSIPIVYND
10 20 30

960 970 980 990 1000 1010
Cry1Ac ELSVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVVEEQNNQR
gi|152 WLSVDPGMNYDIYVELDARVAQARYLYDTRNIKNGDFTQGVMGVHWVTGNADVQ-QIDGV
40 50 60 70 80 90

1020 1030 1040 1050 1060 1070
Cry1Ac SVLVVPEWEAEVSVQEVVRCVGRGYILRVTAAYKEGYEGCVTIHEIENNTDELKFSNCVEE
gi|152 SVLVLSNWSAGVSNVHLQHNHGYVLRVIAKKEGPG
100 110 120

1080 1090 1100 1110 1120 1130
Cry1Ac EIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRENPC

>>gi|22002424|dbj|BAC06484.1| Cry21Ba1 [Bacillus thuring (1286 aa)
initn: 665 initl: 202 opt: 356 Z-score: 408.1 bits: 87.6 E(): 8.2e-14
Smith-Waterman score: 781; 24.277% identity (51.528% similar) in 1211 aa overlap
(44-1065:70-1244)

20 30 40 50 60
Cry1Ac CIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLE---FVPGAG---FVLGLVDI
gi|220 EEFAKTGYKDPLEQHLKIAWNASQNGTIDYLALTKASISFIGLIPDADAVVFFINMVFDF
40 50 60 70 80 90

70 80 90 100 110
Cry1Ac IWG-IFGP-----SQWDAFLVQIEQ---LINQRIIEFARNQAISRLEGLSNLYQIYAESF
gi|220 IFPKLFBEGSQNSQAQFFELIIEKVKIIVDQEFRNFTLNTLLNDLDMQMTTLEHFQNDV
100 110 120 130 140 150

```

```

120 130 140 150 160
Cry1Ac R-----EWEADPTNFPALREEMRIQ--FNDMNSALTTAIPLFA--VQNYQVP-
gi|220 QIAICQGEQPLILDEKHPCTPTKNHLVSVKESFKNARTSIEIETVLPHPKFNPMNTNKTTPD
160 170 180 190 200 210

170 180 190 200
Cry1Ac -----LLSVYVQAANLHLSVLRDVSVFGQRW---GFDAATINSRYNDLTRLIGNYTD
gi|220 FNSDTVLLTLPMTTAAATLNLILHQGYIQFVERWKSVDYDEAFINQTKADLQHRIQEYST
220 230 240 250 260 270

210 220 230 240 250 260
Cry1Ac HAVRWYNTGLERVWGPDSRDWRYNQFRRELTLTVLDIVSLFNPYDSRTPYIRTVSOL--
gi|220 TVSTTFEK--FKPTLSNKKSSINTYKYNKYSMTLNCLDIAATWPTLDNVNYPNSVEIQLDQ
280 290 300 310 320 330

270 280 290 300 310
Cry1Ac TREIYTN---VPLENFD-----GSFRGSAQIEGSIKSPHMLDILNSITIIY
gi|220 TRLVFVSNLVGPFEGNDDISTYTRRSIMNYSKGDTPGDVNSAIQSLRYRPLE--LSKVQFY
340 350 360 370 380 390

320 330 340 350
Cry1Ac TDAHRGEY---YWSGHQI-----MASPVGFSG---PEFTFPLYGTMGNAAPQQR--
gi|220 THDQRSNGVRHCYTSGFNLTFFNDNSSMSAKQDESATADSPPLTAPIKMNANNSQNSQYYD
400 410 420 430 440 450

360 370 380 390
Cry1Ac -----IVAQLGGQV-----YRTLSSSTLYRRPFNI---GINNQQLS--VLD-GTEFAYG-
gi|220 YSSINIDNQGSGGSFAFSPYQSNPILPNQKINVFYYPYSSAHPIDPHTTDPDTWFKLGY
460 470 480 490 500 510

400 410 420 430 440 450
Cry1Ac TSSNLPSAVYRKS--GTVDLDEIIPPQN--NNVPPRQGFHSHLSHVSMFRSGFSNSVSI-
gi|220 VSSHIPYDLTPQNVIGEIQDQTKQPSLILKGFPAEKYGGSIYVSEPLNGANAAKLTLN
520 530 540 550 560 570

460 470 480
Cry1Ac -----IRAPMFS-----WIHRSAEFNIIIASDSITQIPAVKGNFLF
gi|220 QILYMQVTNLTQKYQIRLRYATKNDTTASVWFHIIIGPNNQDIINHS-PDIPPRSNKMF
580 590 600 610 620 630

490 500 510 520 530
Cry1Ac ---NG-----SVISGPGFTGGDLVRLNSSGNNIQNR--GYIE-VPIHFPSTSTRYRVRV
gi|220 VQGENKGYVLDLTVDSIELPSGQLTILIQININPDQDLFLDRIEFVPI--PTLPTNPNISI
640 650 660 670 680 690

540 550 560 570 580
Cry1Ac RYASVTPIHNLNVWNGNSS--IFSNTVPATATSLDNLQSSDFGYFESANAFTS-----
gi|220 PKTDTSPKDKSVLWEASPDPIANTITLTGSVYD-FADITFELYKNGMVTSYPIKGPGP

```

```

700      710      720      730      740      750
Cry1Ac 590      600      610
----SLGNIV----GVRNFSGTAGVIIDRFE-----F-----I
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 IPHRSHGNYVSCSQGILSYNYENKPVLDGFDQLRININSDPSFYDSNSGCDTKNQYSAEI
760      770      780      790      800      810
Cry1Ac 620      630      640      650      660      670
PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFCLEDEKR
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 KINPNLSATTDLKITNQVNQLFTSSQTELANTITDYRIDQIVMKVDALSNNVFGVEKK
820      830      840      850      860      870
Cry1Ac 680      690      700      710      720
ELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG--WGGSTGITIQGGDDVFKENYVTLN
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 ALRKLVNQAKQLSKARNVLAGGNF-----EKGHEWVLGREATMIANHELKFGDHLPLP
880      890      900      910      920
Cry1Ac 730      740      750      760      770      780
GTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNVPGTGS
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 P--PTLYPSYAYQKIDESKLSNTRYTVSGFIAQSEHLEIVSRYGKEVHMDLDPYEEA
930      940      950      960      970      980
Cry1Ac 790      800      810      820      830      840
LWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSLDIDVGCIDLNED
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 L-----PISSDESPNCKPATCQCP----SC-DGSQ--PDSHFFSYSIDVGSVQSDVN
990      1000      1010      1020
Cry1Ac 850      860      870      880      890      900
LGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYK
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 LGIEFGLRIAKPNGFAKISNLEIKEDRPLTDQEIKKIQKQKWKKAPDQEQAEVAATFQ
1030      1040      1050      1060      1070      1080
Cry1Ac 910      920      930      940      950      960
EAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSVIPGVNAAFEELE
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 PTLQINALYQNEQWNG-SLHPHVTYQHLSAVVLPPLKQRHWFMEDREGEHYGVTQQFQ
1090      1100      1110      1120      1130      1140
Cry1Ac 970      980      990      1000      1010      1020
GRIFTAFSLYDARNVIKNGDFNNGLSWVNVKGHVDEQNNQSRVSVVPEWAEVSEQEVR
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 QALDRGFQQIEEQNLHNGSFANGLTDWTVTGDALQTLT-IFDEDPVLELAHWDAVSQTIIE
1150      1160      1170      1180      1190      1200
Cry1Ac 1030      1040      1050      1060      1070      1080
VCPGRG---YLLRVTAAYKEGYGEGCVTIIHEIENNTDELKFSNCVVEEIEYPNNTVTCNDYT
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|220 IMDFEEETEYKLRV----RGKKGKGTVTVQHGEEELETMTFNNTSFTTQEQTFYFEGDVTD
1210      1220      1230      1240      1250      1260
Cry1Ac 1090      1100      1110      1120      1130      1140
VNQEEYGGAYTSRNRGYNEAPVPADYASVYEEKSYTDGRRENPCFENRGRYRDYTPLVPG

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```

gi|220 VHVQSENNTFLVDSVELIEVVEE
1270      1280
>>gi|134274695|emb|CAJ43600.1| pesticidal crystal protei (686 aa)
initn: 658 initl: 213 opt: 352 Z-score: 407.4 bits: 86.6 E(): 9e-14
Smith-Waterman score: 755; 29.264% identity (58.372% similar) in 639 aa overlap
(50-635:72-686)
Cry1Ac 20      30      40      50      60      70
LSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIHWGIFGSPQ---
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 KDWMHMCETPTPFASIIISVISIFGRVLGLSSSFANTSKYI-AIITGILGLGSSSSSGS
50      60      70      80      90      100
Cry1Ac 80      90      100      110      120      130
---WDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNPALREE
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 TNVWDNLKIHIEELDRFIDTSVRFMGSTVNLGNSQYLYLDLFDWYEDQNNQKRN
110      120      130      140      150      160
Cry1Ac 140      150      160      170      180
MRIQFNDMNSALTTAIPFAVQN-----YQVPLLSVYVQAANLHLSVLRDVSFVG
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 LVGTFTLGLAFINALGYRNTNGQEVGRGTLSTAYEVQFLPSYAQAANLHLLKDAVTVG
170      180      190      200      210      220
Cry1Ac 190      200      210      220      230      240
QRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGP--DSRDWIRYNQFRREL
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 DKWILIEPTSN--YINRFKDNARIYTDYCTEYFHKGLDNLKPKGSDAVSWLRFNGFRDM
230      240      250      260      270
Cry1Ac 250      260      270      280      290
LTVLDIVSLFPNYDSRYPRTVSQLTREIYTNPV-----LENFDGSRFGSAQ--GIEG
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 LMVLDLITLFLPLYDSVQYPLPTQIELSRQIYTDVPGATFSDPSNWTLTNRTLANFNDL
280      290      300      310      320      330
Cry1Ac 300      310      320      330      340
SIR-SPHLMIDILNSITTYT---DAHR---GEYY--WSGHQIMASPVGFSGPEFTFPLYG
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 EVTDPASLLKWLNSIEVYTGALDSHRPTSPGERIGVWYGNR--NTYINPDTNEVSYRFTG
340      350      360      370      380      390
Cry1Ac 350      360      370      380      390
TMGNAAPQQRIVAQLGQGVYRT-----LSSTLYRRPFNIGINNQLSVDLGTETAYGTS
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 ELAYENPYTFIGSFFDNDIYKVALRAAAVSTTFGSNDSTFGVSSSFFNRRGIHQLYESS
400      410      420      430      440      450
Cry1Ac 400      410      420      430      440      450
SNLPSAVYRKSGTVDLSLEIPPQNNVPPRQGFSHRSLSHVSMFRSFGSNSSVSIIRAPMF
: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|134 QPIPSWIPITLA-----FPGEESSEGNANDYSHRLCDVKNITGGLRGTTPARG-RSSLL
460      470      480      490      500
Cry1Ac 460      470      480      490      500      510
S--WIHRSAEFNNIASDSITQIPAVKGNFLFNG--SVISGPGFTGGDLVRLNSSGNNIQ
: : : : : : : : : : : : : : : : : : : : : : : : : :

```







Regulatory Product Characterization Team

initn: 548 initl: 189 opt: 338 Z-score: 386.9 bits: 83.7 E(): 1.3e-12
Smith-Waterman score: 759; 24.309% identity (51.855% similar) in 1267 aa overlap
(10-1110:45-1267)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIET--GY
gi|344 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY
Cry1Ac ---TPIDISLSLTQFLLE---FVPGAGFVLGLVDIIWGI FGP SQWDAFLVQ---IEQLINQ
gi|344 QTYVNI GLSLITLAVPEIGIFTPF IGLFFAALNKHDAPP PPPNAKDI FEAMKPAIQEMIDR
Cry1Ac RI---EEFARNQAI SRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
gi|344 TLTADEQTFLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVD SGLIKKFTDEVLSLNSFYT
Cry1Ac TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVS VFGQRW---GFDAATINSRYND
gi|344 DRLP VFITDNTADR TLLGLPPYAILASMHMLLRDI ITKGPTWDSKINF TPD AIDSFKTD
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELT LTVL DIVSLFPNYDSRT
gi|344 IKNNIKLYSKTIYDVFQKGLASVYGTSPDLESFAKKQKYIEIMTTHCLDFARLFTFD PDL
Cry1Ac YP-----IRTVSQLT---REIYTN--PVLENFDGSRFGSAQ----
gi|344 YPTGSGDISLQKTRRILSPFIPIRTADGLTLMNNTSIDTSNWPNYENGAFNPKERILK
Cry1Ac -----GIEGSIRSPHL--MDILNSIT--IY----TDAHRGEYYWS---GHQIM-
gi|344 QFKLYPSWRAGQYGGLLQPYLWAI EVQDSVETRLYGLPAVDPQAGPNVYSIDSSNPIIQ
Cry1Ac -----ASPVGFSGPEFTFPPLYGTMGNAAPQORIVAQLGQGVYRTLSTLYRRPFNIGI
gi|344 INMDTWKTPPQASGWNTNL-MRGSVSGLSFLQRDGR LRSAGMGGGFADTIYSLP-----
Cry1Ac NNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTVD---SLDEI---PPQNNV P---PRQ
gi|344 ATHYLSYLYGT--PYQTS DNYSGHV GALVGVSTPQEBATLPNI IGQPDEQGNVSTMGFPFPE
Cry1Ac 430 440 450 460 470

Cry1Ac GFSHRLSHVSMFRSGFSNSSVSI---IRAPMFSWIHRSAEFNNIIASDSITQI-----
gi|344 KASYGGTVVKEWLNANAMKLSFGQSIGIPITNVTSGEYQIRCRYASNDNTNFFNVDTG
Cry1Ac ---PAVKGNFLFNQSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPS--TS
gi|344 GANPIFQ-QINFAS TVDNN TG VQGANGVVVKSIATTDNSFTVKI PAKTINVHLTNQGGSS
Cry1Ac TRYRVRVRYASVTPHILNVNWGNSSIF--SNTVPATA---TSLDN-----LQ
gi|344 DVFLDRIEFVPILESNTVTIFNNSYTTGSANLIPAIAPLWSTSSDKALTGSMITGR TTP
Cry1Ac SSD---FGYFE-----SANAF TSSL--GNIVGVRNFSGTAGVIID---RFEFI
gi|344 NSDDALLRFFKTNYDTQTIPGSGKDFNTLEIQDIVSIDIFVGSGLHSGDSGSKLDFT
Cry1Ac PVTA-----TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
gi|344 NNSGSGGSPKSFTEQNLENIT TQVNALFTSNTQDALATDVSDHDIEEVVLKVDALSDE
Cry1Ac FCLDEKRELSKVHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFKEN
gi|344 VFGKEKTLRFVNVQAKRLSKARNLLVGGNF DNLD----AWYRGRNVVNSHLLKSD
Cry1Ac YVTLSGTFDECYPTYLYQKIDE SKLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
gi|344 HVLLPPP--GLSPSYIFQKVEESKLRNTRYTVSGFIAHATDLEIVVSRYGQEIKKVVQV
Cry1Ac PGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR DGEKCAHSHHFLSLDIDVGCT
gi|344 P-YGEAFPLTSSGPV--C-----CIPHSTSNGLTG-----NPHFFSYSDV GAL
Cry1Ac DLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWET
gi|344 DVD TNP GIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNWRTEYKERA EV
Cry1Ac NIVYKEAKESVDALFVNSQYD-QLQADTNIA MIHA-ADKRVHSIREAYLP ELSVIPGVNA
gi|344 TSLIQPVINRINGLYDNGNNGSIRS DISYQNIDAIVLPTLPKLRHWFMSDRFSEQG---

```

          970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFAFSLYDARNVIKNGDFNNGLSCWNVKGHVDEEQQNNQRSVLVPWEWA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |344 DIMAKFQGGALNRAYAQLQNTLLHNGHFTKDAANWTVEGDAHQVVLDEGKRVLRPLDWSS
      1120      1130      1140      1150      1160      1170

```

```

          1030      1040      1050      1060      1070
Cry1Ac EVSQEVRVC---PGRGYILRVYTAYKEGYEGCVTIHEIENN---TDELKFSNCVEEIIY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |344 SVSQTIEIENFDPDKKEYQLVF---HGQEGEIVTLEHGEEETKYIETHHFFANFTTSQ-R
      1180      1190      1200      1210      1220      1230

```

```

          1080      1090      1100      1110      1120      1130
Cry1Ac PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRENPCEFNR
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |344 QGLTFESNKVTVTISSEDEGFLVDNIALVEAP-LPTDDQNSEGTASSTNSDTSMMNNQ
      1240      1250      1260      1270      1280

```

```

          1140      1150      1160      1170      1180
Cry1Ac GYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

```

>>gi|40159629|gb|AAR66713.1| Sequence 4 from patent US 6 (1289 aa)  
 initn: 548 initl: 189 opt: 338 Z-score: 386.9 bits: 83.7 E(): 1.3e-12  
 Smith-Waterman score: 756; 24.309% identity (51.855% similar) in 1267 aa overlap  
 (10-1110:45-1267)

```

          10      20      30
Cry1Ac          CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIET--GY
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKINAGTYSKAIADVLKGFIDDTINY
      20      30      40      50      60      70

```

```

          40      50      60      70      80      90
Cry1Ac -TPIDISLSLTQFLLE---FVPGAGFVLGLVDIIWGFIPGSPQWDAFLVQ---IEQLINQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 QTYVNIGLSLITLAVPEIGIFTPFIFGLFFAALNKHDAPPPNAKDI FEAMKPAIQEMIDR
      80      90      100      110      120      130

```

```

          100      110      120      130      140
Cry1Ac RI---EEFARNQAISRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 TLTADEQTFNLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVDGSLIKKFTDEVLSLSNSFYT
      140      150      160      170      180      190

```

```

          150      160      170      180      190
Cry1Ac TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVSFVGQRW---GFDAATINSRYND
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 DRLPVFITDNTADRTLGLPYAILASMHMLLRDIITKPGTWDKINFTPDADISFKTD
      200      210      220      230      240      250

```

```

          200      210      220      230      240      250
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELTTLVLDIVLSFPNYDSRT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 IKNNIKLYSKTIYDVQKGLASYGTPSDLESFAKKQKYIEIMTTHCLDFARLFPFPDPL
      260      270      280      290      300      310

```

```

          260      270      280      290
Cry1Ac YP-----IRTVSQLT---REIYTN--PVLENFDSFRGSAQGI--
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

gi |401 YPTGSGDISLQKTRILSPFPIRTADGLTLNNTSIDTSNWPNYENGNAGFPNPKERILK
      320      330      340      350      360      370

```

```

          300      310      320
Cry1Ac -----EGSIRSPHL--MDILNSIT--IY-----TDAHRGEYYWS---GHQIM-
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 QFKLYPSWRAAQYGLLQPYLWAIQVQDSVETRLYGQLPAVDPPQAGPNYVSIDSSNPIIQ
      380      390      400      410      420      430

```

```

          330      340      350      360      370
Cry1Ac -----ASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRITLSSTLYRRPFNIGI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 INMDTWKTPPQAGSAGWNTNL-MRGSVSGLSFLQRDGTSLRSLAGMGGGFADTIYSLP-----
      440      450      460      470      480

```

```

          380      390      400      410      420
Cry1Ac NNQQLSVLDGTEFAYGTSSNLPSAVYRKSQGTVD---SLDEI---PPQNNNVV---PRQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 ATHYLSYLYGT--PYQTSNDYSGHVGALVGVSTPQEATLPNIIGQPDEQGNVSTMGFPPE
      490      500      510      520      530      540

```

```

          430      440      450      460      470
Cry1Ac GFSHRLSHVSMFRSGFSNSSVSI---IRAPMFSWIHRSAEFNIIASDSITQI-----
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 KASYGGTVVKEWLNGANAMKLSPGQSIGIPITNVTSGEYQIRCRYASNDNTNVFNVDTG
      550      560      570      580      590      600

```

```

          480      490      500      510      520
Cry1Ac ---PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP----IHFPS--TS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 GANPIFQ-QINFASVVDNNTGVQGVVVKSIATTDNSFTVKIPAKTINVHLTNQSS
      610      620      630      640      650      660

```

```

          530      540      550      560      570
Cry1Ac TRYRVVRYASVTPIHLLNVNWNSSIF--SNTVPATA---TSLDN-----LQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 DVFLDRIEFVPILESNTVTIFNNSYTTGSANLIPAIAPLWSTSSDKALTGSMITGRTTP
      670      680      690      700      710      720

```

```

          580      590      600      610
Cry1Ac SSD---FGYFE-----SANAFSSL--GNIVGVNRFSGTAGVIID---RFEFI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 NSDDALLRFFKTNQYDTQTIPIPGSGKDFNTNLEIQDIVSIDIFVSGSLHSGSDGSIKLDFT
      730      740      750      760      770      780

```

```

          620      630      640      650      660
Cry1Ac PVTA-----TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 NNNSGSGGSPKSFTEQNDLENITQVNALFTSNTQDALATVSDHDIIEVVLKVDALSDE
      790      800      810      820      830      840

```

```

          670      680      690      700      710      720
Cry1Ac FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKEN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |401 VFGKEKTLRKFVNQAKRLSKARNLLVGGNFDNLD-----AWYGRGNVNVSNHELLKSD
      850      860      870      880      890      900

```

```

          730      740      750      760      770      780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGIYEDSQDLEIYSIRYNAK-HETVNV

```





```

380      390      400      410      420
Cry1Ac NNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVD---SLDEI---PPQNNNVP---PRQ
gi|183 ATHYLSYLYGT--PYQTSNDYSGHVGALVGVSTPQEQATLPNIIGQPDEQGNVSTMGFPFE
490      500      510      520      530      540

430      440      450      460      470
Cry1Ac GFSHRLSHVSMFRSGFSNSSVSI---IRAPMFSWIHRSAEFNIIASDSITQI-----
gi|183 KASYGGTVVKEWLNANAMKLSPGQSIGIPITNVTSGEYQIRCRYASNDNTNVFFNVDTG
550      560      570      580      590      600

480      490      500      510      520
Cry1Ac ---PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPS--TS
gi|183 GANPIFQ-QINFASVTDNNTGVQGGANGVYVVKSIATTDNSFTVKIPAKTINVHLTNQGSS
610      620      630      640      650      660

530      540      550      560      570
Cry1Ac TRYRVRVRYASVTPHLLNVNNGNSSIF--SNTVPATA-----TSLDN-----LQ
gi|183 DVFLDRIEFVPILESNTVTIFNNSYTTGSANLIPAIAPLWSTSSDKALTGSMISITGRTPP
670      680      690      700      710      720

580      590      600      610
Cry1Ac SSD---FGYFE-----SANAFSSL--GNIVGVRNFSGTAGVIID---RFEFI
gi|183 NSDALLRFFKTYNDTQTIPIPGSGKDFNTLEIQDIVSIDIFVSGSLHGSDGSIKLDFT
730      740      750      760      770      780

620      630      640      650      660
Cry1Ac PVTA-----TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
gi|183 NNSGSGGSPKSFTEQNDLENITTQVNALFTSNTQDALATDVSDHDIIEVVLKVDALSDE
790      800      810      820      830      840

670      680      690      700      710      720
Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKEN
gi|183 VFGKEKTLRKFVNQAKRLSKARNLLVGGNFDNLD----AWYGRNVVNVSNHELLKSD
850      860      870      880      890      900

730      740      750      760      770      780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK--HETVNV
gi|183 HVLLPPP--GLSPSYIFQKVESKLRNTRYTVSGFIAHATDLEIVSRYGQEIKKVVQV
910      920      930      940      950

790      800      810      820      830      840
Cry1Ac PGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDKGKCAHSHHFLSLDIDVGCT
gi|183 P-YGEAFPLTSSGPV--C-----CIPHSTSNGLG-----NPHFFSYSIDVGAL
960      970      980      990

850      860      870      880      890      900
Cry1Ac DLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWET
gi|183 DVDNTNPGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNWRTEYEKERAEV
1000     1010     1020     1030     1040     1050

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910      920      930      940      950      960
Cry1Ac NIVYKEAKESVDALFVNSQYD-QLQADTNIAMIIHA-ADKRVHSIREAYLPELSVIPGVNA
gi|183 TSLIQPVINRINGLYDNGNWNWSIRSISYQNIIDAVLPTLPKLRHWFMSDRFSEQG---
1060     1070     1080     1090     1100     1110

970      980      990      1000     1010     1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVVEEQNNQSVLVPEWEA
gi|183 DIMAKFQGANRAYAQLEQNTLLHNGHFTKDAANWTVEGDAHQVVELEDGKRVLRPLDWSS
1120     1130     1140     1150     1160     1170

1030     1040     1050     1060     1070
Cry1Ac EVSQEVRVC---PGRGYILRVYAYKEGYGEGCVTTHEIENN---TDELKFSNCVEEIEY
gi|183 SVSQTEIENFDPDKKEYQLVF---HGQEGEVTLEHGEETKYIETHTHHFANFTTSQ-R
1180     1190     1200     1210     1220     1230

1080     1090     1100     1110     1120     1130
Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENCEFN
gi|183 QGLTFESNKVTVTISSEDEGFLVDNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNNQ
1240     1250     1260     1270     1280

1140     1150     1160     1170     1180
Cry1Ac GYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE

>>gi|12810188|gb|AAE44103.1| Sequence 4 from patent US 6 (1289 aa)
initn: 548 initl: 189 opt: 338 Z-score: 386.9 bits: 83.7 E(): 1.3e-12
Smith-Waterman score: 756; 24.309% identity (51.855% similar) in 1267 aa overlap
(10-1110:45-1267)

10      20      30
Cry1Ac CMQAMDNPNINICIPYNCLSNPEVEVLGGERIET--GY
gi|128 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY
20      30      40      50      60      70

40      50      60      70      80      90
Cry1Ac -TPIDISLSLTQFLLESE---FVPAGFVLGLVDIIWGFGPSQWDAFLVQ---IEQLINQ
gi|128 QTYVNIGLSLITLAVPEIGIFTFPFIQLFFAALNKHDPAPPPNAKDI FEAMKPAIQEMIDR
80      90      100     110     120     130

100     110     120     130     140
Cry1Ac RI---EEFARNQAISRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
gi|128 TLTADEQTLFNGEISGLQNLAAARYQSTMDDIQSHGGFNKVDVSGGLIKKFTDEVLSLNSFTY
140     150     160     170     180     190

150     160     170     180     190
Cry1Ac TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVSVFGQRW---GPDAAATINSRYND
gi|128 DRLPVFTDNTADRTLGLPYAYAILASMHLMLLRDIITRGPWDSKINFTPDAIDSFKTD
200     210     220     230     240     250

200     210     220     230     240     250
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELTLTLDVLSLFPNYSRT

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      . . . . .
gi|128 IKNNIKLYSKTIYDVFKGLASLYGTPSDLESFAKKQKYIEIMTTHCLDFARLFPTTFDPDL
      260      270      280      290      300      310

      260      270      280      290
Cry1Ac YP-----IRTVSQLT---REIYTN--PVLENFDGSRGSAQGI--
      ::      ::      ::      ::      ::      ::
gi|128 YPTGSGDISLQKTRRILSPFPIRTADGLTLNNTSIDTSNWPNYENGGAFNPKERILK
      320      330      340      350      360      370

      300      310      320
Cry1Ac -----EGSIRSPHL--MDILNSIT--IY----TDAHRGEYYS--GHQIM-
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 QFKLYPSWRAAQYGGLLQPYLWAIQVQDSVETRLYGQLPAVDPQAGPNVYSIDSSNPIIQ
      380      390      400      410      420      430

      330      340      350      360      370
Cry1Ac -----ASPVGSFGEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGI
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 INMDTWKTPPQASGWNNTNL--MRGSVSGLSFLQRDGTSLRSLAGMGGGFADTIYSLP----
      440      450      460      470      480

      380      390      400      410      420
Cry1Ac NNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTVD---SLDEI---PPQNNNVP---PRQ
      . . : : : : : : : : : : : : : : : : : : : :
gi|128 ATHYLSYLYGT--PYQTSDNYSGHVGVALVGVSTPQEAATLPIIGQDPDEQGNVSTMGPFPE
      490      500      510      520      530      540

      430      440      450      460      470
Cry1Ac GFSHRLSHVSMFRSFGSNSSVSI---IRAPMFSWIHRSAEFNIIASDSITQI-----
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 KASYGGTVVKEWLNANAMKLSPPGQSIGIPITNVTSGEYQIRCRYASNDNTNVFFNVDTG
      550      560      570      580      590      600

      480      490      500      510      520
Cry1Ac ---PAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNGYIEVP----IHFPS--TS
      : . . . . . : : : : : : : : : : : : : : : : :
gi|128 GANPIFQ--QINFASVTDNNTGVQGANVYVVKSIATTDNSFTVKIPAKTINVHLTNQGSS
      610      620      630      640      650      660

      530      540      550      560      570
Cry1Ac TRYRVRVRYASVTPPIHLNVNNGNSSIF--SNTVPATA---TSLDN-----LQ
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 DVFLDRIEFVPILESNTVTIFNNSYTTGSANLIPAIAPLWSTSSDKALTGSMSTGRTP
      670      680      690      700      710      720

      580      590      600      610
Cry1Ac SSD---FGYFE-----SANAFSSL--GNIVGVRNFSGTAGVIID---RFEFI
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 NSDDALLRFKTYNDTQTIPGSGKDFNTLEIQDIVSIDIFVGSGLHSGSDGSIKLDFT
      730      740      750      760      770      780

      620      630      640      650      660
Cry1Ac PVTA-----TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVLYLSDE
      . . . . . : : : : : : : : : : : : : : : : :
gi|128 NNSGSGGSPKSFTEQNDLENITQVNALFTSNTQDALATDVSDHDIEEVLKVDALSDE
      790      800      810      820      830      840

      670      680      690      700      710      720

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Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKEN
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 VFGKEKTLRKFVFNQAKRLSKARNLLVGGNFDNLD----AWYGRNVNVSNHELLKSD
      850      860      870      880      890      900

      730      740      750      760      770      780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK--HETVNV
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 HVLLPPP--GLSPSYIFQKVEESKLRNTRYTVSGFIAHATDLEIVVSRYQFIKKVVQV
      910      920      930      940      950

      790      800      810      820      830      840
Cry1Ac PGTGSLWLPSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEGKCAHHSHHFLDIDVCGT
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 P--YGEAFPLTSSGPV--C----CIPHSTSNGLTLG-----NPHFFYSIDVGDAL
      960      970      980      990

      850      860      870      880      890      900
Cry1Ac DLNEDLVGVVIFIKIKTQDGHARLGNLEFLLEKPLVGEALARVKRAEKKWRDKREKLEWET
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 DVDTNPGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNWRTEYKERAEV
      1000      1010      1020      1030      1040      1050

      910      920      930      940      950      960
Cry1Ac NIVYKEAKESVDALFVNSQYD--QLQADTNIAMIAH--ADKRVHSIREAYLPELSVIPGVNA
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 TSLIQPVINRINGLYDNGNNGSIRSISYQNIIDAVLPTLPKLRHWFMSDRFSEQG---
      1060      1070      1080      1090      1100      1110

      970      980      990      1000      1010      1020
Cry1Ac AIFEELEGRIFTAFSLYDARNVIKNGDFNNGLSNWKVGHVDVEEQNNQRSVLVPEWEA
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 DIMAKFQAGALNRAYAQLEQNTLLHNGHFTKDAANWTVEGDAHQVVEDEGKRVRLPDWSS
      1120      1130      1140      1150      1160      1170

      1030      1040      1050      1060      1070
Cry1Ac EVSQEVRVC---PGRGYILRVTAKEGYGEGCVTIHEIENN----TDELKFSNCVVEEIIY
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 SVSQTEIENFDPDKEYQLVF---HGQEGTVTLEHGEETKYIETHHHFANFTTSQ--R
      1180      1190      1200      1210      1220      1230

      1080      1090      1100      1110      1120      1130
Cry1Ac PNNTVTCNDYTVNQEYGGAYTSRNRGYNAPSVPADYASVYEEKSYTDGRRENPCFN
      : : : : : : : : : : : : : : : : : : : : : :
gi|128 QGLTFESNKVTVTISSEDEGFLVDNIALVEAP-LPTDDQNSEGNTASSTNSDTSMN
      1240      1250      1260      1270      1280

      1140      1150      1160      1170      1180
Cry1Ac GYRDYTPLPVGVVTKLEYFPEPDKVWIEIGTEGTFIVDSVELLMEE

>>gi|34427044|gb|AAQ70971.1| Sequence 3 from patent US 5 (1289 aa)
      initn: 548 initl: 189 opt: 338 Z-score: 386.9 bits: 83.7 E(): 1.3e-12
      Smith-Waterman score: 759; 24.309% identity (51.855% similar) in 1267 aa overlap
      (10-1110:45-1267)

      10      20      30
Cry1Ac          CMQAMDNPNINECIPYCNLSNPEVEVLGGERIET--GY
      : : : : : : : : : : : : : : : : : : : : : :
gi|344 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY

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Regulatory Product Characterization Team

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20      30      40      50      60      70
Cry1Ac  40      50      60      70      80      90
--TPIDISLSLTQFLLE---FVPGAGFVLGLVDI IWGIFGPSQWDAFLVQ---IEQLINQ
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  QTYVNIIGLSLITLAVPEIGIFTFPIGLFFAALNKHDAPPPNAKIDIFEAMKPAIQEMIDR
80      90      100     110     120     130
Cry1Ac  100     110     120     130     140
--RI---EEFARNQAISRLEGLSNLYQIYAESFREWEA-DPTN PALREEMRIQFNDMNSALT
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  TLTADEQTFLLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVD SGLIKKFTDEVLSLNSFYT
140     150     160     170     180     190
Cry1Ac  150     160     170     180     190
--TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVS VFGQRW---GFDAATINSRYND
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  DRLPVFI TDNTADRTLLGLPYAILASMHMLLRDIITKGP TWDSKINFTPD AIDSFKTD
200     210     220     230     240     250
Cry1Ac  200     210     220     230     240     250
--LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRT
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  IKNNIKLYSKTIYDVFKGLASYGTPSDLESFAKKQKYLEIMTTHCLDFARLFPTFD PDL
260     270     280     290     300     310
Cry1Ac  260     270     280
--YP-----IRTVSQLT---REIYTN--PVLENFDG SFRGSAQ----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344  YPTGSGDISLQKTRRLISLPPFIPIRTADGLTLNNTSIDTSNWNPNYENGGA FPNPKERILK
320     330     340     350     360     370
Cry1Ac  290     300     310     320
-----GIEGSI RSPHL--MDILNSIT--IY----TDAHRGEYYWS---GHQIM-
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344  QFKLYPSWRAGQYGGLLQPYLWAI EVQDSVETRLYQQLPAVD PQAAGPNYVSIDSNPIIQ
380     390     400     410     420     430
Cry1Ac  330     340     350     360     370
-----ASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQGVYRTLSTLYRRPFNIGI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344  INMDTWKTPPGASGWNNTNL-MRGSV SGLSFLQRDGRTRLSAGMGGGFADTIYSLP-----
440     450     460     470     480
Cry1Ac  380     390     400     410     420
--NNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTVD---SLDEI---PPQNNVNP---PRQ
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  ATHYLSYLYGT--PYQTS DNYSGHV GALVGVSTPQEATLPNIIGQPDEQGNVSTMGFPFE
490     500     510     520     530     540
Cry1Ac  430     440     450     460     470
--GFSHRLSHVSMFRSGFSNSSVSI---IRAPMFSWIHRSAEFNNI IASDSITQI-----
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  KASYGGTVVKEWLNGANAMKLSPGQSIGIPITNVTSGEYQRCRYASNDNTNVFFNVDTG
550     560     570     580     590     600
Cry1Ac  480     490     500     510     520
---PAVKGNFLNGSVISGPGFTGGDLVRLN SSGNNIQNRGYIEVP-----IHFPS--TS
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .

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gi|344  GANPIFQ-QINFASTVDNNTGVQ GANGVYVVKSIATTDNSFTVKIPAKTINVHLTNQSSS
610     620     630     640     650     660
Cry1Ac  530     540     550     560
--TRYRVRYASVTPIHLNVNWNSSIF--SNTVPATA---TSLDN-----LQ
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  DVFLDRIEFVPILESNTVTIFNNSYTTGSANLIPAIAPLWSTSSDKAL TGSMSTIGTRTTP
670     680     690     700     710     720
Cry1Ac  580     590     600     610
--SSD---FGYFE-----SANAF TSSL--GNIVGVRNFSGTAGVIID---RFEPFI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344  NSSDALLRFFKTN YDTQTIPIPGSGKDFNTNLEIQDIVSIDIVFGSGLHSGDSGSIKLDFT
730     740     750     760     770     780
Cry1Ac  620     630     640     650     660
--PVTA-----TLEAEYNLERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDE
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  NNNSGSGGSPKSFTEQNDLENIT TQVNALFTSNTQDALATDVSDHDIEEVVKVDALSDE
790     800     810     820     830     840
Cry1Ac  670     680     690     700     710     720
--FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD VFKEN
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  VFGKEKTLRKFVNQAKRLSKARNLLVGGNF DNLD----AWYGRGNVNVSNHELLKSD
850     860     870     880     890     900
Cry1Ac  730     740     750     760     770     780
--YVTLSGTFDECYPTYLYQKIDESK LKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|344  HVLLPPP--GLSPSYIFQKVEESK LKRNTRYTVSGFIAHATDLEIVVSRYGQEI KKVQVQ
910     920     930     940     950
Cry1Ac  790     800     810     820     830     840
--PGTGSWLPLSAQSPIGKCGEPNRCAP HLEWNPDLDCSCRDEKCAHSHHSLDIDVGCT
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  P-YGEAFPLTSSGPPV--C-----CIPHST SNGTLG-----NPHFFSYSIDVGAL
960     970     980     990
Cry1Ac  850     860     870     880     890     900
--DLNEDLGVWVIFKIKTQDGHARLGNLEFLE EKPLVGEALARVKRAEKKWRDKREKLEWET
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  DVDTPNGIEFGLRIVNPTGMARVSNLEI REDRPLAANEIRQVQRVARNWRTEYEKERA EV
1000    1010    1020    1030    1040    1050
Cry1Ac  910     920     930     940     950     960
--NIVYKEAKESVDALFVNSQYD-QLQAD TNIAMIHA-ADKRVHSIREAYLPELSVIPGVNA
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  TSLIQPVINRINGLYDNGNWN SIRSISYQNI DAIVLPTLPKLRHWFMSDRFSEQG---
1060    1070    1080    1090    1100    1110
Cry1Ac  970     980     990     1000    1010    1020
--AIFEELEGRIFTAFSLYDARNVIKNGDF NNLSCWNVKGHV DVEEQNNQRSVLVPEWEA
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .
gi|344  DIMAKFQGALN RAYAQLEQNTLLHNGHF TKDAANWTVEGDAHQVLEDKGRVLR LRPDWSS
1120    1130    1140    1150    1160    1170
Cry1Ac  1030    1040    1050    1060    1070
--EVSQEVRC---PGRGYILRV TAYKEGYGEGCVTIHEIENN----TDELKFSNCV EEEIY

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960      970      980      990
Cry1Ac  850      860      870      880      890      900
DLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWET
. . . . .
gi|142  DVDTNPGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNRWTEYEKERAEV
1000     1010     1020     1030     1040     1050

910      920      930      940      950      960
Cry1Ac  NIVYKEAKESVDALFVNSQYD-QLQADTNIAIHA-ADKRVHSIREAYLPELSVIPGVNA
. . . . .
gi|142  TSLIQPVINRINGLYDNGNWNWSIRSDISYQNIIDAVLPTLPLKLRHWFMSDRFSEQG---
1060     1070     1080     1090     1100     1110

970      980      990      1000     1010     1020
Cry1Ac  AIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVVDVEEQNNQRSVLVPEWEA
. . . . .
gi|142  DIMAKFQGALNRAYAQLQNTLLHNGHF*TKDAANWTVEGDAHQVVLEDKRVLRLPDWSS
1120     1130     1140     1150     1160     1170

1030     1040     1050     1060     1070
Cry1Ac  EVSQEVRVC---PGRGYILRVTAAYKEGYEGCVTIHEIENN---TDELKFSNCVEEBEYI
. . . . .
gi|142  SVSQTIIEIENFPDPKKEYQLVF---HGQEGTVTLEHGEETKYIETHTHHFANFTTSQ-R
1180     1190     1200     1210     1220     1230

1080     1090     1100     1110     1120     1130
Cry1Ac  PNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFENR
. . . . .
gi|142  QGLTFESNKVTVTISSEDEGFLVDNIALVEAP-LPTDDQNSEGTASSTNSDTSMNNNQ
1240     1250     1260     1270     1280

1140     1150     1160     1170     1180
Cry1Ac  GYRDYTPLPVGYVTKLEYFPETDKVWIBIGETEGTFIVDSVELLMEE

>>gi|56664647|gb|AAW18072.1| Sequence 32 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100      110      120      130      140      150
Cry1Ac  ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
. . . . .
gi|566  TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10      20      30

160      170      180      190      200      210
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
. . . . .
gi|566  NYQVPLLSVYVQAANLHLSV
40      50

>>gi|14112750|gb|AAE58165.1| Sequence 30 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100      110      120      130      140      150
Cry1Ac  ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
. . . . .

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. . . . .
gi|141  TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10      20      30

160      170      180      190      200      210
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
. . . . .
gi|141  NYQVPLLSVYVQAANLHLSV
40      50

>>gi|14112752|gb|AAE58167.1| Sequence 32 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100      110      120      130      140      150
Cry1Ac  ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
. . . . .
gi|141  TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10      20      30

160      170      180      190      200      210
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
. . . . .
gi|141  NYQVPLLSVYVQAANLHLSV
40      50

>>gi|23325092|gb|AAN23792.1| Sequence 32 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100      110      120      130      140      150
Cry1Ac  ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
. . . . .
gi|233  TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10      20      30

160      170      180      190      200      210
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
. . . . .
gi|233  NYQVPLLSVYVQAANLHLSV
40      50

>>gi|56642280|gb|AAW11998.1| Sequence 32 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100      110      120      130      140      150
Cry1Ac  ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
. . . . .
gi|566  TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10      20      30

160      170      180      190      200      210
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
. . . . .
gi|566  NYQVPLLSVYVQAANLHLSV

```

40 50  
 >>gi|56664645|gb|AAW18070.1| Sequence 30 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|566      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|566 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|158456677|gb|ABW41350.1| Sequence 30 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|158      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|158 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|56642278|gb|AAW11996.1| Sequence 30 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|566      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|566 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|17920881|gb|AAE86501.1| Sequence 30 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
  
```

```

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|179      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|179 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|158456679|gb|ABW41352.1| Sequence 32 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|158      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|158 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|17920883|gb|AAE86503.1| Sequence 32 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|179      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
gi|179 NYQVPLLSVYVQAANLHLSV
      :
      40 50
  
```

>>gi|23325090|gb|AAN23790.1| Sequence 30 from patent US (50 aa)  
 initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12  
 Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap  
 (126-175:1-50)

```

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
gi|233      TNPALREEMRIQFNDMNSALTTAIPLFAVQ
      :
      10 20 30
  
```

```

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      :
  
```

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gi|233 NYQVPLLSVYVQAANLHLSV
40 50

>>gi|14103745|gb|AAE55179.1| Sequence 30 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|141 TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10 20 30
160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|141 NYQVPLLSVYVQAANLHLSV
40 50

>>gi|14103747|gb|AAE55181.1| Sequence 32 from patent US (50 aa)
initn: 313 init1: 313 opt: 313 Z-score: 378.4 bits: 77.4 E(): 3.7e-12
Smith-Waterman score: 313; 100.000% identity (100.000% similar) in 50 aa overlap
(126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|141 TNPALREEMRIQFNDMNSALTTAIPLFAVQ
10 20 30
160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|141 NYQVPLLSVYVQAANLHLSV
40 50

>>gi|12810187|gb|AAE44102.1| Sequence 2 from patent US 6 (1385 aa)
initn: 534 init1: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
(373-1110:652-1363)

350 360 370 380 390 400
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQLS--VLDGTEFAYGTSSNL
gi|128 DNNTGVQGGANGVYVVKSIATTDNSFTEIPAKTINVHLTNQGSDDVFLDRIF--IPFSL
630 640 650 660 670
410 420 430 440 450
Cry1Ac PSAVYRKSQVDSLDLDEIPPQNN-----VPPRQGFHSHLSSHVMFRSGFSNNSVSII-
gi|128 PLIYHGSYNTSSGADDVLWSSSNMNYDIIVNGQANSSSIASSMHLNKGKVIKTIDIPG
680 690 700 710 720 730
460 470 480 490 500 510
Cry1Ac -RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNMSGN-
gi|128 HSETFFATFPVPEGFNEV---RILAGLPEVSGNITVQSNNPQPQSNNGGGGGGGGGGGD
740 750 760 770 780 790

520 530 540 550 560
Cry1Ac ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHNLVNWGNSIFSNTVPATATSL
gi|128 GQYNFSLSGSDHTTIYHGKLETGIVHQGNNTYTGTPVLLNAYRNNTVVS-SIPVYSPFD
800 810 820 830 840 850
570 580 590 600 610 620
Cry1Ac DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQ
gi|128 ITIQTE-----ADSLELELQPRYGAFATVNGTATV---KSPNVNYDRSFKLPIDLQNI
860 870 880 890 900
630 640 650 660 670 680
Cry1Ac KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVHAKRLSDER
gi|128 TQVNALFASGTQNMALAHNVSDHDIIEVVLLKVDALSDVEVFGDEKKALRKLNVNQAKRLSRAR
910 920 930 940 950 960
690 700 710 720 730 740
Cry1Ac NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
gi|128 NLLIGGSFENWD----AWYKGRNVTVSDHELFKSDHVLPPP--GLSPSYIFQKVEES
970 980 990 1000 1010
750 760 770 780 790 800
Cry1Ac KLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNVPGTGSLLWPLSAQSPIGKCGPENR
gi|128 KLKPNTRYIVSGFIAHGKDLIVVSRYGQEVQKVVQVP-YGEAFPLTSGNPV--C-----
1020 1030 1040 1050 1060
810 820 830 840 850 860
Cry1Ac CAPHLEWNPDLDCSCRDEKCAHSHHFLSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARL
gi|128 CPPRSTSNGLT-----GDP-----HFFSYSIDVGALDLQANPGIEFGLRIVNPTGMARV
1070 1080 1090 1100 1110
870 880 890 900 910 920
Cry1Ac GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD-Q
gi|128 SNLEIREDRPLAANEIRQVQVARNWRTEYEKERAEVTSLIQPVINRINGLYENGNWNGS
1120 1130 1140 1150 1160 1170
930 940 950 960 970 980
Cry1Ac LQADNTIAMIHA-ADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDARNVI
gi|128 IRSDISYQNIDAVLPTLPKLRHWFMSDRFSEQ--DIMAKFQGALNRAYAQLEQSTLL
1180 1190 1200 1210 1220 1230
990 1000 1010 1020 1030 1040
Cry1Ac KNGDFNNGLSQVNVKGVHVDVEEQNNQRSVLVPEWEAEVSVQVVRV---CPGRGYILRVTA
gi|128 HNGHFTKDANWTIEGDAHQITLEDGRRVLRLPDWSSSVSQMIEIENFNPDKEYNLVVF--
1240 1250 1260 1270 1280 1290
1050 1060 1070 1080 1090
Cry1Ac YKEGYGEGCVTIIHEIENN----TDELKFSNCVVEEIPYNNVTVCNDYTVNQEEYGGAYTS
gi|128 --HGQEGVTLEHGBETKYIETHTHHFANFTTSQ-RQGLTFESKNVTVTISSEDEGEFLV

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1300      1310      1320      1330      1340      1350
1100      1110      1120      1130      1140      1150
Cry1Ac  RNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGVVTKLEYFPET
      . . . . .
gi|128  DNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNNQ
      1360      1370      1380

>>gi|142869|gb|AAA67694.1| delta-endotoxin (1385 aa)
      initn: 534 initl: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
(373-1110:652-1363)

350      360      370      380      390      400
Cry1Ac  GTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQLS--VLDGTEFAYGTSNNL
      . . . . .
gi|142  DNNTGVQGGANGVYVVKSIATDINSFTEIPAKTINVHLTNQSSDVFLDRIEF---IPFSL
      630      640      650      660      670

410      420      430      440      450
Cry1Ac  PSAVYRKSQGTVDLSEIIPPQNNN-----VPPRQGFHRLSHVSMFRSGFSNSSVSII-
      . . . . .
gi|142  PLYIHGYSYNTSSGADDVLWSSSNMNYDIIVNGQANSSSIASSMHLNKGKVIKTIDIPG
      680      690      700      710      720      730

460      470      480      490      500      510
Cry1Ac  -RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGN-
      . . . . .
gi|142  HSETFFATFPVPEGFNEV---RILAGLPEVSGNITVQSNPPQPSNNGGGGGGGGGG
      740      750      760      770      780      790

520      530      540      550      560
Cry1Ac  ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHLLNVNWNSSIFSNTVPATATSL
      . . . . .
gi|142  GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTYTGTPLVILNAYRNNTVVS-SIPVYSPFD
      800      810      820      830      840      850

570      580      590      600      610      620
Cry1Ac  DNLQSSDFGYFESANAFSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAYNLERAQ
      . . . . .
gi|142  ITIQTE-----ADSLLELQPRYGFATVNGTATV---KSPNVNDRSFKLPIDLQINIT
      860      870      880      890      900

630      640      650      660      670      680
Cry1Ac  KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
      . . . . .
gi|142  TQVNALFASGTQNMLAHNVSDHDIEEVVLKVDALSDEFVGEKKALRKLNVQAKRLSRAR
      910      920      930      940      950      960

690      700      710      720      730      740
Cry1Ac  NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
      . . . . .
gi|142  NLLIGGSFENWD----AWYKGRNVVTVSDHELFSKSDHVLPPP--GLSPSYIFQKVEES
      970      980      990      1000      1010

750      760      770      780      790      800
Cry1Ac  KLKAFTRYQLRGIYEDSQDLEIYSIRYNAK-HETVNVPGTGLSLWPLSAQSPIGKCGEPNR
      . . . . .
gi|142  KLKPNTRYIVSGFIAHGKLDLIVVSRYGQEVQKVVQVP-YGEAFPLTNSGPP--C-----

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1020      1030      1040      1050      1060
810      820      830      840      850      860
Cry1Ac  CAPHLEWNPDLDCSCRDEKCAHHSHHFLSDIDVGCCTDLNEDLGWVVIKIKTQDGHARL
      . . . . .
gi|142  CPPERSTSNGL-----GDP-----HFFSYSIDVGALDLQANPGIEFGLRIVNPTGMARV
      1070      1080      1090      1100      1110

870      880      890      900      910      920
Cry1Ac  GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD-Q
      . . . . .
gi|142  SNLEIREDRPLAANEIRQVQVARNWRTEYEKERAEVTSLIQPVINRINGLYENGNWNGS
      1120      1130      1140      1150      1160      1170

930      940      950      960      970      980
Cry1Ac  LQADNTNAMIHA-ADKRVHSIREAYLPELSVIPGVNAEIFEELGRIFTAFLSYDARNVI
      . . . . .
gi|142  IRSDISYQNIIDAVLPTLPKLRHWFMSDRFSEQG---DIMAKFQALNRAYAQLQESTLL
      1180      1190      1200      1210      1220      1230

990      1000      1010      1020      1030      1040
Cry1Ac  KNGDFNGLSCWNVKGVHDVVEEQNNQRSVLVPEWEAEVSVQEVVV---CPGRGYILRVTA
      . . . . .
gi|142  HNGHFTKDAANWTIEGDAHQITLEDGRRVLRPLDWSSSVSQMIEIENFNPKKEYNLVVF--
      1240      1250      1260      1270      1280      1290

1050      1060      1070      1080      1090
Cry1Ac  YKEGYGEGCVTIHEIENN---TDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTS
      . . . . .
gi|142  --HGQEGEVTVLEHGEEKYIETHTHHFANFTTSQ-RQGLTFESNKVTVTIISSDEGFLV
      1300      1310      1320      1330      1340      1350

1100      1110      1120      1130      1140      1150
Cry1Ac  RNRGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDYTPLPVGVVTKLEYFPET
      . . . . .
gi|142  DNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNNQ
      1360      1370      1380

>>gi|1831841|gb|AAB46295.1| Sequence 2 from patent US 55 (1385 aa)
      initn: 534 initl: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
(373-1110:652-1363)

350      360      370      380      390      400
Cry1Ac  GTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQLS--VLDGTEFAYGTSNNL
      . . . . .
gi|183  DNNTGVQGGANGVYVVKSIATDINSFTEIPAKTINVHLTNQSSDVFLDRIEF---IPFSL
      630      640      650      660      670

410      420      430      440      450
Cry1Ac  PSAVYRKSQGTVDLSEIIPPQNNN-----VPPRQGFHRLSHVSMFRSGFSNSSVSII-
      . . . . .
gi|183  PLYIHGYSYNTSSGADDVLWSSSNMNYDIIVNGQANSSSIASSMHLNKGKVIKTIDIPG
      680      690      700      710      720      730

460      470      480      490      500      510
Cry1Ac  -RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGN-
      . . . . .
gi|183  HSETFFATFPVPEGFNEV---RILAGLPEVSGNITVQSNPPQPSNNGGGGGGGGGG

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740      750      760      770      780      790
Cry1Ac  ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHLNVNWGNSSIFSNTVPATATSL
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTGTGTPVLILNAYRNNTVVS-SIPVYSPFD
      800      810      820      830      840      850

570      580      590      600      610      620
Cry1Ac  DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQ
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  ITIQTE-----ADSLELELQPRYGFATVNGTATV---KSPNVNYDRSFKLPIDLQINIT
      860      870      880      890      900

630      640      650      660      670      680
Cry1Ac  KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  TQVNALFASGTQMLAHNVSDHDIIEVVLKVDALSDVDFGDEKKALRKLNVQAKRLSRAR
      910      920      930      940      950      960

690      700      710      720      730      740
Cry1Ac  NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  NLLIGGSFENWD----AWYKGRNVTVSDHELKSDHVLPPP--GLSPSYIFQKVEES
      970      980      990      1000     1010

750      760      770      780      790      800
Cry1Ac  KLKAFTRYQLRGIYEDSQDLEIYSIRYNAK-HETVNVPGTGLWPLSAQSPIGKCGEPNR
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  KLPNTRYIVSGFIAHGKDLIEVVSRYGQEVQKVVQVP-YGEAFPLTNSGPV--C-----
      1020     1030     1040     1050     1060

810      820      830      840      850      860
Cry1Ac  CAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGCTDLNEDLGWVVIKIKTQDGHARL
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  CPPRSTSGTL-----GDP-----HFFSYSIDVGALDQANPGIEFGLRIVNPTGMARV
      1070     1080     1090     1100     1110

870      880      890      900      910      920
Cry1Ac  GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD-Q
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  SNLEIREDRPLAANEIRQVQRVARNWRTEYKERA EVTSLIQPVINRINGLYENGNWNGS
      1120     1130     1140     1150     1160     1170

930      940      950      960      970      980
Cry1Ac  LQADNFIAMIHA-ADKRVHSIREAYLPELSIVPGVNAALFEELEGRIFTAFLYDARNVI
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  IRSDISYQNI DAIVLPTLPKLRHWFMSDRFSEQG---DIMAKFQALNRAYAQLEQSTLL
      1180     1190     1200     1210     1220     1230

990      1000     1010     1020     1030     1040
Cry1Ac  KNGDFNNGLSCWNVKGVHDVEEQNNQSVLVVPEWAEVSEVVRV---CPGRGYILRVTA
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  HNGHPTKDAANWTIEGDAHQITLEDGRRVLRPLPDWSSVSQMI E IENFNPKKEYNLVLF--
      1240     1250     1260     1270     1280     1290

1050     1060     1070     1080     1090
Cry1Ac  YKEGYEGECVTIHEIENN---TDELKFSNCVEEEIYPNNTVTCNDYTVNQEEYGGAYTS
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .

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gi|183  --HGQEGEGTTLLEHGEETKYIETHTHHFANFTTSQ-RQGLTFESNKVTVTISSEDEGFLV
      1300     1310     1320     1330     1340     1350

1100     1110     1120     1130     1140     1150
Cry1Ac  RNRGYNEAPSPADYASVYEEKSYTDGRENPCEFNRGYRDYTPLPVGVYTKLEYFPET
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|183  DNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNNQ
      1360     1370     1380

>>gi|34427717|gb|AAQ71352.1| Sequence 1 from patent US 5 (1385 aa)
      initn: 534 initl: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
      Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
      (373-1110:652-1363)

350      360      370      380      390      400
Cry1Ac  GTMGNAAPQQRIVAQLGQGVYRTLSSLYRRPFNIGINNQQLS--VLDGTEFAYGTSSNL
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  DNNTGVQGANVYVVKSIATTDNSFTEIPAKTINVHLTNQSSDVFLDRIEF---IPFSL
      630      640      650      660      670

410      420      430      440      450
Cry1Ac  PSAVYRKSQGTVDLSLEIPPQNNN-----VPPRQGFSHRLSHVSMFRSFGSNTSSVSI--
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  PLYIHGSYNTSSGADDVLWSSNMNYDIIVNQANSSSIASSMHLNKGKVIKTIIDIPG
      680      690      700      710      720      730

460      470      480      490      500      510
Cry1Ac  -RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGN-
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  HSETFATFPVPEGFNEV---RILAGLPEVSGNITVQSNPPQPSNNGGGDGGGGGGGG
      740      750      760      770      780      790

520      530      540      550      560
Cry1Ac  ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHLNVNWGNSSIFSNTVPATATSL
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTGTGTPVLILNAYRNNTVVS-SIPVYSPFD
      800      810      820      830      840      850

570      580      590      600      610      620
Cry1Ac  DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQ
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  ITIQTE-----ADSLELELQPRYGFATVNGTATV---KSPNVNYDRSFKLPIDLQINIT
      860      870      880      890      900

630      640      650      660      670      680
Cry1Ac  KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  TQVNALFASGTQMLAHNVSDHDIIEVVLKVDALSDVDFGDEKKALRKLNVQAKRLSRAR
      910      920      930      940      950      960

690      700      710      720      730      740
Cry1Ac  NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .
gi|344  NLLIGGSFENWD----AWYKGRNVTVSDHELKSDHVLPPP--GLSPSYIFQKVEES
      970      980      990      1000     1010

750      760      770      780      790      800
Cry1Ac  KLKAFTRYQLRGIYEDSQDLEIYSIRYNAK-HETVNVPGTGLWPLSAQSPIGKCGEPNR
      :. . . . . :. . . . . :. . . . . :. . . . . :. . . . . :. . . . .

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gi|344 HSETFFATFPVPEGFNEV--RILAGLPEVSGNITVQSNPPQPSNNGGGGGGGGGG
740 750 760 770 780 790
Cry1Ac ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHLNVNWNSSIFSNTVPATATSL
gi|344 GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTGTPLVILNAYRNNTVVS-SIPVYSPFD
800 810 820 830 840 850
Cry1Ac DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQ
gi|344 ITIQTE-----ADSLELELQPRYGFATVNGTATV---KSPNVNYDRSFKLPIDLQKIT
860 870 880 890 900
Cry1Ac KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
gi|344 TQVNALFASGTQNMLAHNVSDHDIIEEVLKVDALSDEVFGDEKKALRKLVNQAKRLSRAR
910 920 930 940 950 960
Cry1Ac NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
gi|344 NLLIGGSFENWD----AWYKGRNVVTVSDHELFKSDHVLPPP--GLSPSYIFQKVEES
970 980 990 1000 1010
Cry1Ac KLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNVPGTGSLSWPLSAQSPIGKCGEPNR
gi|344 KLKPNTRYIVSGFIAHGKLEIVVSRYGQEVQVQVVP-YGEAFPLTNSGPV--C-----
1020 1030 1040 1050 1060
Cry1Ac CAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVGCTDLNEDLGWVVFVKIKTQDGHARL
gi|344 CPPRSTSNGLT-----GDP-----HFFSYSIDVGDALDQANPGIEFGLRIVNPTGMARV
1070 1080 1090 1100 1110
Cry1Ac GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD-Q
gi|344 SNLEIREDRPLAANEIRQVQRVARNWRTEYKERAEVTSLIQPVINRINGLYENGNWNGS
1120 1130 1140 1150 1160 1170
Cry1Ac LQADTNIAAMIHA-ADKRVHSIREAYLPELSVIPGVNAAIFFELEGRIFTAFSLYDARNVI
gi|344 IRSDISYQNIIDAIVLPTLPKLRHWFMSDRFSEQG---DIMAKFQGALNRAYAQLQESTLL
1180 1190 1200 1210 1220 1230
Cry1Ac KNGDFNNGLSWCNVKGVHDVVEEQNNQSVLVPWEAEVSVQEVVV---CPGRGYILRVTA
gi|344 HNGHFTKDAANWTIEGDAHQITLEDGRVRLRLPDWSSVSQMIENFNPNKKEYNLVF--
1240 1250 1260 1270 1280 1290
Cry1Ac
1050 1060 1070 1080 1090

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Cry1Ac YKEGYGEGCVTIHEIENN----TDELKFSNCVVEEIIYPNNVTVCNDYTVNQEEYGGAYTS
gi|344 --HGQGGEGTVLHGHGEETKYIETHTHHFANFTTSQ-RQGLTFESNKVTYTISSDGEFLV
1300 1310 1320 1330 1340 1350
Cry1Ac RNRGYNEAPSVPADYASVYEEKSYTDGRRNPCEFNRGYRDYTPPLVGVYVTKLEYFPET
gi|344 DNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNNQ
1360 1370 1380
>>gi|2096263|gb|AAB55095.1| Sequence 2 from patent US 56 (1385 aa)
initn: 534 initl: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
(373-1110:652-1363)
Cry1Ac GTMGNAAPQORIVAQLGQGVYRTLSSTLYRPFNIGINNQQLS--VLDGTEFAYGTSSNL
gi|209 DNNTGVQGANVYVVKSIATTDNSFTEIPAKTINVHLTNQGSDDVFLDRIF---IPFSL
630 640 650 660 670
Cry1Ac PSAVYRKSQTVSLDEIPQNNN-----VPPRQGFSHRLSHVSMFRSGFSNSSVSII-
gi|209 PLIYHGSYNTSSGADVLWSSNMNYDIIVNGQANSSSIASSMHLNKGKVIKTIDIPG
680 690 700 710 720 730
Cry1Ac -RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGN-
gi|209 HSETFFATFPVPEGFNEV--RILAGLPEVSGNITVQSNPPQPSNNGGGGGGGGGG
740 750 760 770 780 790
Cry1Ac ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TPIHLNVNWNSSIFSNTVPATATSL
gi|209 GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTGTPLVILNAYRNNTVVS-SIPVYSPFD
800 810 820 830 840 850
Cry1Ac DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQ
gi|209 ITIQTE-----ADSLELELQPRYGFATVNGTATV---KSPNVNYDRSFKLPIDLQKIT
860 870 880 890 900
Cry1Ac KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDER
gi|209 TQVNALFASGTQNMLAHNVSDHDIIEEVLKVDALSDEVFGDEKKALRKLVNQAKRLSRAR
910 920 930 940 950 960
Cry1Ac NLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDES
gi|209 NLLIGGSFENWD----AWYKGRNVVTVSDHELFKSDHVLPPP--GLSPSYIFQKVEES
970 980 990 1000 1010
Cry1Ac
750 760 770 780 790 800

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Regulatory Product Characterization Team

Cry1Ac KLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNVPGTGLWPLSAQSPIGKCGEPNR

gi|209 KLKPNTRYIVSGFIAHGKDL EIVVSRYGQEVQKVVQVP-YGEAFPLTNSGPV--C-----

Cry1Ac CAPHLEWNPDLDCSCRDKGEKCAHSHHFLSLDIDVGTDLNEDLGWVVFIFKIKTQDGHARL

gi|209 CPPERSTSNGLT-----GDP-----HFFSYSIDVGALDLQANPGIEFGLRIVNPTGMARV

Cry1Ac GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYD-Q

gi|209 SNLEIREDRPLAANEIRQVQRVARNRWTEYEKERA EVTSLIQPVINRINGLYENGNWNGS

Cry1Ac LQADTNIA MIHA-ADKRVHSIREAYLPELSVIPGVNA AIFEELEGRIFTAFSLYDARNVI

gi|209 IRSDISYQNIDAIVLPTLPKLRHWFMSDRFSEQG--DIMAKFQALNRAYA QLEQSTLL

Cry1Ac KNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVPEWAEV SQEVRV---CPGRGYILRVTA

gi|209 HNGHFTKDAANWTIEGDAHQITLEDGRRVLR LRPDWSSVSQMI EIEENFNPDKEYNLVF--

Cry1Ac YKEGYGEGCVTIHEIENN---TDELKFSNCV EEEIYPNNTVTCNDYTVNQBEYGGAYTS

gi|209 --HQQGEGTVLEHGEE TKYIETHHFFANFTTSQ-RQGLTFESNKVVTI SSEDEGFLV

Cry1Ac RNRGYNEAPSPADYASVYEEKSYTDGRENPC EFNRGYRDYTPLPVGYVTK ELEYFPET

gi|209 DNIALVEAP-LPTDDQNSEGNTASSTNSD TSMNNQ

>>gi|3994347|gb|AAC87775.1|AR008749 Sequence 2 from pate (1385 aa)
initn: 534 init1: 173 opt: 326 Z-score: 372.2 bits: 81.1 E(): 8.2e-12
Smith-Waterman score: 662; 25.524% identity (54.450% similar) in 764 aa overlap
(373-1110:652-1363)

Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQLS--VLDGTEFAYGTSSNL

gi|399 DNNTGVQGGANGVYVVKSIATTDNSFTEIPAKTINVHLTNQSSDVFDRIEF---IPFSL

Cry1Ac PSVAVYRSGTVDLSDEIIPPQNNN-----VPPRQGF SHRLSHVSMFRSGFSNSSVSII-

gi|399 PLIYHGSYNTSSGADDVLWSSSNMYYDIIVNGQANSSSIASSMHLNKGKVIKIDIPG

Cry1Ac PSVAVYRSGTVDLSDEIIPPQNNN-----VPPRQGF SHRLSHVSMFRSGFSNSSVSII-

Cry1Ac -RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFN GSVISGPGFTGGDLVRLNSSGN-

gi|399 HSETFFATFPVPEGFNEV---RILAGLPEVSGNITVQSN NPQPNSNNGGDDGGGGGGD

Cry1Ac ---NIQNRGYIEVPIHFPSTSTRYRVRVRYASV-TP IHLNVNWNSSSIFSNTPATATSL

gi|399 GQYNFSLSGSDHTTIYHGKLETGIHVQGNYYTGT PVLILNAYRNNTVVS-SIPVYSPFD

Cry1Ac DNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGV IIDRFEPVTPATLEAEYNLERAQ

gi|399 ITIQTE-----ADSL ELELQPRYGFATVNGTATV---KSPNVNYDRSFKLPIDLQ NIT

Cry1Ac KAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYL SDEFCLDEKRELSEKVKHAKRLSDER

gi|399 TQVNALFASGTQNM LAHNVSDHDI EEVVLKVDALSDEVFGDEKKALRKLNVQAKRLSRAR

Cry1Ac NLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFK ENYVTLSGTFDECYPTYLYQKIDES

gi|399 NLLIGGSFENWD----AWYKGRNVVTVSDHEL FFKSDHVLPPP--GLSPSYIFQKVEES

Cry1Ac KLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETV NVPGTGLWPLSAQSPIGKCGEPNR

gi|399 KLKPNTRYIVSGFIAHGKDL EIVVSRYGQEVQKVVQVP-YGEAFPLTNSGPV--C-----

Cry1Ac CAPHLEWNPDLDCSCRDKGEKCAHSHHFLSLDID VGTDLNEDLGWVVFIFKIKTQDGHARL

gi|399 CPPERSTSNGLT-----GDP-----HFFSYSID VGALDLQANPGIEFGLRIVNPTGMARV

Cry1Ac GNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE WETNIVYKEAKESVDALFVNSQYD-Q

gi|399 SNLEIREDRPLAANEIRQVQRVARNRWTEYEKERA EVTSLIQPVINRINGLYENGNWNGS

Cry1Ac LQADTNIA MIHA-ADKRVHSIREAYLPELSVIPGV NA AIFEELEGRIFTAFSLYDARNVI

gi|399 IRSDISYQNIDAIVLPTLPKLRHWFMSDRFSEQG-- DIMAKFQALNRAYA QLEQSTLL

Cry1Ac KNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVPE WAEV SQEVRV---CPGRGYILRVTA

gi|399 HNGHFTKDAANWTIEGDAHQITLEDGRRVLR LRPDWSSVSQMI EIEENFNPDKEYNLVF--

Cry1Ac RNRGYNEAPSPADYASVYEEKSYTDGRENPC EFNRGYRDYTPLPVGYVTK ELEYFPET

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      1050      1060      1070      1080      1090
Cry1Ac YKEGYGEGCVTIHEIENN---TDELKFSNCVVEEIIYPNNTVTCNDYTVNQEEYGGAYTS
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : :
gi|399 --HGQEGEVTVLEHGEEETKYIETHHFFANFTTSQ--RQGLTFESNKVTVTISSEDEGFLV
      1300      1310      1320      1330      1340      1350

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      1100      1110      1120      1130      1140      1150
Cry1Ac RNRGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGRDYRDTPLPVGYVTKELEYFPET
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : :
gi|399 DNIALVEAP-LPTDDQNSEGNTASSTNSDSTSMNNNQ
      1360      1370      1380

```

>>gi|12810205|gb|AAE44120.1| Sequence 43 from patent US (1220 aa)  
 initn: 515 init1: 171 opt: 325 Z-score: 371.9 bits: 80.9 E(): 8.6e-12  
 Smith-Waterman score: 766; 25.021% identity (52.428% similar) in 1215 aa overlap  
 (10-1110:45-1198)

```

      10      20      30
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIET--GY
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY
      20      30      40      50      60      70

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      40      50      60      70      80      90
Cry1Ac --TPIDISLSLTQFLLE---FVPGAGFVLGLVDIIWGFIPGSPQWDAFLVQ---IEQLINQ
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : :
gi|128 QTYVNIGLSLITLAVPEIGITPFIGLFFAALNKHDAPPPNAKDI FEAMKPAIQEMIDR
      80      90      100      110      120      130

```

```

      100      110      120      130      140
Cry1Ac RI---EEFARNQAISRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 TLTADEQTFLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVDGSLIKKFTDEVLSLNSFYT
      140      150      160      170      180      190

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      150      160      170      180      190
Cry1Ac TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVSVFGQRW---GFDAATINSRYND
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 DRLPVFITDNTADRTLGLPYAILASMHMLLRDIITKGPTWDSKINFPTDAIDSFKTD
      200      210      220      230      240      250

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      200      210      220      230      240      250
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELTTLTVLDIVSLFFPNYDSRT
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 IKNNIKLYSKTIYDVVFQKGLASYGTPSDLESFAKKKYIEIMTTHCLDFARLFPPTDPDL
      260      270      280      290      300      310

```

```

      260      270      280
Cry1Ac YP-----IRTVSQLT---REIYTN--PVLENFDGSRFRGSAQ----
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 YPTGSGDISLQKTRRILSPFIPIRTADGLTLNNTSIDTSNWPNYENGGAFNPNERILK
      320      330      340      350      360      370

```

```

      290      300      310      320
Cry1Ac -----GIEGSI RSPHL--MDILNSIT--IY----TDAHRGEYYS---GHQIM-
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 QFKLYPSWRAGYGGLLQPYLWAI EVQDSVETRLYQQLPAVDPQAGPNVYSIDSNPIIQ
      380      390      400      410      420      430

```

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      330      340      350      360      370
Cry1Ac -----ASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLTSLYRRPFNIGI
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : :
gi|128 INMDTWKTPPQAGASGWNTNL-MRGSVSGLSFLQRDGTRLSAGMGGGFADTIYSLP-----
      440      450      460      470      480

```

```

      380      390      400      410      420      430
Cry1Ac NNQQLSVLDGTEFAFGTSSNLPSAVYRKSQTVDSLDEIP-PQNNVPPRQGFSHRSLSHVS
      . : : : : : . : : : : : . : : : : : . : : : : : . : : : : :
gi|128 ATHYLSYLYGT--PYQTSQSDNY-----SGHVGALVGVSTPQEQATLPNIIGQPEDEQGNVS
      490      500      510      520      530

```

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      440      450      460      470      480      490
Cry1Ac MFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIP--AVKGNFLFNGSVISG-
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 TM--GPFPEKASYGGTGVVKEWLN-GANAMKLSPGQSIG-IPITNVTKHNYQVRCRYASNS
      540      550      560      570      580      590

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```

      500      510      520      530      540
Cry1Ac --PGF---TGGD---LVRLNSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYASVPIIHL
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 DNPVFFNVDTGGANPIFQQINFASVDSNMGVKEENGVVVKSIIK-TVEIPAGSFY-VHV
      600      610      620      630      640      650

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      550      560      570      580      590
Cry1Ac NVNWGNSSIFSNT---VPATATSL---DNLQSSDFGYFESANAFT---SSLGNIVGVRNF
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 T-NQSSDLFLDRIEFVVKIQFQFCDDNNLHCDNNPVDTDCTFCVCVCTSLTD-CDNNP
      660      670      680      690      700      710

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      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEF-IPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN
      . : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 RGIDCTLCCQVENQLPSFVTLT---DLRNITSQVNGLFAPGTQNRLAQNI SDHIDIEVVL
      720      730      740      750      760

```

```

      660      670      680      690      700      710
Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQG
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 KVDALSDEIFGTNKKALRKLQVQAKRLSRARLLIGGSFENWD----AWYKGRNVVTVS
      770      780      790      800      810      820

```

```

      720      730      740      750      760      770
Cry1Ac GDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNA
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 DHLEPKSDHVVLLPPP--GLSPSYIFQKVEESKLANTRYVTSVGFIAHATDLEIVSRYQO
      830      840      850      860      870      880

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      780      790      800      810      820      830
Cry1Ac K-HETVNVPGTSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSHFS
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 EIKKVVQVP-YGEAFPLTSSGPV--C-----CIPHSTSNGLT-----NPHFFS
      890      900      910      920

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      840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      . : : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|128 YSIDVGALVDVTPNGIEFLGRIVNPTGMARVSNLEIREDRPLAANIRQVQRVARNWRTE
      930      940      950      960      970      980

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```

          900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYD-QLQADTNIAMIHA-ADKRVHSIREAYLPEL
      . . . . .
gi|128 YEKERAEVTSLIQPVINRINGLYENENWNGSIRSDISYQNIDAIVLPTLPLTRHWFMSDR
          990      1000      1010      1020      1030      1040

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          960      970      980      990      1000      1010
Cry1Ac SVIPOVNAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNKGVHDVVEEQNNQRSV
      . . . . .
gi|128 FSEQG---DIMAKFQGALNRAYAQLAQSTLLHNGHFTKDAANWTIEGDAHQITLEDGRRV
          1050      1060      1070      1080      1090

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          1020      1030      1040      1050      1060
Cry1Ac LVVPEWEAEVVSQEVVV---CPGRGYILRVYAYKEGYGEGCVTIHEIENN---TDELKFS
      . . . . .
gi|128 LRLPDWSSSVSQMIEIENFNPDKEYNLVVF---HGQEGEVTLEHGEETKYIETHTHHFA
          1100      1110      1120      1130      1140      1150

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          1070      1080      1090      1100      1110      1120
Cry1Ac NCVVEEIIYPNNTVTNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRR
      . . . . .
gi|128 NFTTSQ-RQGLTFESNKVTVTISSEDEGFLVDNIALVEAP-LPTDDQNSEGNTAFSTNSD
          1160      1170      1180      1190      1200      1210

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          1130      1140      1150      1160      1170      1180
Cry1Ac ENPCEFNRRGYRDTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . .
gi|128 TSMNNNQ
          1220

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>>gi|1831859|gb|AAB46313.1| Sequence 43 from patent US 5 (1220 aa)  
 initn: 515 init1: 171 opt: 325 Z-score: 371.9 bits: 80.9 E(): 8.6e-12  
 Smith-Waterman score: 766; 25.021% identity (52.428% similar) in 1215 aa overlap  
 (10-1110:45-1198)

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          10      20      30
Cry1Ac      CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIET--GY
      . . . . .
gi|183 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY
          20      30      40      50      60      70

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          40      50      60      70      80      90
Cry1Ac -TPIDISLSLTQFLLE---FVPGAGFVLGLVDIIWGFGPSQWDAFLVQ---IEQLINQ
      . . . . .
gi|183 QTYVNIIGLSLITLAVPEIGIFTPFIFGLFFAALNKHDAPPPNAKDI FEAMKPAIQEMIDR
          80      90      100      110      120      130

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          100      110      120      130      140
Cry1Ac RI---EEFARNQAI SRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
      . . . . .
gi|183 TLTADEQTFLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVD SGLIKKFTDEVLSLNSPYT
          140      150      160      170      180      190

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          150      160      170      180      190
Cry1Ac TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVSVFGQRW---GFDAATINSRYND
      . . . . .
gi|183 DRLPVFITDNTADRLLGLPPYAILASMHMLLRDIITKGP TWSKINFTPAIDAFSKTD
          200      210      220      230      240      250

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          200      210      220      230      240      250
Cry1Ac LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFRRELTLTVLDIVSLFPNYSRT
      . . . . .
gi|183 IKNNIKLYSKTIYDVFQKGLASYGTPSDLESFAKKKYIEIMTTHCLDFARLFPFPDPDL
          260      270      280      290      300      310

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          260      270      280
Cry1Ac YP-----I RTVSQLT---REIYTN--PVLENFDGSFRGSAQ----
      . . . . .
gi|183 YPTGSGDISLQKTRRILSPFIPIRTADGLTLNNTSIDTSNWPNYENGN GAFPNPKRIRLK
          320      330      340      350      360      370

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          290      300      310      320
Cry1Ac -----GIEGSIRSPHL--MDILNSIT--IY----TDAHRGEYYS--GHQIM-
      . . . . .
gi|183 QFKLYPSWRAGQYGGLLQPYLWAI EVQDSVETRLYGQLPAVDPQAGPNYVSIDSSNPIIQ
          380      390      400      410      420      430

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          330      340      350      360      370
Cry1Ac -----ASPVGFSGPEFTFPLYGTMGNAAPQORIVAQLGQVYR TLSSTLYRRPFNIGI
      . . . . .
gi|183 INMDTWKTPPQGASGWNTNL-MRGSVSGLSFLQRDGR LRSAGMGGGFADTIYSLP-----
          440      450      460      470      480

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          380      390      400      410      420      430
Cry1Ac NNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIP-PQNNVPPRQGF SHRLSHVS
      . . . . .
gi|183 ATHYLSYLYGT--PYQTS DNY-----SGHV GALVGVSTPQEATLPNIIGQPDEQGNVS
          490      500      510      520      530

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          440      450      460      470      480      490
Cry1Ac MFRSGFSNSSVSIIRAPMF SWIHRSAEFNIIASDSITQIP--AVKGNFLPNGSVISG-
      . . . . .
gi|183 TM--GPFPEKASYGGTVVKEWLN-GANAMKLSPGQSIG-IPITNVTKHNYQVRCRYASNS
          540      550      560      570      580      590

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          500      510      520      530      540
Cry1Ac --PGF---TGGD---LVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASV TPIHL
      . . . . .
gi|183 DNPVFNVDTGGANPIFQQINFAS TVDSNMGVKEENG VYVKS IK-TVEIPAGSFY-VHV
          600      610      620      630      640      650

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          550      560      570      580      590
Cry1Ac NVNWNSSIFSNT---VPATATSL---DNLQSSDFGYFESANAFT---SSLGNIVGVRNF
      . . . . .
gi|183 T-NQSSDLFLDRIEFVPKIQFQCDNNNLHCD CNPVDTDCTFCVCVCTSLTD-CDCNPN
          660      670      680      690      700      710

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          600      610      620      630      640      650
Cry1Ac SGTAGVIDRFEF-IPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTYHIDQVSN
      . . . . .
gi|183 RGIDCTLCCQVENQLPSFVTLT---DLRNITSQVNLGFAPGTQNR LAQNISDHIDIEEVL
          720      730      740      750      760

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          660      670      680      690      700      710
Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWGGSTGITIQG
      . . . . .
gi|183 KVDALSDEIFGTNKKALRKLVLNQA KRLSRARNLLIGGSFENWD----AWYKGRNVVTVS

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Regulatory Product Characterization Team

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770      780      790      800      810      820
Cry1Ac  720      730      740      750      760      770
GDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNA
. . . . .
gi|183  DHELFPKSDHVLPPP--GLSPSYIFQKVEESKFKANTRYTVSGFIAHATDLEIVVSRYGQ
830      840      850      860      870      880

780      790      800      810      820      830
Cry1Ac  K-HETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFS
. . . . .
gi|183  EIKKVVQVP-YGEAFPLTSSGPV--C----CIPHSTSNGLTG-----NPHFFS
890      900      910      920

840      850      860      870      880      890
Cry1Ac  LDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
. . . . .
gi|183  YSIDVGALDVTNPGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNRWTE
930      940      950      960      970      980

900      910      920      930      940      950
Cry1Ac  REKLEWETNIVYKEAKESVDALFVNSQYD-QLQADTNIAAMIHA-ADKRVHSIREAYLPEL
. . . . .
gi|183  YEKERAEVTSLIQPVINRINGLYENENWNGSIRSISYQNIDAIVLPPLTRHWFMSDR
990      1000     1010     1020     1030     1040

960      970      980      990      1000     1010
Cry1Ac  SVIPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHV DVEEQNNQRVS
. . . . .
gi|183  FSEQG---DIMAKFQGALNRAYAQLQSTLLHNGHFTKDAANWTIEGDAHQITLEDGRRV
1050     1060     1070     1080     1090

1020     1030     1040     1050     1060
Cry1Ac  LVVPEWEAEVSEQEVRV---CPGRGYILRV TAYKEGYEGCVTIHEIENN---TDELKFS
. . . . .
gi|183  LRLPDWSSSVSQMIEIENFNPDKEYNLVF---HGQEGTVTLEHGEETKYIETHHFFA
1100     1110     1120     1130     1140     1150

1070     1080     1090     1100     1110     1120
Cry1Ac  NCVEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRR
. . . . .
gi|183  NFTTSQ-RQGLTFESNKVTVTISSEDEFLVDNIALVEAP-LPTDDQNSEGNTAFSTNSD
1160     1170     1180     1190     1200     1210

1130     1140     1150     1160     1170     1180
Cry1Ac  ENPCEFNRGYRDYTPLPVGYVTKLELYFPETDKVWIEIGETEGTFIVDSVELLMEE
gi|183  TSMNNNQ
1220

>>gi|5972730|gb|AAE12621.1| Sequence 43 from patent US 5 (1220 aa)
  initn: 515 init1: 171 opt: 325 Z-score: 371.9 bits: 80.9 E(): 8.6e-12
Smith-Waterman score: 766; 25.021% identity (52.428% similar) in 1215 aa overlap
(10-1110:45-1198)

10      20      30
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIET--GY
. . . . .
gi|597  VLAYTPPSFLPDAGTQATPADLTAYEQLLKNLEKGINAGTYSKAIADVLKGFIDDTINY

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20      30      40      50      60      70
Cry1Ac  -TPIDISLSLTQFLLE---FVPGAGFVLGLVDIIWGFQPSQWDAFLVQ---IEQLINQ
. . . . .
gi|597  QTYVNIGLSLITLAVPEIGIFTFPIGLFFAALNKHDAPPPNNAKDI FEAMKPAIQEMIDR
80      90      100     110     120     130

100     110     120     130     140
Cry1Ac  RI---EEFARNQAIRLEGLSNLYQIYAESFREWEA-DPTNPALREEMRIQFNDMNSALT
. . . . .
gi|597  TLTADEQTFLNGEISGLQNLAAARYQSTMDDIQSHGGFNKVD SGLIKKFTDEVLNSLNSFYT
140     150     160     170     180     190

150     160     170     180     190
Cry1Ac  TAIPLFAVQNY-QVPLLSV--YVQAANLHLSVLRDVS VFGQRW---GFDAATINSRYND
. . . . .
gi|597  DRLPVFITDNTADRTLLGLPYAILASMHLMLLRDIITK GPTWDSKINFTPDAIDSFKTD
200     210     220     230     240     250

200     210     220     230     240     250
Cry1Ac  LTRLIGNYTDHAVRWYNTGLERVWGP-DSRDWIRYNQFR RELTLTLDIVSLFPNYDSRT
. . . . .
gi|597  IKNNIKLYSKTIYDVFKGLASYGTPSDLESFAKKKYIE IMTTHCLDFARLFPFPDPL
260     270     280     290     300     310

260     270     280
Cry1Ac  YP-----IRTVSQLT---REIYTN--PVLENFDG SFRGSAQ----
. . . . .
gi|597  YPTGSGDISLQKTRRILSPFIPIRTADGLTLNNTS IDTSNWPNYENGN GAFPNPKERILK
320     330     340     350     360     370

290     300     310     320
Cry1Ac  -----GIBGSIRS PHL--MDILNSIT--IY---- TDAHRGEYYS---GHQIM-
. . . . .
gi|597  QFKLYPSWRAGQYGLLQPYLWAI EVQDSVETRLYGQL PAVDPQAGPNVYSIDSSNPIIQ
380     390     400     410     420     430

330     340     350     360     370
Cry1Ac  -----ASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTL SSTLYRRPFNIGI
. . . . .
gi|597  INMDTWKTPPQGASGWNTNL-MRGSVSGLSFLQRDGR TRLSAGMGGGFADTIYSLP-----
440     450     460     470     480

380     390     400     410     420     430
Cry1Ac  NNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIP-PQNNVPPRQGF SHRLSHVS
. . . . .
gi|597  ATHYLSYLYGT--PYQTS DNY-----SGHVGALVGVSTPQEATLPNIIGQPDEQGNVS
490     500     510     520     530

440     450     460     470     480     490
Cry1Ac  MFRSGFSNSVSIIRAPMFSWIHRSAEFN NIIASDSITQIP--AVKGNFLFNGSVISG-
. . . . .
gi|597  TM--GFPFKEKASYGGTVVKELWN-GANAMKLS PGQSIG-IPITNVTKHNYQVRCRYASNS
540     550     560     570     580     590

500     510     520     530     540
Cry1Ac  --PGF----TGGD---LVRNLSSGNNIQNRG YIEVPIHPSTSTRYRVRVRYASVTP IHL
. . . . .

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gi|597 DNPVFFNVDTGGANPIFQQINFASVTDSNMGVKKEENGVVVKSIIK-TVEIPAGSFY-VHV
      600      610      620      630      640      650
      550      560      570      580      590
Cry1Ac NVNWGNSSIFSNT--VPATATSL--DNLQSSDFGYFESANAFT---SSLGNIVGVRNF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 T-NQGSDDLFLDRIEFVPKIQFQFCNNDNLHDCNPNVDTDCTFCVCTSLTD-CDCNPN
      660      670      680      690      700      710
      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEF-IPVTATLEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSN
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 RGIDCTLCCQVENQLPSFVTLT---DLRNITSQVNGLFAPGTQNRLAQNISDHDIIEVVL
      720      730      740      750      760
      660      670      680      690      700      710
Cry1Ac LVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQG
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 KVDALSDEIFGTNKKALRKLNVQAKRLSRARNLLIGGSFENWD----AWYKGRNVVTVS
      770      780      790      800      810      820
      720      730      740      750      760      770
Cry1Ac GDDVFKENYVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNA
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 DHELFKSDHVLPPP--GLSPSYIFQKVEESKLANTRYTVSGFIAHATDLEIVVSRYQQ
      830      840      850      860      870      880
      780      790      800      810      820      830
Cry1Ac K-HETVNVPGTGSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFFS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 EIKKVVQVP-YGEAFPLTSSGPV--C-----CIPHSTSNGLTG-----NPHFFS
      890      900      910      920
      840      850      860      870      880      890
Cry1Ac LDIDVGCTDLNEDLGVVVFIKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDK
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 YSIDVGALDVDTPNGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVQRVARNWRTE
      930      940      950      960      970      980
      900      910      920      930      940      950
Cry1Ac REKLEWETNIVYKEAKESVDALFVNSQYD-QLQADTNIAIHA-ADKRVHSIREAYLPEL
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 YEKERAEVTSLIQPVINRINGLYENENWNGSIRSISYQNIIDAIVLPPLRHLRFWMSDR
      990      1000      1010      1020      1030      1040
      960      970      980      990      1000      1010
Cry1Ac SVIPGVNAAIFFELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVVEEQNNQRSV
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 FSEQG---DIMAKFQGALNRAYAQLQSTLLHNGHFTKDAANWTIEGDAHQITLEDGRRV
      1050      1060      1070      1080      1090
      1020      1030      1040      1050      1060
Cry1Ac LVPPEWAEVQEVV---CPGRGYILRVTAIYKEGYEGCVTIHEIENN---TDELKFS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 LRLPDWSSSVSQMIEIENFNPDKEYNLVF---HGQEGGTVLEHGEETKYIETHTHHFA
      1100      1110      1120      1130      1140      1150
      1070      1080      1090      1100      1110      1120
Cry1Ac NCVVEEIIYPNNVTTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRR

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      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 NPTTSQ-RQGLTFESNKVITVTTISSEDEGEFLVDNIALVEAP-LPTDDQNSEGTAFSTNSD
      1160      1170      1180      1190      1200      1210
      1130      1140      1150      1160      1170      1180
Cry1Ac ENPCEFNRYRDTPLPVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|597 TSMNNNQ
      1220
>>gi|14103743|gb|AAE55177.1| Sequence 28 from patent US (50 aa)
      initn: 306 initl: 306 opt: 306 Z-score: 370.1 bits: 75.9 E(): 1.1e-11
      Smith-Waterman score: 306; 98.000% identity (100.000% similar) in 50 aa overlap
      (126-175:1-50)
      100      110      120      130      140      150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|141
      TNPALREEMRIQFNDMNSALTTAIPLLAVQ
      10      20      30
      160      170      180      190      200      210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|141 NYQVPLLSVYVQAANLHLSV
      40      50
>>gi|14112748|gb|AAE58163.1| Sequence 28 from patent US (50 aa)
      initn: 306 initl: 306 opt: 306 Z-score: 370.1 bits: 75.9 E(): 1.1e-11
      Smith-Waterman score: 306; 98.000% identity (100.000% similar) in 50 aa overlap
      (126-175:1-50)
      100      110      120      130      140      150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|141
      TNPALREEMRIQFNDMNSALTTAIPLLAVQ
      10      20      30
      160      170      180      190      200      210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|141 NYQVPLLSVYVQAANLHLSV
      40      50
>>gi|56664643|gb|AAW18068.1| Sequence 28 from patent US (50 aa)
      initn: 306 initl: 306 opt: 306 Z-score: 370.1 bits: 75.9 E(): 1.1e-11
      Smith-Waterman score: 306; 98.000% identity (100.000% similar) in 50 aa overlap
      (126-175:1-50)
      100      110      120      130      140      150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|566
      TNPALREEMRIQFNDMNSALTTAIPLLAVQ
      10      20      30
      160      170      180      190      200      210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|566 NYQVPLLSVYVQAANLHLSV

```



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Cry1Ac PFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPR-QGFSH
gi|100 ITDINVNSQNSQYLDLNSVMVNGGQKVTGCSPLSSNGNSNNAALPNQKINVIYSVQSNDK
450 460 470 480 490 500

440 450 460 470 480 490
Cry1Ac RLSHVSVMFRS-GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNQSV
gi|100 PEKHADTYRKGWYMSHIPPYDLVPE--ENVIGDIDPDTKQPSLLLKGFPAEKG---YGDSI
510 520 530 540 550 560

500 510 520 530 540
Cry1Ac --ISGPGTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPIHNLNVNW
gi|100 AYVSEP-LNGANAVKL-TSYQVLQ---MEVT---NQTTQKYRIRIRYATGGDTAASIW
570 580 590 600 610

550 560 570 580 590
Cry1Ac GNSSIFSNTVPATATSLDNLQSSDFGYFESANA-----FTSSL---GN-IVGVRNFSG
gi|100 HIIGPSGNDLTNEGHNFSVSSRNKMFVQGNNGKYVLNLTDSIELPSGQQTILIQN-TN
620 630 640 650 660 670

600 610 620 630 640 650
Cry1Ac TAGVIIDRFEFI--PVTAT-----LEAEBYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
gi|100 SQDLFLDRIEFISLSPSTSTPTSTNFVEPE-SLEKIIINQVNLFSSSSQTELAHTVSDYKI
680 690 700 710 720 730

660 670 680 690 700
Cry1Ac DQVSNLVTYLSDDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG--WGGS
gi|100 DQVVLLKVNALSDVDFGVEKKALRKLNVNQAQQLSKARNLVGGNF-----EKGHEWALS
740 750 760 770 780

710 720 730 740 750 760
Cry1Ac TGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
gi|100 REATMVANHELFPKGDHLLPP--PTLYPSYAYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
790 800 810 820 830 840

770 780 790 800 810 820
Cry1Ac YSIRYNAC-HETVNVPGTGSWPLSA-QSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC
gi|100 VVSRYGKEVHMDLDIPYEEAL-PISSDESP--NCCKPAAC-----QCSSCDGSQ-
850 860 870 880 890

830 840 850 860 870 880
Cry1Ac AHHSHHFLSLDIDVGTDLNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKR
gi|100 -SDSHFFSYSIDVGSLSQSDVNLGIEFGLRIAKPNGFAKISNLEIKEDRPLTEKEIKKVQR
900 910 920 930 940

890 900 910 920 930 940
Cry1Ac AEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIAHADKRVH--SI
gi|100 KEQKWKAFNQEAQEVATTLQPTLDQINALYQNEEDWN-----GSVHPASDYQHLSAV
950 960 970 980 990 1000

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950 960 970 980 990
Cry1Ac REAYLPE-----LSVIPGVNAALFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKG
gi|100 VVPTLPKQRHWFMEGREGEHVLTQQFQQALDRAFQIEEQNLIHNGNLANGLTDWTVTG
1010 1020 1030 1040 1050 1060

1000 1010 1020 1030 1040 1050
Cry1Ac HVDVEEQNNQRSVLLVPEWEAEVSVQEVVCP--GRGYILRVAYKEGYGEGCVTTHIEIEN
gi|100 DAQLT-IFDEDPVLELAHWDAISQITIEIMDFEGRHRIQTACTWKRQRNSYRSTWRKRL
1070 1080 1090 1100 1110 1120

1060 1070 1080 1090 1100 1110
Cry1Ac NTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEE
gi|100 TMTFNTTSFTTQEQTFYFEGDVTVDVHVQSENNTFLIDSVELIEIEE
1130 1140 1150 1160

>>gi|5977359|gb|AAE14769.1| Sequence 6 from patent US 58 (1167 aa)
initn: 694 initl: 192 opt: 321 Z-score: 367.4 bits: 80.0 E(): 1.5e-11
Smith-Waterman score: 826; 24.658% identity (55.890% similar) in 1095 aa overlap
(42-1042:70-1105)

20 30 40 50 60
Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAG---FVLGLVDI
gi|597 EEFGKTGYMDPLKQHLQIAWDTSQNGTVDYLALTKASISLIGLIPGADAVVPFINMFVDF
40 50 60 70 80 90

70 80 90 100 110
Cry1Ac IWG-IFG-PSQWDA-----FLVQIEQLINQRIEEFARNQAISRLEGLS-----NLY
gi|597 IFPKLFGSGSQNAQAQFFELIEKVKELVDEDFRNFNLTNNLLNLDGMQATLSHFQNDV
100 110 120 130 140 150

120 130 140 150
Cry1Ac QIYAESFRE---WEADPT--NPALREEMRIQ--FNDMNSALTTAIPLFA---VQNYQV
gi|597 QIAICQEQPGLMLDQTPACTPTTDHLISVRESFKDARTTIETALPHFKNPMLSTNDNT
160 170 180 190 200 210

160 170 180 190 200
Cry1Ac P-----LLSVYVQAANLHLSVLRDVSFVFGQRW--GFDAATINSRYNDLTRLIGNY
gi|597 PDFNSDVTLLTLPMTTGTATLNLILHQGYIQFAERWKSVMYDESFINQTKVDLQRRIQDY
220 230 240 250 260 270

210 220 230 240 250 260
Cry1Ac TDHAVRWYNTGLERWGPDSRDWI-RYNQFRRELTLTVLDIVSLFPNYSRTPYPIRTVSQ
gi|597 STTVSTTFEK-FKPTLNPNSKESVKNYRYSRMTLQSLDIAATWPTLDNVNYPNSVDIQ
280 290 300 310 320 330

270 280 290 300 310
Cry1Ac LTREIYTNPVLNFDGSRGSAQGIIEGSIKRSPLHMDILNSITI-----YTDHARGEY--
gi|597 LQQ---TRLVFSVAGVPWEGN-----DNITS-NIIDVLTPIINTGIGFQESSDLRKFYTPR
340 350 360 370 380

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320      330      340      350      360      370
Cry1Ac -YWSGHQIMASPVGFSGPEFTFP--LYGTMGNAAPQQRI--VAQLGQQGVYRTLSSLTLYRR
      . . . . .
gi|597 IELQSMQFHGQYVNSKSVHEHCYSDDLKLNKNTITAGVSNIDESNQNNKHNYGPVINS
390      400      410      420      430      440

      380      390      400      410      420      430
Cry1Ac PFNIGINNQQLSVLDGTEFAYGTSNLPSSAVYRKSGTVDSLDEIPPQNNVPPR-QGFSSH
      . . . . .
gi|597 ITDINVNSQNSQYLDLNSVMVGGQKVTGCSPLSSNGSNNAALPNQKINVIYSVQSNDK
450      460      470      480      490      500

      440      450      460      470      480      490
Cry1Ac RLSHVSFMFRS-GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLNGSV
      . . . . .
gi|597 PEKHADTYRKWGYMSSHIPYDLVP--ENVIGDIDPDTKQPSLLKGFPAEKG--YGDSDI
510      520      530      540      550      560

      500      510      520      530      540
Cry1Ac --ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHPSTSTRYRVRVRYASVTPIHNLNVW
      . . . . .
gi|597 AYSVEP-LNGANAVKL-TSYQVLQ---MEVT---NQTTQKYRIRIRYATGGDTAASIVF
570      580      590      600      610

      550      560      570      580      590
Cry1Ac GNSSIFSNTVPATATSLDNLQSSDFGYFESANA-----FTSSL---GN-IVGVRNFSG
      . . . . .
gi|597 HIIGPSGNDLTNEGHNFSVSSRNKMFVQGNNGKYVLNLTDSIELPSSQQTILIQN-TN
620      630      640      650      660      670

      600      610      620      630      640      650
Cry1Ac TAGVIIDRFEFI--PVTAT-----LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
      . . . . .
gi|597 SQDLFLDRIEFISLPSSTPTSTNFVEPE-SLEKIINQVNLFSSSSQTELAHTVSDYKI
680      690      700      710      720      730

      660      670      680      690      700
Cry1Ac DQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERG--WGGS
      . . . . .
gi|597 DQVVLKVNALSDDVFGVEKKALRKLNVQAKQLSKARNVLVGGNF-----EKGHEWALS
740      750      760      770      780

      710      720      730      740      750      760
Cry1Ac TGITIQQGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEI
      . . . . .
gi|597 REATVANHELFGDHLPP--PTLYPSYAYQKIDESKLNTRTYTSGVIAQSEHLEV
790      800      810      820      830      840

      770      780      790      800      810      820
Cry1Ac YSIRYNAK-HETVNVPGTGLWPLSA-QSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCK
      . . . . .
gi|597 VVSRYGKEVHMDLIPYEEAL-PISSDESP--NCKPAAC-----QCSSCDGSQ-
850      860      870      880      890

      830      840      850      860      870      880
Cry1Ac AHHSHHFLSDIDVGCIDLNEDLGVVVIKIKTQDGHARLGNLEFLLEEKPLVGEALARVKR
      . . . . .
gi|597 -SDSHFFSYSIDVGLSDVNLGIEFGLRIAKPNGFAKISLNLEIKEDRPLTEKEIKKQVR
900      910      920      930      940

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890      900      910      920      930      940
Cry1Ac AEKKWRDRKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVH--SI
      . . . . .
gi|597 KEQKWKAFNQEQAEVATTLPQPTLDQINALYQNEWDN-----GSVHPASDYQHLSAV
950      960      970      980      990      1000

      950      960      970      980      990
Cry1Ac REAYLPE----LSVIPGVNAAIPEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVK
      . . . . .
gi|597 VVPTLQKQRHWFMEGREGEHVLTQQFQQALDRAFFQIEEQNLIHNGNLANGLTDWTVTG
1010      1020      1030      1040      1050      1060

      1000      1010      1020      1030      1040      1050
Cry1Ac HVDVEEQNNQSRVSLVPEWEAEVSQEVVCP--GRGYILRVTAAYKEGYGECVTHEIEN
      . . . . .
gi|597 DAQLT-IPDEDVLELAHWDAISQTIEMDFEGRHRIQTACTWKRQRNSYRSTWRKRL
1070      1080      1090      1100      1110      1120

      1060      1070      1080      1090      1100      1110
Cry1Ac NTDELKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEE
      . . . . .
gi|597 TMTFNNTSFTTQEQTFYFEGDVTDVHVQSENNTFLIDSVELIEIIEE
1130      1140      1150      1160

>>gi|1830715|gb|AAB45169.1| Sequence 6 from patent US 55 (1167 aa)
initn: 694 initl: 192 opt: 321 Z-score: 367.4 bits: 80.0 E(): 1.5e-11
Smith-Waterman score: 826; 24.658% identity (55.890% similar) in 1095 aa overlap
(42-1042:70-1105)

      20      30      40      50      60
Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAG---FVLGLVDI
      . . . . .
gi|183 EEFGKTYGMDPLKQHLQIAWDTSQNGTVDYLALTKASISLIGLIPGADAVVFPINMVFDF
40      50      60      70      80      90

      70      80      90      100      110
Cry1Ac IWG-IFG-PSQWDA-----FLVQIEQLINQRIEFARNQAIISRLEGLS-----NLY
      . . . . .
gi|183 IFPKLFGSGSQNAQAQFFELIEKVKELVDEDFRNTLNNLLNLYLDGMQTALSHFQNDV
100      110      120      130      140      150

      120      130      140      150
Cry1Ac QIYAESFRE---WEADPT--NPALREEMRIQ--FNDMNSALTTAIPFLFA---VQNYQV
      . . . . .
gi|183 QIAICQGEQPLMLDQTPACTPTDHLISVRESFKDARTTIETALPHFKNPMLSTNDNT
160      170      180      190      200      210

      160      170      180      190      200
Cry1Ac P-----LLSVYVQAANLHLSVLRDVSVFGQRW---GFDAATINSRYNDLTRLIGNY
      . . . . .
gi|183 PDFNSDTVLLTLPMYTTGATLNLILHQGYIQFAERKWSVNYDESFINQTKVDLQRRIQDY
220      230      240      250      260      270

      210      220      230      240      250      260
Cry1Ac TDHAVRWYNTGLERVWGPDSRDWI--RYNQFRELTTLTVLDIVSLFNPYDSRTPYPIRTVSO
      . . . . .
gi|183 STTVSTTFEK-FKPTLNPNSKESVKNYRYSMTLQSLDIAATWPTLNDVNYPSNVDIQ
280      290      300      310      320      330

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      270      280      290      300      310
Cry1Ac  LTREIYTNVPLENFDGSRFRGSAQIEGSIKSPHMLDILNSITI-----YTDahrGEY--
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  LDQ---TRLVFSVAVAGPWEGN-----DNITS-NIIDVLTPIINTGIGFOESSDLRKFYTPR
      340      350      360      370      380
Cry1Ac  -YWSGHQIMASPVGFSGPEFTFP--LYGTMGNAAPQORI--VAQLGQGVYRSLSTLYRR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  IELQSMQPHGQVYVNSKSVHEHCYSGLKLNKNTITAGVSNIDESNQNKKNHYGPVINSF
      390      400      410      420      430      440
Cry1Ac  PFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIIPQNNVPPR-QGFSH
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  ITDINVNSQNSQYLDLNSVMVNGGQKVTGCSPLSSNGNSMNAALPNQKINVIYSVQSNDK
      450      460      470      480      490      500
Cry1Ac  RLSHVSMFRS-GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSV
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  PEKHADTYRKGWYMSHIPPYDLVP--ENVIGDIDPDTKQPSLLLKGFPAEKG---YGDISI
      510      520      530      540      550      560
Cry1Ac  --ISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLVNW
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  AYWSEP-LNGANAVKL-TSYQVLQ---MEVT---NQTTQKYRIRIRYATGGDTAASIWF
      570      580      590      600      610
Cry1Ac  GNSSIFSNTVPATATSLDNLQSSDFGYFESANA-----FTSSL---GN-IVGVRNFSG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  HIIGPSGNDLTNEGHNFSVSSRNKMFVQNGNGKYVLNLTDSIELPSGQQTILIQN-TN
      620      630      640      650      660      670
Cry1Ac  TAGVIIDRFEFI--PVTAT-----LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  SQDLFLDRIEFISLPSTSTPTSTNFVEPE-SLEKIIINQVNLFSSSSQTELAAHTVSDYKI
      680      690      700      710      720      730
Cry1Ac  DQVSNLVTYLSDDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERG--WGGS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  DQVVLKVNALSDVDFGVEKKALRKLNVNQAQLSKARNVLVGGNF-----EKGHEWALS
      740      750      760      770      780
Cry1Ac  TGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLLKAFTRYQLRGYIEDSQDLEI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  REATMVANHELFGDHLPP--PTLYPSYAYQKIDESKLLKSNTRYTVSGFIAQSEHLEV
      790      800      810      820      830      840
Cry1Ac  YSIRYNAK-HETVNVPGTGLWPLSA-QSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKC
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  VVSRYGKEVHMLDIPYEEAL-PISSDESP--NCCKPAAC-----QCSSCDGSQ-

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      850      860      870      880      890
Cry1Ac  AHHSHHFLSDIDVGCCTDLNEDLGVVWIFKIKTQDGHARLGNLFLEEKPLVGEALARVKR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  -SDSHFFSYSIDVGLSQSDVNLGIEFGLRIAKPNGFAKISNLEIKEDRPLTEKIKKVR
      900      910      920      930      940
Cry1Ac  AEKKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNIAIMIHAADKRVH--SI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  KEQKWKAFNQAEVATTLPQTLQINALYQNEWDN-----GSVHPASDYQHLSAV
      950      960      970      980      990      1000
Cry1Ac  REAYLPE-----LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVVKGNDFNGLSCWNVKG
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  VVPTLPKQRHWFMEGREGEHVLTQQFQALDRAFQQIEEQNLIHNGNLANGLTDWTVTG
      1010      1020      1030      1040      1050      1060
Cry1Ac  HVDVEEQNNQSRVSVLWPEWAEVSVQEVVRCVCP--GRGYILRVTAKEGEGCVTIHEIEN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  DAQLT-IFDEDVLELAHWDAISQTIEMDFEGRHRIQTACTWKRQRNSYRSTWRKRLK
      1070      1080      1090      1100      1110      1120
Cry1Ac  NTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|183  TMTFNNTSFTTQEQTFYFEGDVTVDVHVQSENNTFLDLSVELIEIEE
      1130      1140      1150      1160
>>gi|14112751|gb|AAE58166.1| Sequence 31 from patent US (50 aa)
      initn: 303 initl: 303 opt: 303 Z-score: 366.6 bits: 75.3 E(): 1.7e-11
      Smith-Waterman score: 303; 96.000% identity (100.000% similar) in 50 aa overlap
      (126-175:1-50)
      100      110      120      130      140      150
Cry1Ac  ARNQAISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTPAIPFAVQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|141  TNPALREEMRIQFNDMNSALTTPAIPFTVQ
      10      20      30
Cry1Ac  NYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLRLIGNYTDHAVRWY
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|141  NYQVPLLSVYVQAVNLHLSV
      40      50
>>gi|17920882|gb|AAE86502.1| Sequence 31 from patent US (50 aa)
      initn: 303 initl: 303 opt: 303 Z-score: 366.6 bits: 75.3 E(): 1.7e-11
      Smith-Waterman score: 303; 96.000% identity (100.000% similar) in 50 aa overlap
      (126-175:1-50)
      100      110      120      130      140      150
Cry1Ac  ARNQAISRLLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTPAIPFAVQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|179  TNPALREEMRIQFNDMNSALTTPAIPFTVQ
      10      20      30

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>>gi|53970029|gb|AAV19122.1| Sequence 41 from patent US (137 aa)
initn: 308 init1: 129 opt: 307 Z-score: 364.8 bits: 76.4 E(): 2.1e-11
Smith-Waterman score: 307; 39.437% identity (73.944% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
gi|539 PGFTGGDILRRTNAGNFGDMRVNITAPL--
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANA
gi|539 ---SQRYRVRIRYASTANLQFHTSINGRAINQANFPATMNSGENLQSGSFRVAGFTTPTFT
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGL
gi|539 FSDALSTFTIGAFSFSNNNEVYIDRIEFVPAEVTFATESDQDRAQKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|16240180|gb|AAE79628.1| Sequence 41 from patent US (137 aa)
initn: 308 init1: 129 opt: 307 Z-score: 364.8 bits: 76.4 E(): 2.1e-11
Smith-Waterman score: 307; 39.437% identity (73.944% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
gi|162 PGFTGGDILRRTNAGNFGDMRVNITAPL--
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANA
gi|162 ---SQRYRVRIRYASTANLQFHTSINGRAINQANFPATMNSGENLQSGSFRVAGFTTPTFT
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGL
gi|162 FSDALSTFTIGAFSFSNNNEVYIDRIEFVPAEVTFATESDQDRAQKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504407|gb|AAM57105.1| Sequence 41 from patent US (137 aa)
initn: 308 init1: 129 opt: 307 Z-score: 364.8 bits: 76.4 E(): 2.1e-11
Smith-Waterman score: 307; 39.437% identity (73.944% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF

gi|215 PGFTGGDILRRTNAGNFGDMRVNITAPL--
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANA
gi|215 ---SQRYRVRIRYASTANLQFHTSINGRAINQANFPATMNSGENLQSGSFRVAGFTTPTFT
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNALFTSTNQLGL
gi|215 FSDALSTFTIGAFSFSNNNEVYIDRIEFVPAEVTFATESDQDRAQKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|56642277|gb|AAW11995.1| Sequence 29 from patent US (50 aa)
initn: 300 init1: 300 opt: 300 Z-score: 363.1 bits: 74.6 E(): 2.7e-11
Smith-Waterman score: 300; 96.000% identity (98.000% similar) in 50 aa overlap
(126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|566 TNPALTEEMRIQFNDMNSALTTAIPLFTVQ
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|566 NYQVPLLSVYVQAANLHLSV
40 50

>>gi|17920880|gb|AAE86500.1| Sequence 29 from patent US (50 aa)
initn: 300 init1: 300 opt: 300 Z-score: 363.1 bits: 74.6 E(): 2.7e-11
Smith-Waterman score: 300; 96.000% identity (98.000% similar) in 50 aa overlap
(126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|179 TNPALTEEMRIQFNDMNSALTTAIPLFTVQ
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|179 NYQVPLLSVYVQAANLHLSV
40 50

>>gi|14112749|gb|AAE58164.1| Sequence 29 from patent US (50 aa)
initn: 300 init1: 300 opt: 300 Z-score: 363.1 bits: 74.6 E(): 2.7e-11
Smith-Waterman score: 300; 96.000% identity (98.000% similar) in 50 aa overlap
(126-175:1-50)

100 110 120 130 140 150



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          340      350              360      370      380
Cry1Ac  GNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIG-INNQQLSVLDGTEFAYGTSSNLPSAV
          350      360      370      380      390      400
gi|160  YNSG--EPFLTNLNG-----KPGNNPVPNSRDNP IISAKGSRPSANYVGMNF
          390              400      410      420

          410      420      430      440      450      460
Cry1Ac  YRKSQTVDSLDEIPPQNNVPPRQGFSSHRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSA
          410      420      430      440      450      460
gi|160  QRANKTVVSNQYVIPNDNYTVPA--GHKLGWISALHDELNANNADLVVSV--WVKNDI
          430      440      450      460      470      480

          470      480      490              500      510
Cry1Ac  EFNIIASDSITQIPAVKGNFLFNGSVISGPG-----FTGGDLVRLNSSGN
          470      480      490      500      510
gi|160  FQENIIGS--IKVTDDGTENRQIIIGIPADKHMTRSTKRMELEFINGTNGSMSLSST
          490      500      510      520      530      540

          520      530      540      550      560      570
Cry1Ac  NIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQ
          520      530      540      550      560      570
gi|160  NDQLYYTIN----PIVSQRYQIRYRVATTSAESLDL-WIDG-YKRGTTPLPNTSSTSTQ
          550      560      570      580      590

          580      590      600      610      620
Cry1Ac  SSDF-----GYFESANAFTSSL---GNIVGVR-NFSGTAGVIIDRFEFIPVTATLEAEY
          580      590      600      610      620
gi|160  TQKVIIQQLGQKYLINGPTLDLDTAGSHTFGIMLTANASQNVFIDRIEFVPIATTEPVTI
          600      610      620      630      640      650

          630      640      650      660      670
Cry1Ac  NLERAQKAVNA----LFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
          630      640      650      660      670
gi|160  PNTPIKTYTNPENPQQLVWTAQPGILGDIVNYHINLYNHL
          660      670      680      690

          680      690      700      710      720      730
Cry1Ac  KHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGDDVFKENYVTLSTGTFDECYP
>>gi|33731233|gb|AAQ37296.1| Sequence 15 from patent US (137 aa)
  initn: 298 init1: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11
Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap
(495-633:1-137)

          470      480      490      500      510      520
Cry1Ac  EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
          470      480      490      500      510      520
gi|337  PGFTGGDILRRTSPGQISTLRVNITAPL--
          10              20

          530      540      550      560      570      580
Cry1Ac  PSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
          530      540      550      560      570      580
gi|337  ---SQRYRVRIRYASTTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRVVGFTTTPFN
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac  SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
          590      600      610      620      630      640
gi|337  FSNSSVFTLSAHVFNMSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVASLF
          90      100      110      120      130

          650      660      670      680      690      700
Cry1Ac  KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

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Cry1Ac  SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
          90      100      110      120      130
gi|337  FSNSSVFTLSAHVFNMSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVASLF
          90      100      110      120      130

          650      660      670      680      690      700
Cry1Ac  KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
>>gi|53970027|gb|AAV19120.1| Sequence 37 from patent US (137 aa)
  initn: 298 init1: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11
Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap
(495-633:1-137)

          470      480      490      500      510      520
Cry1Ac  EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
          470      480      490      500      510      520
gi|539  PGFTGGDILRRTSPGQISTLRVNITAPL--
          10              20

          530      540      550      560      570      580
Cry1Ac  PSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
          530      540      550      560      570      580
gi|539  ---SQRYRVRIRYASTTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRVVGFTTTPFN
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac  SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
          590      600      610      620      630      640
gi|539  FSNSSVFTLSAHVFNMSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVASLF
          90      100      110      120      130

          650      660      670      680      690      700
Cry1Ac  KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
>>gi|16240162|gb|AAE79615.1| Sequence 15 from patent US (137 aa)
  initn: 298 init1: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11
Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap
(495-633:1-137)

          470      480      490      500      510      520
Cry1Ac  EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
          470      480      490      500      510      520
gi|162  PGFTGGDILRRTSPGQISTLRVNITAPL--
          10              20

          530      540      550      560      570      580
Cry1Ac  PSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
          530      540      550      560      570      580
gi|162  ---SQRYRVRIRYASTTNLQFHSTIDGRPINQGNFSATMSSGSNLQSGSFRVVGFTTTPFN
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac  SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
          590      600      610      620      630      640
gi|162  FSNSSVFTLSAHVFNMSGNEVYIDRIEFVPAEVTFAEYDLERAQKAVASLF
          90      100      110      120      130

          650      660      670      680      690      700
Cry1Ac  KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|53970016|gb|AAV19109.1| Sequence 15 from patent US (137 aa)  
 initn: 298 initl: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11  
 Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539          PGFTGGDILRRTSPGQISTLRVNITAPL--
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 ---SQRVYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFSTPPFN
      30          40          50          60          70          80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 FSNSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
      90          100         110         120         130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|16240178|gb|AAE79626.1| Sequence 37 from patent US (137 aa)  
 initn: 298 initl: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11  
 Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162          PGFTGGDILRRTSPGQISTLRVNITAPL--
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 ---SQRVYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFSTPPFN
      30          40          50          60          70          80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 FSNSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
      90          100         110         120         130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|33731244|gb|AAQ37307.1| Sequence 37 from patent US (137 aa)  
 initn: 298 initl: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11  
 Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520

```

```

Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337          PGFTGGDILRRTSPGQISTLRVNITAPL--
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 ---SQRVYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFSTPPFN
      30          40          50          60          70          80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 FSNSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
      90          100         110         120         130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|21504404|gb|AAM57103.1| Sequence 37 from patent US (137 aa)  
 initn: 298 initl: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11  
 Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215          PGFTGGDILRRTSPGQISTLRVNITAPL--
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215 ---SQRVYRVRIRYASTTNLQFHTSIDGRPINQGNFSATMSSGSLQSGSFRTVGFSTPPFN
      30          40          50          60          70          80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIV---GVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215 FSNSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
      90          100         110         120         130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|21504390|gb|AAM57092.1| Sequence 15 from patent US (137 aa)  
 initn: 298 initl: 143 opt: 304 Z-score: 361.2 bits: 75.7 E(): 3.4e-11  
 Smith-Waterman score: 304; 42.254% identity (69.014% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215          PGFTGGDILRRTSPGQISTLRVNITAPL--
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT

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gi|597 ADTENLIKLI DEEI QKQLNKALLDQDRNNWTSFLESIFDTSATVSNAIIDAQWSGTVDTT
110 120 130 140 150 160

Cry1Ac N-----PALREEMRI--QFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
130 140 150 160 170
gi|597 NRQOKTPTTSDYLVNVVGFDSADSSIIITNENQIMNGNPDVAAPYFVIGATLRLSLYQSY
170 180 190 200 210 220

Cry1Ac SVFGQRW----GFDAATINSRYNDLTRL-----IGNYTDHAVRWYNTGLER-VWGPDS
180 190 200 210 220
gi|597 IKFCNSWIDAVGFSTNDANTQKANLARTKLTMRITINEYTQRVMKVFKDSKNMPTIGTNK
230 240 250 260 270 280

Cry1Ac RDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV--LENFDGSRF
230 240 250 260 270 280
gi|597 FSVDAYNVVYKGMTLNVLDMVAIWSLSPNDYTSQTAIEQTRVTFNSMVGQEEGTDGTLK
290 300 310 320 330 340

Cry1Ac GSAQGIIEGSI RSPHLM---DILNSITIIYTDHRGEYWSGHQIMASPVGFSGPEFTFPLY
290 300 310 320 330 340
gi|597 --IYNTFDSL S YQHS LIPNNVNLISYYTDELQ----NLELAVVTPKGGSG--YAYP-Y
350 360 370 380 390

Cry1Ac GTMGNAAPQQRIV AQLGQGVYRTLSSSTLYRR--PFN-IGINNQQLSVLDGTEFAYGTSSN
350 360 370 380 390
gi|597 GFILNYAN-----SNKYGDNDPTGKPLNKQDGIQIINAATQNSKYLDG-ETINGIGAS
400 410 420 430 440

Cry1Ac LP-----SAV---YRKSGTVDSLDE-I PPQNNN--VP PRQGF SHRLSHVSMFRSGFSN
400 410 420 430 440
gi|597 LPGYCTTGCSATEQPFSCSTSTANSYKASCNP SDTNQKINALYAFQTQNVKSGTGKLGVLA
450 460 470 480 490 500

Cry1Ac SSVSII RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFN GS-VISGPGFTGGDLVRL
450 460 470 480 490 500
gi|597 SLVPYDLNPKNVF GELSDSTNNVI---LKGIPAEKGYFPNNARPTVVKEWINGASAVPF
510 520 530 540 550 560

Cry1Ac NSSGNNIQRNGYIEVPIHFPSTSTRYRVRVRYA---SVTPIHLNVNWNSSIFSNTVPAT
510 520 530 540 550 560
gi|597 YS-GNTL----FMTAT---NLTATQYKIRIRYANPNSDTQIGVLITQNGSQI-SNSNLTL
570 580 590 600 610

Cry1Ac ATSLDNLQSSDF-----GYFESANAFTS---SLGNIVGVRNFSGTAGVIIDRFE
570 580 590 600
gi|597 YSTTSSMSSNLPQNVVYVTGENGNVTLDDLSTNNVLTGDIT-LKLTGGNKQIFIDRIE
620 630 640 650 660 670

610 620 630

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```

Cry1Ac FIP-----VTAT-----LEAEYNLERAQKAVN
::: . . . . . : : : : :
gi|597 FIPTMPVPAPTNTNTNNGDNGNPPHHC A IAGTQQQLCSGPPKFEQVSDLEKITTVYVY
680 690 700 710 720 730

Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE-FCLDEKRELSEKVKHAKRLSDERNLL
640 650 660 670 680
gi|597 MLFKSSSYEELALKVSSYQINQVALKVMALSDEKFC-EEKRLRLKLVNKANQLLEARNLL
740 750 760 770 780 790

Cry1Ac QDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTYLYQKIDESKLG
690 700 710 720 730 740
gi|597 VGGNF----ETTQNVWLGTNAYINYSFLFNGNYLSLQPA-SGFFTSYAYQKIDESTLK
800 810 820 830 840

Cry1Ac AFTRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGTGS LWPLSAQSPIGKCGEPNRCAP
750 760 770 780 790 800
gi|597 PYTRYKVSFGFIGQSNQVELIISRYGKEIDKILNVPYAGPL-PITADASI-TC----CAP
850 860 870 880 890 900

Cry1Ac HLEWNPDLDCSCRDEKCAHSHHFSLDIDVGCTDLNEDLGVWVIFKIKTQDGHARLGNL
810 820 830 840 850 860
gi|597 EID-----QCDGGQS---DSHFFNYSIDVGALHPPELNPGLIEIGLKI VQSNGYITISNL
910 920 930 940 950

Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNI--VYKEAKESVDALFVNSQYDQLQ
870 880 890 900 910 920
gi|597 EIIEERPLTEMEIQAVNRKDKHW--KREKLECASVSELLQPIINQIDSLFKDANW----
960 970 980 990 1000

Cry1Ac ADTNIAMIHAAADKRVHSIREAYLPELSV-----IPGVNAAI FEELEGRIFTAFSLYDARN
930 940 950 960 970 980
gi|597 --YNDILPHVVTYQTLKNIIVPDLPLK LKHWFDHLPGEYHEIEQOMKEALKHAFTQLDEKN
1010 1020 1030 1040 1050 1060

Cry1Ac VIKNGDFNNGLS CWNVKGHV DVEEQNNQRSVLVVPEWEAEVSQEVRCV---GRGYILRV
990 1000 1010 1020 1030
gi|597 LIHNGHFATNLIDWQVEGDARMKVLENNALALQLSNWSSVSQSIDILEFDEDKAYKLRV
1070 1080 1090 1100 1110 1120

Cry1Ac TAYKEGYGEGCVTIHEIENNTDELKFSNCEVEEIIYPNNTVTNCNDYTVNQEYGGAYTSRN
1040 1050 1060 1070 1080 1090
gi|597 --YAQSGT-----IQFGNCEDEAIQFNTNSFVYKEKIIYFDTPSINLHIQ
1130 1140 1150 1160

Cry1Ac RGYNEAPSPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKLEYFPETDK
1100 1110 1120 1130 1140 1150
gi|597 SEGSEFVVSSIDLVELSDDE
1170 1180

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>>gi|10051729|gb|AAE28636.1| Sequence 4 from patent US 5 (1186 aa)
initn: 505 init1: 153 opt: 307 Z-score: 350.8 bits: 76.9 E(): 1.3e-10
Smith-Waterman score: 778; 25.196% identity (53.269% similar) in 1147 aa overlap
(50-1075:75-1143)

20 30 40 50 60 70
Cry1Ac LSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVGLVDIIWGFPGSQWDA
gi|100 SFSLTALQQGFASQGGAFNYLTLLQSGISLAGSFVPGGTFVAPIVNMVIGWLWPHKNKT

80 90 100 110 120
Cry1Ac F----LVQ-----IEQLINQRIEEFARNQAIRLEGLSNLYQIYAESF--REWEA--DPT
gi|100 ADTENLIKLIIDEEIQQLNKALLDQRNNWTSFLESIFDTSATVSNAIIDAQWSGTVDDT

130 140 150 160 170
Cry1Ac N----PALREEMRI--QFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
gi|100 NRQOKTPTTSDYLNIVGKFDSDASSIIITNENQIMNGNFDVAAAPYFVIGATLRLRLSLYQSY

180 190 200 210 220
Cry1Ac SVFGQRW---GFDAATINSRYNDLTRL-----IGNYTDHAVRWYNTGLER-VWGPDS
gi|100 IKFCNSWIDAVGFSTNDANTQKANLARTKLTMRITINEYTRVMVFKDSKNMPTIGTNK

230 240 250 260 270 280
Cry1Ac RDWIRYNQFRELTLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV--LENFDGSFR
gi|100 FSVDAYNVYVKGMTLNVLDMAIVAIWSSLYPNDYTSQTAIEQTRVTFNSNMVGGQEEGDGTLK

290 300 310 320 330 340
Cry1Ac GSAQGIIEGSIRSPHLM---DILNSITTYDAHRGEYYSWGHQIMASPVGFGSPEFTFPLY
gi|100 --IYNTFDSLQSLIPNNVNLISYYTDELQ----NLELAVYTPKGGSG--YAYP-Y

350 360 370 380 390
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSTLYRR--PFN-IGINNQLSVLDGTEFAYGTSSN
gi|100 GFILNYAN-----SNKYGDNDPTGKPLNKQDGPQQINAATQNSKYLQD--ETINGIGAS

400 410 420 430 440
Cry1Ac LP-----SAV---YRSGTVDSLDE-IPPQNNN--VPPRQGFSHRLSHVSMFRSGFSN
gi|100 LPGYCTTGCSATEQPFSCSTSTANSYKASCNPSDTNQKINALYAFQTNTVKGSTGKLGVLVA

450 460 470 480 490 500
Cry1Ac SSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRL
gi|100 SLVPYDLNPKNVFGEKLDSDTNNVI----LKGIPAEKGYFPNNARPTVVKEWINGASAVFPF

510 520 530 540 550 560
Cry1Ac NSSGNNIQNRGYIEVPIHPFSTSTRYRVRVRYA---SVTPIHLNVNWGSSIFSNTVPAT
gi|100 YS-GNTL---FMTAT---NLTATQYKIRIRYANPNSDTQIGVLITQNGSQI-SNSNLTLL

570 580 590 600
Cry1Ac ATSLDNLQSSDF-----GYFESANAFTS----SLGNIVGVNRNFGSGTAGVIIDRFE
gi|100 YSTTDSMSSNLPQNVVYVTGNGNYTLDDLSTTNVLSTGDIT-LKLTGGNKQIFIDRIE

610 620 630
Cry1Ac FIP-----VTAT-----LEAEYNLERAQKAVN
gi|100 FIPTMPVPAPTNNNTNNNGDNGNPNPHHGCAIAGTQQLCSGPPKFEQVSDLEKITTQVY

640 650 660 670 680
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE-FCLDEKRELSEKVKHAKRLSDERNLL
gi|100 MLFKSSSYEELALKVSSYQINQVALKVMALSDEKFC-EEKRLRLKLVNKANQLEARNLL

690 700 710 720 730 740
Cry1Ac QDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLG
gi|100 VGGNF-----ETTQNVVLGTNAYINYSPLFNGNYLSLQPA-SGFFTSYAYQKIDESTLK

750 760 770 780 790 800
Cry1Ac AFTRYQLRGYIEDSODLEIYSIRYNAKHETV-NVPGTGSWLPLSAQSPIGKCGEPNRCAP
gi|100 PYTRYKVSFGFIQSNQVELIISRYKEIDKILNVYPYAGPL-PITADASI-TC----CAP

810 820 830 840 850 860
Cry1Ac HLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTDLNEDLGVVWVIFKIKTQDGHARLGNL
gi|100 EID-----QCDDGQS---DSHFFNYSIDVGALHPENLPGIEIGLKIYQSNGYITISNL

870 880 890 900 910 920
Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNI--VYKEAKESVDALFVNSQYDQLQ
gi|100 EIIEERPLTEMIQAVNRKDKHW--KREKLLCASVSELLQPIINQIDSLFKDANW----

930 940 950 960 970 980
Cry1Ac ADTNIAAMIHAADKRVHSIREAYLPESV----IPGVNAAIFEELGRIFTAFSLYDARN
gi|100 --YNDILPHVYTYQTLKNIIVPDLPLKPKLHWFIDHLPGEYHEIEQQMKEALKHAFTQLDEKN

990 1000 1010 1020 1030
Cry1Ac VIKNGDFNGLSCWNVKGVVDVEEQNNQRSVLVVPEWEAEVSVQEVRCV---GRGYILRV
gi|100 LIHNGHFATNLDWQVEGDARMKVLNENALALQLSNWDSVSSQSIDILEFDEDKAYKLRV

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1040      1050      1060      1070      1080      1090
Cry1Ac TAYKEGYGBGCVTIHEIENNTDELKFSNCEVEEIIYPNNTVTCNDYTVNQEEYGGAYTSRN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|100 --YAQGSQT-----IQFGNCEDEAIQFNTNSFVYKEKIIIFYDTPSINLHIQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      1130      1140      1150      1160

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```

1100      1110      1120      1130      1140      1150
Cry1Ac RGYNEAPSVPADYASVYEEKSYTDGRRENPCFNRGYRDTPLPVGYVTKELEYFPETDK
gi|100 SEGSEFVVSIDLVELSDDE
      1170      1180

```

>>gi|1830714|gb|AAB45168.1| Sequence 4 from patent US 55 (1186 aa)  
 initn: 505 initl: 153 opt: 307 Z-score: 350.8 bits: 76.9 E(): 1.3e-10  
 Smith-Waterman score: 778; 25.196% identity (53.269% similar) in 1147 aa overlap  
 (50-1075:75-1143)

```

20      30      40      50      60      70
Cry1Ac LSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGFGPSQWDA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 SFSLTALQGFASQGGAFNYLTLLQSGISLAGSFVPGGTFVAPIVMVMVIGWLWPHKNTK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      50      60      70      80      90      100

```

```

80      90      100      110      120
Cry1Ac F----LVQ----IEQLINQRIEEFARNQAISRLEGLSNLYQIYAESF--REWEA--DPT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 ADTENLIKLIIDEIQQLNKALLDQRNNTWTSFLESIFDTSATVSNAIIDAQWGTVDTT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      110      120      130      140      150      160

```

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130      140      150      160      170
Cry1Ac N----PALREEMRI--QFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 NRQQTPTTSDYLVNVVGFDSADSSIITNENQIMNGNFDVAAPYFVIGATRLRLSLSYQSY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      170      180      190      200      210      220

```

```

180      190      200      210      220
Cry1Ac SVFGQRW---GFDAATINSRYNDLTRL-----IGNYTDHAVRWYNTGLER--VWGPDS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 IKFCNSWIDAVGFSTNDANTQKANLARTKLTMRRTINEYTQRVMKVFKDKSNMPTIGTNK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      230      240      250      260      270      280

```

```

230      240      250      260      270      280
Cry1Ac RDWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPV--LENFDGFSFR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 FSVDAYNVVYKGMTLNVLDMAIWSLSLYPNDYTSQTAIEQTRVTFSNMVGQEEGTGTLK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      290      300      310      320      330      340

```

```

290      300      310      320      330      340
Cry1Ac GSAQIEGSIRSPHLM---DILNSITTYDAHRGEYYWSGHQIMASPVGFSGPEFTFPFLY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 --IYNTFDSLQSLIPNNVNLISYTYDELQ----NLELAVYTPKGGSG--YAYP-Y
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      350      360      370      380      390

```

```

350      360      370      380      390
Cry1Ac GTMGNAAPQQRIVALGQGVYRTLSTLYRR--PFN-IGINNQQLSVLDGTEFAYGTSSN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 GFILNYAN-----SNYKYGNDPTGKPLNKQDGPQQNAATQNSKYLDG--ETINGIGAS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      400      410      420      430      440

```

```

400      410      420      430      440
Cry1Ac LP-----SAV---YRKSQTVDSLDE-IPPQNNN--VPFRQGFSHRLSHVSMFRSGFSN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 LPGYCTTGCSATFQPFSCSTSTANSYKASCNPSTDTNQKINALYAFTQTNVKGSTGKLGVLVA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      450      460      470      480      490      500

```

```

450      460      470      480      490      500
Cry1Ac SSVSIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGS-VISGPGFTGGDLVRL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 SLVVPYDLNPKNVFGEELSDTNNVI----LKGIPAEKGYFPNARNPTVVKKEWINGASAVPF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      510      520      530      540      550      560

```

```

510      520      530      540      550      560
Cry1Ac NSSGNNIQNRGYIEVPIHFPSTSTRYRVRYA--SVTPIHNLVNWGSSIFSNTVPAT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 YS-GNTL---FMTAT---NLTATQYKIRIRYANPNSDTQIGVLITQNGSQI-SNSNLTL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      570      580      590      600      610

```

```

570      580      590      600
Cry1Ac ATSLDNLQSSDF-----GYFESANAFTS---SLGNIVGVVRFSGTAGVIIDRFE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 YSTTDSMSSNLPQNVVYVTGENGNITLLDLYSTTNVLSTGDIIT-LKLTGGNKQIFIDRIE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      620      630      640      650      660      670

```

```

610      620      630
Cry1Ac FIP-----VTAT-----LEAEYNLERAQKAVN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 FIPTMPVPAPTNNNTNNGDNGNPPHGCALAGTQQLCSGPPKFEQVSDLEKITTQVY
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      680      690      700      710      720      730

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640      650      660      670      680
Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVTVLSDE-FCLDEKRELSEKVKHAKRLSDERNLL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 MLFKSSSYEELALKVSSYQINQVALKVMAALSDEKFC-EEKRLRLKLVNKANQLEARNLL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      740      750      760      770      780      790

```

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690      700      710      720      730      740
Cry1Ac QDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKILK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 VGGNF----ETTQNVVLGTNAYINYSFLFNGNYSLSLQPA-SGFFTSYAYQKIDESTLK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      800      810      820      830      840

```

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750      760      770      780      790      800
Cry1Ac AFTRYQLRGYIEDSQDLEIYSIRYNKAKHETV-NVPGTGLSLWPLSAQSPIGKCGEPNRCAP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 PYTRYKVSFGIQSNQVELIISRYGKEIDKILNVVPYAGPL-PITADASI-TC----CAP
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      850      860      870      880      890      900

```

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810      820      830      840      850      860
Cry1Ac HLEWNPDLDCSRDGEKCAHSHHFLSLDIVGCTDLNEDLGVVWVIFKIKTQDGHARLGNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 EID-----QCDGGQS---DSHFFNYSIDVGALHPELNPGBIEIGLKIYQSNNGYITISNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      910      920      930      940      950

```

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870      880      890      900      910      920
Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNI--VYKEAKESVDALFVNSQYDQLQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 EIIEERPLTEMEIQAVNRKDKHW--KREKLLCASVSELLQPIINQIDSLFKDANW----

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gi|248 PYTRYKVSFGFIGSQSNOVELIISRYGKEIDKILNVPYAGPL-PITADASI-TC----CAP
850      860      870      880      890      900

      810      820      830      840      850      860
Cry1Ac HLEWNPDLDCSRDGEKCAHSHHFLSLDIDVGCTDLNEDLGVVWIFKIKTQDGHARLGNL
...      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|248 EID-----QCDDGQS---DSHFFNYSIDVGALHPPELNPGEIIGLKVQSNQNGYITISNL
      910      920      930      940      950

      870      880      890      900      910      920
Cry1Ac EFLEEKPLVGEALARVKRAEKKWRDKREKLEWETNI--VYKEAKESVDALFVNSQYDQLQ
...      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|248 EIIIEERPLTEMEIQAVNRKDKHW--KREKLLECASVSELLQPIINQIDSLFKDANW----
      960      970      980      990      1000

      930      940      950      960      970      980
Cry1Ac ADTNIAMIIHAADKRVHSIREAYLPELSV-----IPGVNAAIFEELEGRIFTAFSLYDARN
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|248 --YNDILPHVTTYQTLKNIIVPDLPLKHKHWFIDHLPGEYHEIEQQMKEALKHAFTQLDEKN
1010     1020     1030     1040     1050     1060

      990      1000     1010     1020     1030
Cry1Ac VIKNGDFNNGLSQWNVKGVHVDVEEQNNQRSVLVPEWEAEVSEQEVRVCP---GRGYILRV
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|248 LIHNGHFATNLIDWQVEGDARMKVLNENALALQLSNWSSVSQSIDILEFDEDKAYKLRV
1070     1080     1090     1100     1110     1120

      1040     1050     1060     1070     1080     1090
Cry1Ac TAYKEGYGEGCVTIHEIENNTDELKFSNCVVEEIIYPNNVTVCNDYTVNQEEYGGAYTSRN
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|248 --YAQSGT-----IQFGNCEDEAIQFNTNSFVYKEKIIYFDTPSINLHIQ
      1130     1140     1150     1160

      1100     1110     1120     1130     1140     1150
Cry1Ac RGYNEAPSVPADYASVYEEKSYTDGRENPCFNRGYRDYTPLVGYVTKLELYFPETDK

gi|248 SEGSEFVVSSIDLVELSDDE
1170     1180

```

>>gi|160724712|emb|CAP40038.1| unnamed protein product [ (1235 aa)  
 initn: 872 initl: 298 opt: 306 Z-score: 349.4 bits: 76.7 E(): 1.5e-10  
 Smith-Waterman score: 935; 26.394% identity (55.052% similar) in 1148 aa overlap  
 (33-1044:64-1170)

```

      10      20      30      40      50
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLS---EFVPGAG
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 QFNKNKNWEDALKLLEKFFYSGLTQDAIDIFLGDGSGFDY-LSLVNVIKSIAGSFIPIYVG
40      50      60      70      80      90

      60      70      80      90      100      110
Cry1Ac FVLGLVDIIWGFIFG-PSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLS---LYQIYA
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 ALVPIINLLFGSESKPDVFEQMRARIEALIHKELSADHVQTLKAEIKLKDGTGDLYQKDV
100     110     120     130     140     150

      120      130      140      150      160
Cry1Ac ESFREWEADPTNP-----ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQA
..      .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:

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gi|160 NAVAGRTNGPTPPSFDSENTDALKAEIERSQITATNTLFLVQRMQFAIEGYEIEITLPLHTIA
160      170      180      190      200      210

      170      180      190      200      210      220
Cry1Ac ANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRYNTGLERVWGPDSR
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 ASMHLIFLKDVCHEGAEWGIANTTLTNYQQQLQDCIREYSNKAYSFMNIGLQRAKNNNGN
220     230     240     250     260     270

      230      240      250      260      270      280
Cry1Ac DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGS---FR
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 MWNVNVMNIRYRTMKNALDVAQWPILDKVITYPLDITLQQTGRGIFSD--LSRGGTQSNYR
280     290     300     310     320     330

      290      300      310      320      330
Cry1Ac GSAQGIIEGSIKSPHMLDILNSITITYDAHRGEYY---WSGHQIMASPVGF---SGPEFT
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 YDYDAVQG--YAPSFVGFDELNVVDFGYKDLTAIQPTGDRIDSIWQSFKYNSEGEPL
340     350     360     370     380

      340      350      360      370      380
Cry1Ac FPL-YGTMGN--AAPQQR---IVAQLGQGVYRTLSSTLYRR-----PFNIGINNQQLSV
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 TNLGNGKRGNNVPIPNRDNPIISAKGSRPSANYVGMNFORADKTVVPNGYVIPNDNYTV
390     400     410     420     430     440

      390      400      410      420
Cry1Ac LDGTEFAY-----GTSSNLPASAVYRKS-----GTV-----DSLDEIPPQNN
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 PAGHKLGWISALHDELNDANNADLVSVWVKNDIFQENIIGSKIKVTDDGTENRQQII
450     460     470     480     490     500

      430      440      450
Cry1Ac NVPPRQGFSHRLSHVSM-FRSGFSNSSVSIIRA-----PMFS-----
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 GIPADKHMTRSTRKMELEFING-TNGSMLSSSTNDQLYITINPIVSRVQIRYRVATSA
510     520     530     540     550     560

      460      470      480      490      500
Cry1Ac ----WI---HR-SAEFNIIASDSITQ---IPAVKGNF-LFNGSVI--SGPGFTGGDLV
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 ESLDLWIDGYKRGTTPLPNTSSTSTQTKVVIQGLQKQYQLINGPILDLTAGSHTFGIAL
570     580     590     600     610     620

      510      520      530      540
Cry1Ac RLNSSGNNIQNRGYIE-VPIH-----FPS---TSTRYRVRYAS-----VTPIH---
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 TATPSQNVFIDR--IEFVPIGSPCQNIIPAGPFTVDNGRKTVWTSSTGTAFSVENIQGVF
630     640     650     660     670     680

      550      560      570      580      590
Cry1Ac --LNVNW-----GNSSIFSNIVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGRNF
.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|160 GMRNFWRIEFLQKGVTLSSQYTIPIITGASFDHYS---FGPFSKDIPEGFDTIQIVSP-DF
690     700     710     720     730     740

      600      610      620      630      640      650
Cry1Ac SGTAGVIIDRFEFIPVTA-TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSN

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gi|160 PIVITPIDGKVCFDTS... 750 760 770 780 790

Cry1Ac LVTYLSDEFCLDEKRE... 660 670 680 690 700 710

gi|160 KVNALSDDLFGTEKER... 800 810 820 830 840 850

Cry1Ac GDDVFKENYVTLGTF... 720 730 740 750 760 770

gi|160 DNPLFAGTYVSLPP... 860 870 880 890 900 910

Cry1Ac AKHETV-NVPGTGS... 780 790 800 810 820 830

gi|160 KEIDTAFTVPYQEA... 920 930 940 950

Cry1Ac SLDIDVGCTDLNED... 840 850 860 870 880 890

gi|160 SYTIDVGALQLESN... 960 970 980 990 1000 1010

Cry1Ac KREKLEWETNIVYK... 900 910 920 930 940 950

gi|160 LSQKQSQQLQKQY... 1020 1030 1040 1050 1060 1070

Cry1Ac ELSVIPGVNAAIFE... 960 970 980 990 1000

gi|160 QLR--RTSSPMIE... 1080 1090 1100 1110 1120 1130

Cry1Ac RSVLVVPEWEAEV... 1010 1020 1030 1040 1050 1060

gi|160 ISVLHVPSWDETV... 1140 1150 1160 1170 1180 1190

Cry1Ac CVEEEIYPNNTVTC... 1070 1080 1090 1100 1110 1120

gi|160 NTFVTKEISFYPT... 1200 1210 1220 1230

>>gi|21504393|gb|AAM57094.1| Sequence 19 from patent US (137 aa)
initn: 287 initl: 143 opt: 293 Z-score: 348.3 bits: 73.3 E(): 1.8e-10
Smith-Waterman score: 293; 40.845% identity (68.310% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIP... 470 480 490 500 510 520

gi|215 PGFXGGDILRRTSPGQ... 10 20

Cry1Ac PSTSTRYRVRVRYAS... 530 540 550 560 570 580

gi|215 ---SQRYRVRIRYAX... 30 40 50 60 70 80

Cry1Ac SSLGNIV---GVRNF... 590 600 610 620 630 640

gi|215 FSNSSVFTLSAHVFN... 90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSN... 650 660 670 680 690 700

>>gi|33731235|gb|AAQ37298.1| Sequence 19 from patent US (137 aa)
initn: 287 initl: 143 opt: 293 Z-score: 348.3 bits: 73.3 E(): 1.8e-10
Smith-Waterman score: 293; 40.845% identity (68.310% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIP... 470 480 490 500 510 520

gi|337 PGFXGGDILRRTSPGQ... 10 20

Cry1Ac PSTSTRYRVRVRYAS... 530 540 550 560 570 580

gi|337 ---SQRYRVRIRYAX... 30 40 50 60 70 80

Cry1Ac SSLGNIV---GVRNF... 590 600 610 620 630 640

gi|337 FSNSSVFTLSAHVFN... 90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSN... 650 660 670 680 690 700

>>gi|53970018|gb|AAV19111.1| Sequence 19 from patent US (137 aa)
initn: 287 initl: 143 opt: 293 Z-score: 348.3 bits: 73.3 E(): 1.8e-10
Smith-Waterman score: 293; 40.845% identity (68.310% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIP... 470 480 490 500 510 520

gi|539 PGFXGGDILRRTSPGQ... 10 20

Cry1Ac PSTSTRYRVRVRYAS... 530 540 550 560 570 580

gi|539 ---SQRYRVRIRYAXTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTVGFTTTPFN
30 40 50 60 70 80

Cry1Ac SSLGNIV---GVRNFGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|539 FSNNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDSNFKDINRQP
650 660 670 680 690 700

>>gi|16240166|gb|AAE79617.1| Sequence 19 from patent US (137 aa)
initn: 287 init1: 143 opt: 293 Z-score: 348.3 bits: 73.3 E(): 1.8e-10
Smith-Waterman score: 293; 40.845% identity (68.310% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNNIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
470 480 490 500 510 520

gi|162 PGFXGGDILRRITSPGQISTLRVNITAPL--
10 20

Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNNGNSSIFSNTPATATSLDNLQSSDFGYFESANAFT
530 540 550 560 570 580

gi|162 ---SQRYRVRIRYAXTTNLQFHTSIDGRPINQGNFSATMSSGSNLQSGSFRVTVGFTTTPFN
30 40 50 60 70 80

Cry1Ac SSLGNIV---GVRNFGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|162 FSNNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKREKSEKVKHAKRLSDERNLLQDSNFKDINRQP
650 660 670 680 690 700

>>gi|14103753|gb|AAE55187.1| Sequence 38 from patent US (50 aa)
initn: 284 init1: 284 opt: 284 Z-score: 344.2 bits: 71.1 E(): 3e-10
Smith-Waterman score: 284; 88.000% identity (96.000% similar) in 50 aa overlap
(126-175:1-50)

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
100 110 120 130 140 150

gi|141 TNPALKEEMRTQFNDMNSILVTAIPLFSVQ
10 20 30

Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
160 170 180 190 200 210

gi|141 NYQVPFLSVYVQAANLHLSV
40 50

>>gi|56642286|gb|AAW12004.1| Sequence 38 from patent US (50 aa)
initn: 284 init1: 284 opt: 284 Z-score: 344.2 bits: 71.1 E(): 3e-10
Smith-Waterman score: 284; 88.000% identity (96.000% similar) in 50 aa overlap
(126-175:1-50)

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
100 110 120 130 140 150

gi|566 TNPALKEEMRTQFNDMNSILVTAIPLFSVQ
10 20 30

Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
160 170 180 190 200 210

gi|566 NYQVPFLSVYVQAANLHLSV
40 50

>>gi|17920889|gb|AAE86509.1| Sequence 38 from patent US (50 aa)
initn: 284 init1: 284 opt: 284 Z-score: 344.2 bits: 71.1 E(): 3e-10
Smith-Waterman score: 284; 88.000% identity (96.000% similar) in 50 aa overlap
(126-175:1-50)

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
100 110 120 130 140 150

gi|179 TNPALKEEMRTQFNDMNSILVTAIPLFSVQ
10 20 30

Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
160 170 180 190 200 210

gi|179 NYQVPFLSVYVQAANLHLSV
40 50

>>gi|14112758|gb|AAE58173.1| Sequence 38 from patent US (50 aa)
initn: 284 init1: 284 opt: 284 Z-score: 344.2 bits: 71.1 E(): 3e-10
Smith-Waterman score: 284; 88.000% identity (96.000% similar) in 50 aa overlap
(126-175:1-50)

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
100 110 120 130 140 150

gi|141 TNPALKEEMRTQFNDMNSILVTAIPLFSVQ
10 20 30

Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
160 170 180 190 200 210

gi|141 NYQVPFLSVYVQAANLHLSV
40 50

>>gi|158456685|gb|ABW41358.1| Sequence 38 from patent US (50 aa)
initn: 284 init1: 284 opt: 284 Z-score: 344.2 bits: 71.1 E(): 3e-10
Smith-Waterman score: 284; 88.000% identity (96.000% similar) in 50 aa overlap
(126-175:1-50)

Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
100 110 120 130 140 150

gi|158 TNPALKEEMRTQFNDMNSILVTAIPLFSVQ
10 20 30

160 170 180 190 200 210





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Cry1Ac HRLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNNIIAS-DSITQIP--AVKGNFLFN
gi|183 -VLYPITETVKNKTGGNLGVISA---YVPMELVPENVIGDYNADTKLPLTQLKG-FPFE
520 530 540 550 560

490 500 510 520 530 540
Cry1Ac --GSVISGPGFTGGDLVRLNSSGNN---IQNRGYIEVPIHFPSTSTRYRVRVRYASV--T
gi|183 KYGSEYNNRGIS---LVREWINGNNAVKLSNSQSVGIQIT-NQTKQKYEIRCRYASKGDN
570 580 590 600 610 620

550 560 570 580 590
Cry1Ac PIHLNVNWNSSIFSNVTVP--ATATSLDNLQSSDFGY-FESANAFTSSLGNI-VGVRNFS
gi|183 NVYFNVLDLSENP-FRNSISFGSTESSVVGQGENGYILKSITTVVEIPAGSFYVHITN-Q
630 640 650 660 670 680

600 610 620
Cry1Ac GTAGVIIDRFEFIP-----VTATLEAEYN-----
gi|183 GSSDLFLDRIEFVVKIQFQFCNNDNLHDCNPNVDTDCFCVCVCTSLTDCDCNPRGLDC
690 700 710 720 730 740

630 640 650 660
Cry1Ac -----LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
gi|183 TLCCQVENQLPSFVTLTDLQNIITQVNALVASSEHDTLATDVSDYEIEEVVLKVDALSGE
750 760 770 780 790 800

670 680 690 700 710 720
Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGGDDVFKEN
gi|183 VFGKKAALRKLKLVNHTKRLSKARNLLIGGNFDNLD---AWYRGRNVVNVSDHELKFSK
810 820 830 840 850

730 740 750 760 770 780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
gi|183 HVLLPP--PTLYSSYMFQKVEESKLNTRYTVSGFIAHAEDLEIVVSRYGQEVKVVQV
860 870 880 890 900 910

790 800 810 820 830 840
Cry1Ac PGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCDRDGEKCAHSHHFSLDIDVGTCT
gi|183 P-YGEAFLTSRGAII-C-----CPPR-----STSNKPKA--DPHFFSYSIDVGTLL
920 930 940 950

850 860 870 880 890 900
Cry1Ac DLNEDLGWVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLEWET
gi|183 DVEANPGIELGLRIVERTGMARVSNLEIREDRPLKKNELRNVRQARNWRRTAYDQERAEV
960 970 980 990 1000 1010

910 920 930 940 950
Cry1Ac NIVYKEAKESVDALFVNSQYDQLQADTNLAMIHAADKRVHSIREAYLPEL-----SV
gi|183 TALIQQVNLQINALYENE-----DWNGAIRSGVS--YHLEAIVLPTLPKLNHWFMMSD
1020 1030 1040 1050 1060

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960 970 980 990 1000 1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNNQRSVLV
gi|183 MLGEEQGSILAQFQEAALDRAYTQLEESTILHNGHFTTDAANWTIEGDAHHAILEDGRRVLR
1070 1080 1090 1100 1110 1120

1020 1030 1040 1050 1060
Cry1Ac VPEWEAEVSEQEVRVC---PGRGYILRVTAKEGYGEGCVTIHEIENN---TDELKFSNC
gi|183 LPDWSSSVSQTIEIENFDKQYQLVFHAQ---GEGTVSLQHGEEGEVVETHPHKSNANF
1130 1140 1150 1160 1170 1180

1070 1080 1090 1100 1110 1120
Cry1Ac VEEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYTDGRREN
gi|183 TTSH-RQGVTTFETNKVTVETSEDGEFLVDHIALVEAP-LPTDDQSSDGNNTSNTSNTS
1190 1200 1210 1220 1230 1240

1130 1140 1150 1160 1170 1180
Cry1Ac PCEFNRGRYRDYTPLVGYVTKELEYFPETDKVWIEIGETEGTFIVDSVELLLMEE
gi|183 MNNNQ

>>gi|12810190|gb|AAE44105.1| Sequence 8 from patent US 6 (1245 aa)
initn: 537 initl: 178 opt: 293 Z-score: 334.0 bits: 73.9 E(): 1.1e-09
Smith-Waterman score: 725; 24.013% identity (52.303% similar) in 1216 aa overlap
(43-1113:71-1226)

20 30 40 50 60
Cry1Ac ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGA---GFVLGLVDII
gi|128 EWGKTGQKLFDEHLLTIAWNLYKTGKLDYFALTAKASISLIGFIPGAEAAVPPINMVFDFV
50 60 70 80 90 100

70 80 90 100 110
Cry1Ac WG-IFGPSQ-----WDAFLVQIEQLINQRIEEF---ARNQAISRLEGLSNLYQ-----
gi|128 WPKLFGANTEGKQQQLFNAIMDAVNKMVDNKFLSYNLSTLNKTIIEGLQGNLGLFQNAIQV
110 120 130 140 150 160

120 130 140 150
Cry1Ac -IYAESFRE----WEADPTNPAL--REEM-RI--QFNDMNSALTTAIPLF-----A
gi|128 AICQGSTPERVNFQDQNTPCNPNQPKDLDLDRVASRFDTANSQFTQHLPEFKNPWSDENS
170 180 190 200 210 220

160 170 180 190 200
Cry1Ac VQNYQ---VPL-LSVYVQAANLHLSVLRDVSVFGQRWGF-DAATINSRNDLTRLIGNYT
gi|128 TQEFKRTSVELTLPMTTATLHLLLYEGYIEFMTKWNFHNEQYLNKLVKQQLIHSYS
230 240 250 260 270 280

210 220 230 240 250 260
Cry1Ac DHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLT
gi|128 ETVRTSFLQFLPTLNNRSKSSVNAVYVRNMTVNCLEIAATWPTFDTHNYHGQGLDLT
290 300 310 320 330 340

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270      280      290      300      310      320
Cry1Ac REIYTN---PVLENFDGSRFRGSAQIEGSIRSPH-LMDILNSITITYTDAHRGEYVWSG--
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 RIILSDTAGPIEYYTTGD---KTSGPEHSNITPNNILDTPSPPTYQHSFVSVDSIVYSRKE
      350      360      370      380      390

      330      340      350      360      370
Cry1Ac -HQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTL---YRRPFNI
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 LQQLDIATYSTNNSNNCHP-YGLRLSYTDGSRDYDGNQDPDFTSNNNYCHNSYAPITL
400      410      420      430      440      450

      380      390      400      410      420      430
Cry1Ac GINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV--DS-LDEI-PPQN--NNVPPRQGF
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 -VNAHRLYNKGS--LQNVESLVVSTVNGGSGSCICDAWINYLRRPQTSKNESRPDQKIN
460      470      480      490      500      510

      440      450      460      470      480
Cry1Ac HRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNIIIAS-DSITQIP--AVKGNFLFN
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 -VLYPITETVKNKGTGGNLGVISA---YVPMELVPEVIGVDNADTKLPLTLQKGF-PFPE
520      530      540      550      560

      490      500      510      520      530      540
Cry1Ac --GSVISGPGFTGGDLVRLNSSGNN---IQNRGYIEVPIHFPSTSTRYRVRVRYASV--T
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 KYGSEYNNRGIS---LVREWINGNNAVKLSNSQSVGIQIT-NQTKQKYEIRCRYASKGDN
570      580      590      600      610      620

      550      560      570      580      590
Cry1Ac PIHLNVNWNSSIFSNTVP--ATATSLDNLQSSDFGY-FESANAFTSSLGNL-VGVRNFS
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 NVYFNVLDLSENP-FRNSISFGSTESSVVGQGENGYILKSIITVEIPAGSFYVHITN-Q
630      640      650      660      670      680

      600      610      620
Cry1Ac GTAGVIIDRFEFIP-----VTATLEAEYN-----
: : . . . . . : : . . . . . : : . . . . .
gi|128 GSSDLFLDRIEFVPKIQFQCDNNNLHDCDCNNPVDTDCTFCVCTSLTDCDCNNRPLGLDC
690      700      710      720      730      740

      630      640      650      660
Cry1Ac -----LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
: : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 TLCCQVENQLPSFVTLTDLQNIITQVNALVASSEHDTLATDVSDYIEIEVVLKVDALSSE
750      760      770      780      790      800

      670      680      690      700      710      720
Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGGSTGITIQGGDDVFKEN
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 VFGKEKALRKLNVNHTKRLSKARNLLIGGNFDNLD---AWYRGRNVVNVSDHELFPKSD
810      820      830      840      850

      730      740      750      760      770      780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKILKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 HVLLPP--PTLYSSYMFQKVEESKILKANTRYTVSGFIAHAEDLELVVSRYGQEVKVVQV
860      870      880      890      900      910

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      790      800      810      820      830      840
Cry1Ac PGTGSLWPLSAQSPIGKCEPNRCAPHEWNPDLDCSCRDGEKCAHSHHFLSLDIDVCGT
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 P-YGEAFPLTSRGAI--C-----CPPR-----STSNKPA--DPHFFYSYSDVGTL
      920      930      940      950

      850      860      870      880      890      900
Cry1Ac DLNEDLGVNVVIFKIKTQDGHARLGNLEFLLEEKPLVGEALARVKRAEKKWRDKRELEWET
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 DVEANPGIELGLRIVERTGMARVSNLEIREDRPLKKNELRNVRQRAARNWRTAYDQRAEV
960      970      980      990      1000      1010

      910      920      930      940      950
Cry1Ac NIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPEL-----SV
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 TALIQPVLNQINALYENE-----DWNGAIRSGVS--YHDLEAIVLPTLPKLNHFMSD
1020      1030      1040      1050      1060

      960      970      980      990      1000      1010
Cry1Ac IPGVNAAIFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHVDVEEQNNQRSLV
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 MLGEEQSILAQFQALDRAYTQLEESTILHNGHFTTDAANWTIEGDAHHAILEDGRRVLR
1070      1080      1090      1100      1110      1120

      1020      1030      1040      1050      1060
Cry1Ac VPEWEAEVSEQEVRVC---PGRGYILRVTAAYKEGYGEGCVTIHEIENN---TDELKFSNC
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 LPDWSSSVSQTTEIENFDPDKEYQLVFHAQ---GEGTVSLQHGEEGEYVETHPHKSANF
1130      1140      1150      1160      1170      1180

      1070      1080      1090      1100      1110      1120
Cry1Ac VEEIIPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPVSPADYASVYEEKSYTDGRREN
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|128 TTSH-RQGVTFETNKVTVTEITSEDGEFLVDHIALVEAP-LPTDDQSSDGNNTSNTNSNTS
1190      1200      1210      1220      1230      1240

      1130      1140      1150      1160      1170      1180
Cry1Ac PCEFNRGRYDYTPLVGVYTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|128 MNNNQ

>>gi|2096266|gb|AAB55098.1| Sequence 8 from patent US 56 (1245 aa)
initn: 537 initl: 178 opt: 293 Z-score: 334.0 bits: 73.9 E(): 1.1e-09
Smith-Waterman score: 725; 24.013% identity (52.303% similar) in 1216 aa overlap
(43-1113:71-1226)

      20      30      40      50      60
Cry1Ac ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGA---GFVLGLVDII
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|209 EWGKTGQKQLFDEHDLTIAWNLYKTGKLDYFALTKASISLIGFIPGAEAAVPPINMFVDFV
      50      60      70      80      90      100

      70      80      90      100      110
Cry1Ac WG-IFGPSQ-----WDAFLVQIEQLINQRIEEF---ARNQAIISRLEGLSNLYQ-----
: : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . . : : . . . . .
gi|209 WPKLFGANTEGKQQQLFNAIMDAVNKMVDNKFSLSYNLSTLNKTIIEGLQGNLGLFQNAIQV
110      120      130      140      150      160

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          120          130          140          150
Cry1Ac -IYAESFRE----WEADPTNPAL--REEM-RI--QFNDMNSALTTAIPLF-----A
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 AICQGSTPERVNFQDQCTPCPNPQCKDDLDRVASRFDTANSQFTQHLEPEFKNPWSDENS
          170          180          190          200          210          220

          160          170          180          190          200
Cry1Ac VQNYQ---VPL-LSVYVQAANLHLSVLRDVSVFGQWGF-DAATINSRYNDLTRLIGNYT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 TQEFKRTSVELTLPMTTAVTLHLLLYEGYIEFMTKWNFHNEQYLNLLKVELQQLIHSYS
          230          240          250          260          270          280

          210          220          230          240          250          260
Cry1Ac DHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 ETVRTSFLQFLPTLNNRSKSSVNAVYRVRNMTVNCLEIAATWPTFDTHNYHQGGKLDLT
          290          300          310          320          330          340

          270          280          290          300          310          320
Cry1Ac REIYTN--PVLENFDGSRGSAQIEGSIKSPH-LMDILNSITTYTDAHRGEYWSG--
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 RIILSDTAGPIEEYTTGD---KTSQPEHSNITPNNILDTPSPYQHSFVSVDSIVYSRKE
          350          360          370          380          390

          330          340          350          360          370
Cry1Ac -HQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL----YRRPFNI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 LQQLDIATYSTNNSNCHP-YGLRLSYTDGSRDYGDNPDPFTTSNNNYCHNSYTAIPITL
          400          410          420          430          440          450

          380          390          400          410          420          430
Cry1Ac GINNQQLSVLDGTEFAYGTSSNLPSAVYRKSQTV--DS-LDEI-PPQN--NNVPPRQGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 -VNARHLYNAKGS--LQNVESLVVSTVNGGSGSCICDAWINYLRRPQTSKNESRPDQKIN
          460          470          480          490          500          510

          440          450          460          470          480
Cry1Ac HRLSHVSMFRSFGSNSSVSIIRAPMFSWIHRSAEFNNIIAS-DSITQIP--AVKGNFLFN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 -VLYPITETVNGTGGNLGIVISA---YVPMELVPENVIGDYNADTKLPLTLQKLG-PPFE
          520          530          540          550          560

          490          500          510          520          530          540
Cry1Ac --GSVISGPGFTGGDLVRLNSSGNN---IQNRGYIEVPIHFPSTSTRYRVRVRYASV--T
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 KYGSEYNNRGIS---LVREWINGNNAVKLSNSQSVGIQIT-NQTKQKYEIRCRYASKGDN
          570          580          590          600          610          620

          550          560          570          580          590
Cry1Ac PIHLNVNNGNSSIFSNTVP--ATATSLDNLQSSDFGY-FESANAFTSSLGNI-VGVRNFS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 NVYFNVDLSENP-FRNSISFGSTESSVVGQGENGYILKSITTVIIPAGSFYVHITN-Q
          630          640          650          660          670          680

          600          610          620
Cry1Ac GTAGVIIDRFEFIP-----VTATLEAEYN-----
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 GSSDLFLDRIEFVPKIQFQCDNNLHCDNPNVDTDCCTFCCVCTSLTDCCDNNPRGLDC

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          690          700          710          720          730          740
Cry1Ac -----LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 TLCCQVENQLPSFVTLTDLQNITTQVNALVASSEHDTLATDVSDBEIEEVVLKVDALSGE
          750          760          770          780          790          800

          670          680          690          700          710          720
Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKEN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 VFGKEKALRKLWNHTKRLSKARNLLIGGNFDNLD----AWYRGRNVNVSDHDLFKSD
          810          820          830          840          850

          730          740          750          760          770          780
Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 HVLLPP--PTLYSSYMFQKVEESKLANTRYTVSGFIAHAEDLEIVVSRYGQEVKVVQV
          860          870          880          890          900          910

          790          800          810          820          830          840
Cry1Ac PGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDVGCT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 P-YGEAFPLTSRGAI--C-----CPPR-----STSNKPA--DPHFFSYSIDVGTL
          920          930          940          950

          850          860          870          880          890          900
Cry1Ac DLNEDLGWVVIKIKTQDGHARLGNLEFLKPLVGEALARVKRAEKWRDKREKLEWET
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 DVEANPGIELGLRIVERTGMARVSNLEIREDRPLKKNELRNVRARNWRTAYDQERAEV
          960          970          980          990          1000          1010

          910          920          930          940          950
Cry1Ac NIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAAKRVHSIREAYLPEL-----SV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 TALIQVVLNQINALYENE-----DWNGAIRSGVS--YHDLAIVLPTLPKLNHWFMDS
          1020          1030          1040          1050          1060

          960          970          980          990          1000          1010
Cry1Ac IPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVEEQNNQRSVLV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 MLGEEQSILAQFQALDRAYTQLEESTILHNGHFTTDAANWTIEGDAHHAILEDGRRVLR
          1070          1080          1090          1100          1110          1120

          1020          1030          1040          1050          1060
Cry1Ac VPWEAEVSVQEVRC---PGRGYILRVYAYKEGYGECVTIHEIENN---TDELKFSNC
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 LPDWSSSVSQTIEIENFDPDKEYQLVFHAQ---GEGTVSLQHGEGEYVETHPHKSNANF
          1130          1140          1150          1160          1170          1180

          1070          1080          1090          1100          1110          1120
Cry1Ac VEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNAPSVPADYASVYEEKSYTDGRRN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|209 TTSH-RQGVTFETNKVTVETSEDGEFLVDHIALVEAP-LPTDDQSSDGNTTNTSNTS
          1190          1200          1210          1220          1230          1240

          1130          1140          1150          1160          1170          1180
Cry1Ac PCFENRGRDYTPLPVGVYVKELEYFPETDKVWIEIGETEGTFIVDSVELLMEE

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gi|597 MLGEGQSILAQFQAEALDRAYTQLEESTILHNGHFTTDAANWTIEGDAHHAILEDGRRVLR
1070 1080 1090 1100 1110 1120

Cry1Ac VPWEAEVSQEVRC---PGRGYILRVTAKEGYGEGCVTIHEIENN---TDELKFSNC
1020 1030 1040 1050 1060

gi|597 LPDWSSSVSQTIEIENFDPKEYQLVFHAQ---GEGTVSLQHGEEGEYVETHPHKSAF
1130 1140 1150 1160 1170 1180

Cry1Ac VEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYTDGRREN
1070 1080 1090 1100 1110 1120

gi|597 TTSH-RQGVTFETNKVTVETSEDGEFLVDHIALVEAP-LPTDDQSSDGNNTSNTSNTS
1190 1200 1210 1220 1230 1240

Cry1Ac PCEFNRGVRDYTPLPVGVVTKLEYFPETDKVWIEIGTEGTFIVDSVELLMEE
1130 1140 1150 1160 1170 1180

gi|597 MNNNQ

>>gi|862637|gb|AAA68598.1| delta endotoxin (1245 aa)
initn: 537 init1: 178 opt: 293 Z-score: 334.0 bits: 73.9 E(): 1.1e-09
Smith-Waterman score: 725; 24.013% identity (52.303% similar) in 1216 aa overlap
(43-1113:71-1226)

Cry1Ac ECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGA---GFVLGLVDII
20 30 40 50 60
gi|862 EWGKTGQKLFEDHLTIWANLYKTKGLDYFALTKASISLIGFIPGAEAAVFPINMFVDFV
50 60 70 80 90 100

Cry1Ac WG-IFGPSQ-----WDAFLVQIEQLINQRIEEF---ARNQAISRLEGLSNLYQ-----
70 80 90 100 110
gi|862 WPKLFGANTEGKQQFLFNAIMDAVNKMDNKFLSYNLSTLNKTIIEGLQGNLGLFQNAIQV
110 120 130 140 150 160

Cry1Ac -IYAESFRE----WEADPTNPAL--REEM-RI--QFNDMNSALTTAIPLF-----A
120 130 140 150
gi|862 AICQGSTPERVNFQNCPTCPNPNQCKDDLDRVASRFDTANSQFTQHLPEFKNPWSDENS
170 180 190 200 210 220

Cry1Ac VQNYQ---VPL-LSVYVQAANLHLSVLRDVSFQGRWGF-DAATINSRYNDLTRLIGNYT
160 170 180 190 200
gi|862 TQEFKRTSVELTLPMTTAVATLHLLLYEGYIEFMTKWNFNHNEQYLLNNLKVLELQQLIHSYS
230 240 250 260 270 280

Cry1Ac DHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLT
210 220 230 240 250 260
gi|862 ETVRTSFLQFLPTLNNRSKSSVNAYNRYVRNMTVNCLDIAATWPTFDTHNYHQGGKLDLT
290 300 310 320 330 340

Cry1Ac REIYTN---PVLNFDGSGFRGSAQGIIEGSIIRSPH-LMDILNSITITYDAHRGEYWSG--
270 280 290 300 310 320

gi|862 RIILSDTAGPIEEYTTGD--KTSQPEHSNITPNNILDTPSPTYQHSFVSVDSIVYSRKE
350 360 370 380 390

Cry1Ac -HQIMASPVGFGSGPEFTFPPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTL----YRRFPNI
330 340 350 360 370

gi|862 LQQLDIATYSTNNSNCHP-YGLRLSYTDGSRDYGDNPDPFTTNNNCHNSYTAIPITL
400 410 420 430 440 450

Cry1Ac GINNQLSVLDGTEFAFGTSSNLPNAVYRKSGTV--DS-LDEI-PPQN--NNVPRQGF
380 390 400 410 420 430

gi|862 -VNARHLYNAKGS--LQNVESLVVSTVNGGSGSCICDANINYLRRPQTSKNESRPDQKIN
460 470 480 490 500 510

Cry1Ac HRLSHVSMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIAS-DSITQIP--AVKGNFLFN
440 450 460 470 480

gi|862 -VLYPITETVKNKGTGGNLGVIISA---YVPMELVPENVIGDYNADTKLPLTLQKGF-PPFE
520 530 540 550 560

Cry1Ac --GSVISGPGFTGGDLVRLNSSGNN---IQNRGYIEVPIHFPSTSTRYRVRVRYASV--T
490 500 510 520 530 540

gi|862 KYGSEYNNRGIS---LVREWINGNNAVKLSNSQSVGIQIT-NQTKQKYEIRCRYASKGDN
570 580 590 600 610 620

Cry1Ac PIHLNWNWGNSSIFSNITVP--ATATSLDNLQSSDFGY-FESANAFSTSSLGNI-VGVRNFS
550 560 570 580 590

gi|862 NVYFNVDLSENP-FRNSISFGSTESSVVGQGENGKYILKSITTVIIPAGSFVYHITN-Q
630 640 650 660 670 680

Cry1Ac GTAGVIIDRFEPFIP-----VTATLEAEYN-----
600 610 620

gi|862 GSSDLFLDRIEFVPKIQFQCDNNLHCDCCNNPVDTDCTFCVCTSLTDCDCNNPRGLDC
690 700 710 720 730 740

Cry1Ac -----LERAQKAVNALFTSTNQLGLKTNVDYHIDQVSNLVTYLSDE
630 640 650 660

gi|862 TLCCQVENQLPSFVTLTLQNIITQVNALVASSEHDTLATDVSVDYIEEVVLKVDALSGE
750 760 770 780 790 800

Cry1Ac FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGTGITIQGGDVFKEN
670 680 690 700 710 720

gi|862 VFGKEKALRKLNVNHTKRLSKARNLLIGGNFDNLD----AWYRGRNVNVSDHELKFS
810 820 830 840 850

Cry1Ac YVTLSGTFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HETVNV
730 740 750 760 770 780

gi|862 HVLLPP--PTLYSSYMFQKVEESKLANTRYTVSGFIAHAEDLEIVVSRYGQEVKVVQV
860 870 880 890 900 910

Cry1Ac

gi|862

790 800 810 820 830 840

Cry1Ac PGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSLDIDVVGCT

gi|862 P-YGEAFPLTSRGAII--C-----CPPR-----STNSGKPA--DPHFFSYSLDVGTL

Cry1Ac DLNEDLGVVWVIFKIKTQDGHARLGNLEFLFLEEKPLVGEALARVKRAEKKWRDKREKLEWET

gi|862 DVEANPGIELGLRIVERVTGMARVSNLEIREDRPLKKNELRNVRARARNWRTAYDQERAEV

Cry1Ac NIVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPEL-----SV

gi|862 TALIQPVLNQLNALYENE-----DWNGAIRSGVS--YHDLAIVLPTLPKLNHWFMMSD

Cry1Ac IPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDFVEEQNNQSRVSVL

gi|862 MLGEGSILAQFQEALDRAYTQLEESTILHNGHFTDAANWTIEGDAHHAILEDGRRVLR

Cry1Ac VPEWEAEVSQEVVRC---PGRGYILRVYAYKEGYGEGCVTIHEIENN---TDELKFSNC

gi|862 LPDWSSSVSQTIEIENFDPKKEYQLVFHAQ---GEGTVSLQHGEEGEYVETHPHKSAF

Cry1Ac VEEIYPNNTVTCNDYTVNQEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYTDGRREN

gi|862 TTSH-RQGVTFETNKVTVEITSEDEGFLVDHIALVEAP-LPTDDQSSDGNSTNTSNTS

Cry1Ac PCEFNRGRYRDYTPLPVGYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLLMEE

gi|862 MNNNQ

>>gi|152013915|gb|ABS20064.1| dipterans toxic crystal pr (118 aa)
initn: 264 init1: 180 opt: 272 Z-score: 324.5 bits: 68.7 E(): 3.8e-09
Smith-Waterman score: 272; 44.828% identity (68.103% similar) in 116 aa overlap
(934-1048:2-116)

Cry1Ac IVYKEAKESVDALFVNSQYDQLQADTNIAMIHAADKRVHSIREAYLPELSVIPGVNAAIF

gi|152 HILNADRLVQSIPIVYHAWLPDAPGMNYDLY

Cry1Ac EELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDFVEEQNNQSRVSVLVPWEAEVS

gi|152 NNLKVRIEQARYFYDARNVITNGDFTQGLQEWHTGKAAVQ-QMDGASVVLVLSNWSAGVS

Cry1Ac EEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGHVDFVEEQNNQSRVSVLVPWEAEVS

Cry1Ac QEVVPCPRGRYILRVYAYKEGY-GEGCVTIHEIENNTDELKFSNCVEEIEYPNNTVTCND

gi|152 QNLHVQDHHGYLVRVIAKKGRYLGHGY

>>gi|9622198|gb|AAF89667.1|AF169250\_2 parasporal crystal (675 aa)
initn: 127 init1: 81 opt: 281 Z-score: 323.8 bits: 71.1 E(): 4.1e-09
Smith-Waterman score: 281; 23.720% identity (57.682% similar) in 371 aa overlap
(60-414:101-456)

Cry1Ac GERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGIWFGPSQWDAFLVQIEQLIN

gi|962 ENSPFLTAPIVGVVSTLLEALKKQVSRLLMLTNLFPNNSTSMTEEILRATQYVQ

Cry1Ac QRIEEFARNQAISSRLEGLSNLYQIYAESFREW----EADPTNPALREEMRIQFNDMNSA

gi|962 EQLDVTWNRVSQLLEGLKNNLRFNDQIDDFLQNRVEISPTA-----MIDSINTMQQV

Cry1Ac LTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLI

gi|962 FVNRLPQFQLSDYQLLLPLFAQGATLHLTFIRDIIINAGEWNIPEAQLNTCKRYLKQYV

Cry1Ac GNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLFFPNYSRTPYRIVT

gi|962 AQYSNYALSTYEGAFRFRFYPRAT-LENMLQFKTFMTLNVDLVSIVSLKMYNLYISTS

Cry1Ac SQLTREIYNPVLNFDGSRFGSAQIEGSI---RSPHLMILNSITI---YTDHRGEY

gi|962 ANL-YNIGDNKVNE---GEYSISYWPFFNSYIQTKSNYVLSGVSGYAIRWYYLNTFFGEY

Cry1Ac YWSG-HQIMASVPG-FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLSTLYRRPFP

gi|962 IQDNLNIIASVYGVGNGPKIGVQLSTTELDKQIKQARAGMPTGLDLSFNCTLRNPTT

Cry1Ac I---GINNQSLVDLGTGEFAYGTSSNLPSAVYRKSQVSDLSLDEIPPQNNVPPRQGFVSHR

gi|962 VPFACNFQBELTS-SGTA---GTGGFIRSDVFRSEDNICGLGTGYASAWTSYDPYYITNI

Cry1Ac LSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS

gi|962 SATVQVDGINIDITPLCFGEDRAITSTHGKVIIVYRNRKANIAGTQNGTMIHQAPNDG

>>gi|155097716|gb|ABT00647.1| Sequence 261 from patent U (632 aa)

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initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09
Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap
(45-595:56-599)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIWGIF
gi|155 FEHKSLDTIRKEWMEKRTDHSLYVAPIVGTVSSFLKK---VGSLLGKRILSELWGLI

Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
gi|155 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELEGLOANIREFNQVQDNF-LNPQTQN

Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVSFVFGQRWGF
gi|155 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLSFIRDVVLNADEWGI

Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
gi|155 SAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFE

Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRFGSAQGIIEGSIKSPHLMIDILNS
gi|155 YVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNG

Cry1Ac IT-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|155 FSGARLTQTFPNIIGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLT

Cry1Ac GVYRT-LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPP
gi|155 PFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPL

Cry1Ac QNNVPPRQGFVSHRSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIIASDSITQI
gi|155 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS-VHNRK--NNIYAVHE----

Cry1Ac PAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPTSTT
gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQNST

530 540 550 560 570 580

Cry1Ac RYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
gi|155 TARYTLRGNGNSYNYLRLVSSLGNSTIRVTINGRVYTAASNVTNTTND-GVNDNGARFLD

Cry1Ac -SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|155 INMGNVVASDNTNVPLDINVTNFSGTQFELMNMIFVPTNLPPIY

>>gi|112088020|gb|ABI06943.1| Sequence 2 from patent US (632 aa)
initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09
Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap
(45-595:56-599)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIWGIF
gi|112 FEHKSLDTIRKEWMEKRTDHSLYVAPIVGTVSSFLKK---VGSLLGKRILSELWGLI

Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
gi|112 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELEGLOANIREFNQVQDNF-LNPQTQN

Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHLSVLRDVSFVFGQRWGF
gi|112 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLSFIRDVVLNADEWGI

Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
gi|112 SAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFE

Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSRFGSAQGIIEGSIKSPHLMIDILNS
gi|112 YVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNG

Cry1Ac IT-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|112 FSGARLTQTFPNIIGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLT

Cry1Ac GVYRT-LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEIPP
gi|112 PFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPL

420 430 440 450 460 470

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Cry1Ac QNNNVPPRQGFSHRLSHVSMFRSGFSSSV--SIIRAPMFSWIHRSAEFNIIASDSITQI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS--VHNK--NIIYAVHE----
      440          450          460          470

      480          490          500          510          520
Cry1Ac PAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPTST
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNT
      480          490          500          510          520

      530          540          550          560          570          580
Cry1Ac RYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 TARYTLRGNGNSYNLYLRVSSSLGNSTIRVTINGRVYTASNVTNTTND--GVNDNGARFLD
      530          540          550          560          570          580

      590          600          610          620          630          640
Cry1Ac -SLGNIVGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112 INMGNVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPIY
      590          600          610          620          630

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>>gi|158478173|gb|ABW49930.1| Sequence 2 from patent US (632 aa)  
 initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09  
 Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap  
 (45-595:56-599)

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      20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FEHKS LDTIRKEWMEWKRTDHS LYVAPIVGTVSSFLKK---VGLIGKRILSELWGLI
      30          40          50          60          70          80

      80          90          100         110         120
Cry1Ac GPSQWDAFLVQI----EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FPSGSTNMQDILRETEQFLNQLRLNTDTLARVNAELEGLOANIREFNQVQVDF--LNPTQN
      90          100         110         120         130         140

      130         140         150         160         170         180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLFSFIRDVVLNADEWGI
      150         160         170         180         190         200

      190         200         210         220         230         240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 SAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR---GLNTRLHDM---EFRTYMPFLNVFE
      210         220         230         240         250

      250         260         270         280         290         300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSRPHLMDILNS
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 YVSIWLSLFKYQLLVSSGANL----YASGSGPQQTQSPTSQDWPFLYSLFQVNSNYVLMG
      260         270         280         290         300         310

      310         320         330         340         350         360

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Cry1Ac IT-----IYTAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FSGARLTQTFPNIIGLPGTTTTALLAARVNYSGGVSSGDIGAVFNQFSCSTFLPPLLT
      320          330          340          350          360          370

      370          380          390          400          410
Cry1Ac GVYRT--LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCAFTARGNSNYFPDYFIRNISGVPL
      380          390          400          410          420          430

      420          430          440          450          460          470
Cry1Ac QNNNVPPRQGFSHRLSHVSMFRSGFSSSV--SIIRAPMFSWIHRSAEFNIIASDSITQI
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS--VHNK--NIIYAVHE----
      440          450          460          470

      480          490          500          510          520
Cry1Ac PAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPTST
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNT
      480          490          500          510          520

      530          540          550          560          570          580
Cry1Ac RYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 TARYTLRGNGNSYNLYLRVSSSLGNSTIRVTINGRVYTASNVTNTTND--GVNDNGARFLD
      530          540          550          560          570          580

      590          600          610          620          630          640
Cry1Ac -SLGNIVGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 INMGNVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPIY
      590          600          610          620          630

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>>gi|155718050|gb|ABU37566.1| Sequence 2 from patent US (632 aa)  
 initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09  
 Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap  
 (45-595:56-599)

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      20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 FEHKS LDTIRKEWMEWKRTDHS LYVAPIVGTVSSFLKK---VGLIGKRILSELWGLI
      30          40          50          60          70          80

      80          90          100         110         120
Cry1Ac GPSQWDAFLVQI----EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 FPSGSTNMQDILRETEQFLNQLRLNTDTLARVNAELEGLOANIREFNQVQVDF--LNPTQN
      90          100         110         120         130         140

      130         140         150         160         170         180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLFSFIRDVVLNADEWGI
      150         160         170         180         190         200

      190         200         210         220         230         240

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Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTTLTVLD
gi|155 SAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR---GLNTRLHDML---EFRYTMFLNVFE
210 220 230 240 250

Cry1Ac 250 260 270 280 290 300
IVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIIRSPHLMIDILNS
gi|155 YVSIWLSLFKYQLLVSSGANL----YASGSGPQQTQSFQSDWPFLYSLFQVNSNYVLNG
260 270 280 290 300 310

Cry1Ac 310 320 330 340 350 360
IT-----IYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|155 FSGARLTQTFPNIGGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLT
320 330 340 350 360 370

Cry1Ac 370 380 390 400 410
GVYRT-LSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPP
gi|155 PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAFRTARGNSNYFPDYFIRNISGVPL
380 390 400 410 420 430

Cry1Ac 420 430 440 450 460 470
QNNNVPPRQGFHSHRSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQI
gi|155 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS-VHNRK--NNIYAVHE----
440 450 460 470

Cry1Ac 480 490 500 510 520
PAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPTST
gi|155 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQRTTFISEKFGNQGDSLRFEQSNT
480 490 500 510 520

Cry1Ac 530 540 550 560 570 580
RYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
gi|155 TARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTAGSNVNTTTNND-GVNDNGARFLD
530 540 550 560 570 580

Cry1Ac 590 600 610 620 630 640
-SLGNIVGVRNFGSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|155 INMGNVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPYI
590 600 610 620 630

>>gi|33765711|gb|AAQ52362.1| Sequence 2 from patent US 6 (632 aa)
initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09
Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap
(45-595:56-599)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGI
gi|337 FEHKSOLDTIRKEWMEWKRTDHSYLVAPIVGTVSSFLKK---VGSLLGKRIKRLSELWGLI
30 40 50 60 70 80
80 90 100 110 120

Cry1Ac GPSQWDAFLVQI----EQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP
gi|337 FPSGSTNLMDILRETEQFLNQLRNTDTLARVNAELEGLOANIREFNPQQVDNF-LNPTQN
90 100 110 120 130 140

Cry1Ac 130 140 150 160 170 180
ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
gi|337 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQANMHLFSIRDVVLNADEWGI
150 160 170 180 190 200

Cry1Ac 190 200 210 220 230 240
DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTTLTVLD
gi|337 SAATLRTYQNYLKNYTTTEYSNYCINTYQTAFR---GLNTRLHDML---EFRYTMFLNVFE
210 220 230 240 250

Cry1Ac 250 260 270 280 290 300
IVSLFPNYDSRTPYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIIRSPHLMIDILNS
gi|337 YVSIWLSLFKYQLLVSSGANL----YASGSGPQQTQSFQSDWPFLYSLFQVNSNYVLNG
260 270 280 290 300 310

Cry1Ac 310 320 330 340 350 360
IT-----IYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPPLYGTMGNAAPQQRIVAQLGQ
gi|337 FSGARLTQTFPNIGGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLT
320 330 340 350 360 370

Cry1Ac 370 380 390 400 410
GVYRT-LSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSSAVYRKSGETVDSLDEIPP
gi|337 PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAFRTARGNSNYFPDYFIRNISGVPL
380 390 400 410 420 430

Cry1Ac 420 430 440 450 460 470
QNNNVPPRQGFHSHRSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQI
gi|337 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS-VHNRK--NNIYAVHE----
440 450 460 470

Cry1Ac 480 490 500 510 520
PAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPTST
gi|337 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQRTTFISEKFGNQGDSLRFEQSNT
480 490 500 510 520

Cry1Ac 530 540 550 560 570 580
RYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
gi|337 TARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTAGSNVNTTTNND-GVNDNGARFLD
530 540 550 560 570 580

Cry1Ac 590 600 610 620 630 640
-SLGNIVGVRNFGSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|337 INMGNVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPYI
590 600 610 620 630

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>>gi|13537893|emb|CAC35761.1| unnamed protein product [B (632 aa)
initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09
Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap
(45-595:56-599)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDI IWGIF
gi|135 FEHKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFLKK---VGS LIGKRILSELWGLI
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
gi|135 FPGSGTNLMQDILRETEQFLNQLRNTDTLARVNAELEGQA NIREFNQQVDNF-LNPTQN
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGF
gi|135 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHL SFIRDVVLNADEWGI
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRY NQFRRELTLTVLD
gi|135 SAATLRTYQNYLKNYTTEYSNYCINTYQTAFR---GLNTRLHDML ---EFRTYMF LNVPFE
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHLM DILNS
gi|135 YVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFL YSLFQVNSNYV LNG
260 270 280 290 300 310

310 320 330 340 350 360
Cry1Ac IT-----IYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQ
gi|135 FSGARLTQTFPNIGGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLT
320 330 340 350 360 370

370 380 390 400 410
Cry1Ac GVYRT-LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPP
gi|135 PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAF TARGNSNYFPDYFIRNISGVPL
380 390 400 410 420 430

420 430 440 450 460 470
Cry1Ac QNNVPPRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRS AEFNNIIASDSITQI
gi|135 VVRNEDLRRPL----HYNEIRNIESPSGTPGGLRAYMVS-VHNRK-- NNIYAVHE----
440 450 460 470

480 490 500 510 520
Cry1Ac PAVKGNLFLNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP----- IHFPSTST
gi|135 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGD SLRFEQSNT
480 490 500 510 520

530 540 550 560 570 580
Cry1Ac RYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFG YFESANAFTS
gi|135 TARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTASNVNTTTNND -GVNDNGARFLD
530 540 550 560 570 580

590 600 610 620 630 640
Cry1Ac -SLGNIVGVRNFSGTAGVIDRFEFIPVTTATLEAEYNLERAQKAVNALFT STNQGLKTN
gi|135 INMGNVVASDNTNVPLDINVTFNSGTQFELMNMIFVPTNLPP IY
590 600 610 620 630

>>gi|23559624|emb|CAD52947.1| unnamed protein product [B (632 aa)
initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09
Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap
(45-595:56-599)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDI IWGIF
gi|235 FEHKSLDITIRKEWMEWKRTDHSLYVAPIVGTVSSFLKK---VGS LIGKRILSELWGLI
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAES FREWEADPTNP
gi|235 FPGSGTNLMQDILRETEQFLNQLRNTDTLARVNAELEGQA NIREFNQQVDNF-LNPTQN
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV LR DVS VFGQRWGF
gi|235 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHL SFIRDVVLNADEWGI
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRY NQFRRELTLTVLD
gi|235 SAATLRTYQNYLKNYTTEYSNYCINTYQTAFR---GLNTRLHDML ---EFRTYMF LNVPFE
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGI EGSIRSPHLM DILNS
gi|235 YVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFL YSLFQVNSNYV LNG
260 270 280 290 300 310

310 320 330 340 350 360
Cry1Ac IT-----IYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIV AQLGQ
gi|235 FSGARLTQTFPNIGGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLT
320 330 340 350 360 370

370 380 390 400 410
Cry1Ac GVYRT-LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIPP
gi|235 PFVRSWLDSGSDRGVNTVTNWQTESFESTLGLRCGAF TARGNSNYFPDYFIRNISGVPL
380 390 400 410 420 430

Regulatory Product Characterization Team

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420      430      440      450      460      470
Cry1Ac QNNNVPPRQGFHSHLHVSMFRSGFSNSV--SIIRAPMFSWIHRSAEFNIIASDSITQI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|235 VVRNEDLRRPL-----HYNEIRNIESPSGTPGGLRAYMVS--VHNRK--NNIYAVHE----
      440      450      460      470

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480      490      500      510      520
Cry1Ac PAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPSTST
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|235 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNT
      480      490      500      510      520

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530      540      550      560      570      580
Cry1Ac RYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|235 TARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTND--GVNDNGARFLD
      530      540      550      560      570      580

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590      600      610      620      630      640
Cry1Ac -SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|235 INMGNVVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPYI
      590      600      610      620      630

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>>gi|155718053|gb|ABU37569.1| Sequence 8 from patent US (633 aa)  
 initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09  
 Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap  
 (45-595:57-600)

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20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 FEHKS LDTIRKEWMEWKRTDHS LYVAPIVGTVSSFLKK---VGS LIGKRILSELWGLI
      30      40      50      60      70      80

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80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELEGQANIREFNQVDNF--LNPTQN
      90      100      110      120      130      140

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130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLSFIRDVVLNADDEWGI
      150      160      170      180      190      200

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190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 SAATLRTYQNYLKNYTTSEYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMPFLNVFE
      210      220      230      240      250

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250      260      270      280      290      300
Cry1Ac IVSLFPNYDSRTPYIRTVSQTREIYTNVLENFDGSRFGSAQGIIEGSIIRSPHMLDILNS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 YVSIWLSLFKYQSLLVSSGANL----YASGSGPQQTSFTSQDWPFLYLSLFQVNSNYVLNG
      260      270      280      290      300      310

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310      320      330      340      350      360
Cry1Ac IT-----IYTAHRRGEYWSGHQIMASVGVFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 FSGARLTQTTFPNIGGLPGTTTTALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLT
      320      330      340      350      360      370

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370      380      390      400      410
Cry1Ac GVYRT--LSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 PFVRSWLDGSDRGGVNTVTNWQTESFESTLGLRCGAFTARGNSNYFPDYFIRNISGVPL
      380      390      400      410      420      430

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420      430      440      450      460      470
Cry1Ac QNNNVPPRQGFHSHLHVSMFRSGFSNSV--SIIRAPMFSWIHRSAEFNIIASDSITQI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 VVRNEDLRRPL-----HYNEIRNIESPSGTPGGLRAYMVS--VHNRK--NNIYAVHE----
      440      450      460      470

```

```

480      490      500      510      520
Cry1Ac PAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPSTST
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSNT
      480      490      500      510      520      530

```

```

530      540      550      560      570      580
Cry1Ac RYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 TARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTASNVTNTTND--GVNDNGARFLD
      540      550      560      570      580

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590      600      610      620      630      640
Cry1Ac -SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 INMGNVVASDNTNVPLDINVTFNSTQFELMNMIFVPTNLPPYI
      590      600      610      620      630

```

>>gi|158478176|gb|ABW49933.1| Sequence 8 from patent US (633 aa)  
 initn: 222 init1: 177 opt: 276 Z-score: 318.3 bits: 70.0 E(): 8.2e-09  
 Smith-Waterman score: 286; 22.203% identity (52.840% similar) in 581 aa overlap  
 (45-595:57-600)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FEHKS LDTIRKEWMEWKRTDHS LYVAPIVGTVSSFLKK---VGS LIGKRILSELWGLI
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELEGQANIREFNQVDNF--LNPTQN
      90      100      110      120      130      140

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130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|158 PVPLSITSSVNTMQQLFLNRLPQFRVQGYQLLLLPLFAQAANMHLSFIRDVVLNADDEWGI
      150      160      170      180      190      200

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410      420      430      440      450      460
Cry1Ac  SGTVDLSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFNSSSV-SIIRAPMFSWIHRSAEF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112  ----NISGVPLVIRN---EDLTRPL-HYNQIRNIESPSGTPGGLRAYMVS-VHNRK--
      430      440      450      460      470

```

```

470      480      490      500      510      520
Cry1Ac  NNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP---
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112  NNIIAAHE-----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGN
      480      490      500      510      520

```

```

530      540      550      560      570
Cry1Ac  ---IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112  QGDSLRFEQSNNTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTNND
      530      540      550      560      570      580

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```

580      590      600      610      620      630
Cry1Ac  FGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNAL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|112  -GVNDNGARFSDINIGNVVASDNTNVPLDINVTLSNGTQFELMNIMFVPTNLPPPLY
      590      600      610      620      630

```

>>gi|12822553|gb|AAE48994.1| Sequence 4 from patent US 6 (635 aa)  
 initn: 219 init1: 171 opt: 275 Z-score: 317.1 bits: 69.8 E(): 9.6e-09  
 Smith-Waterman score: 282; 23.116% identity (54.606% similar) in 597 aa overlap  
 (45-595:56-602)

```

20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  FEHKSLDTIQEEMWEKRTDHSLYVAPVVGTVSSFLKK---VGSLLGKRILSELWGLI
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac  GPSQWDAFLVQI---EQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  FPSGSTNLMQDILRETEQFLNQLRLNTDTLDRVNAELEGQANIREFNQVDNF-LNPTQN
      90      100      110      120      130      140

```

```

130     140     150     160     170     180
Cry1Ac  ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLFIRDVILNADEWGI
      150     160     170     180     190     200

```

```

190     200     210     220     230     240
Cry1Ac  DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRELTLTVLD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  SAATLRTRYDYLRLNYTRDYSNYCINTYQTAFR---GLNTRLHMDL---EFRTYMFNLVFE
      210     220     230     240     250

```

```

250     260     270     280     290
Cry1Ac  IVSLFPNYDSRITYPIRTVSQLE-----TREIYTN---PVLEN-FDGSFRGSAQGIIEG-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  YVSIWLSLFKYQSLMVSSGANLYASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGN
      260     270     280     290     300     310

```

```

300     310     320     330     340     350
Cry1Ac  --SIRSPHLMIDLNSITIIYT-DAHRGEYVWSGHQIMASPVVGFSGPEFTFPPLYGTMGNAAP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  RLSTTFPNIGGLPGSTTIHSLNSARVNY--SGG-VSSGLIGATNLNHNFNFC-STVLPPLS
      320     330     340     350     360     370

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360     370     380     390     400
Cry1Ac  QQRIVAQLQOGVYR---TLSSLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  TPFVRSWLDSGTDREGVATSTTWQTESFQI-TSGLRCGAFPPS--ARGNSNYFPDYFIR-
      380     390     400     410     420

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410     420     430     440     450     460
Cry1Ac  SGTVDLSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFNSSSV-SIIRAPMFSWIHRSAEF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  ----NISGVPLVIRN---EDLTRPL-HYNQIRNIESPSGTPGGLRAYMVS-VHNRK--
      430     440     450     460     470

```

```

470     480     490     500     510     520
Cry1Ac  NNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP---
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  NNIIAAHE-----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGN
      480     490     500     510     520

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530     540     550     560
Cry1Ac  ---IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSN-----TVPATATSLDNL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  QGDSLRFEQSNNTARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYTPVNVNTNINN-
      530     540     550     560     570

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570     580     590     600     610     620
Cry1Ac  QSSDFGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKA
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|128  ---D-GVIDNGARFSDINIGNVVASDNTNVPLDINGTLSSGTQFELMNIMFVPTNLPPPLY
      580     590     600     610     620     630

```

>>gi|33765733|gb|AAQ52384.1| Sequence 46 from patent US (635 aa)  
 initn: 219 init1: 171 opt: 275 Z-score: 317.1 bits: 69.8 E(): 9.6e-09  
 Smith-Waterman score: 278; 22.934% identity (54.806% similar) in 593 aa overlap  
 (45-595:56-602)

```

20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337  FEHKSLDTIQEEMWEKRTDHSLYVAPVVGTVSSFLKK---VGSLLGKRILSELWGLI
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac  GPSQWDAFLVQI---EQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337  FPSGSTNLMQDILRETEQFLNQLRLNTDTLDRVNAELEGQANIREFNQVDNF-LNPTQN
      90      100      110      120      130      140

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130     140     150     160     170     180
Cry1Ac  ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337  PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLFIRDVILNADEWGI
      150     160     170     180     190     200

```

```

190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 SAATLRTRYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVFE
      210      220      230      240      250

```

```

250      260      270      280      290
Cry1Ac IVSLFPNYDSRTYPIRTVSQLE-----TREIYTN---PVLEN-FDGSFRGSAQGIIEG-
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 YVSIWSLFKYQSLMVSSGANLYASGGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGN
      260      270      280      290      300      310

```

```

300      310      320      330      340      350
Cry1Ac --SIRSPHMLDILNSITTYT-DAHRGEYWSGHQIMASPVGFSGPEFTFFLYGTMGNAAP
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 RLSTTFPNIGGLPGSTTIHSLNSARVNY--SGG-VSSGLIGATNLNHNFNFC-STVLPPLS
      320      330      340      350      360      370

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360      370      380      390      400
Cry1Ac QQRIVVAQLGQGVYR---TSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRK
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 TPFVRSWLDSGTDREGVATSTTWQTESFQI-TSGLRCGAFPPS--ARGNSNYFPDYFIR-
      380      390      400      410      420

```

```

410      420      430      440      450      460
Cry1Ac SGTVDLSLDEIIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 ----NISGVPLVIRN---EDLTRPL-HYNQIRNIESPSGTPGGLRAYMVS-VHNRK--
      430      440      450      460      470

```

```

470      480      490      500      510      520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVPP---
      : : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 NNIYAAHE-----NGTMIHLAPEDYTGTFTISPIHATQVNNQTRTFISEKFGN
      480      490      500      510      520

```

```

530      540      550      560      570
Cry1Ac ----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 QGDSLRFEQSNTTARYTLRGNNGSNLYLRVSSIGNSTIRVTINGRVYTASNVTNTNND
      530      540      550      560      570      580

```

```

580      590      600      610      620      630
Cry1Ac FGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLAEAYNLERAQKAVNAL
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 -GVNDNGARFSDINIGNVVASDNTNVPLDINVTLNSGTQFELMNMIFVPTNLPLLY
      590      600      610      620      630

```

>>gi|5834516|emb|CAA10670.2| Cry2A protein [Bacillus thu (551 aa)  
 initn: 210 init1: 171 opt: 267 Z-score: 308.6 bits: 68.0 E(): 2.9e-08  
 Smith-Waterman score: 267; 25.541% identity (63.203% similar) in 231 aa overlap  
 (45-267:56-275)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|583 FEHKSOLDTIQKEWMEWKRTDHSYVAPVVGTVSSFLKK---VGSLLGKRILSELWGII
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI----EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|583 FPSSSTNLMQDILRETEKFLNQLRLNTDTLARVNAELIGLQANIREFNQVQVDFN-LNPTQN
      90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|583 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|583 SAATLRTRYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVFE
      210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLE-----TREIYTNPVLENFDGSFRGSAQGIIEGSI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|583 YVSIWSLFKYQSLMVSSGANLYASGGPQQTQSFTAQNWPFLYSLFQVNSNYILSGISGT
      260      270      280      290      300      310

```

>>gi|129307220|gb|ABO30519.1| Cry2Af1 [Bacillus thuringi (626 aa)  
 initn: 171 init1: 135 opt: 267 Z-score: 307.8 bits: 68.0 E(): 3.2e-08  
 Smith-Waterman score: 289; 21.837% identity (51.993% similar) in 577 aa overlap  
 (45-595:56-593)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGVDIIWGI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|129 FQHKSLDITQKEWTEWKKNNHLSYVDPIVGTVGSFLLKKVGSLLGKRILSELNLI
      30      40      50      60      70      80

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```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLS---NLYQIYAESFREWEADPTNPA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|129 NTNLMQDILRETEKLLNQLRLNADTLNRVNAELRGLLEANVNEFNQVQVDFN----LNP
      90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|129 VPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|129 AATLRTRYRDHLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVLDY
      210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLE-----TREIYTNPVLENF---DGSFRGSAQGIIEGSI
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|129 VSIWSLFKYQSLMVSSGANL-YACGNSPNTQSFTAQDWPFYSLFQVNSNYILSGISGR
      260      270      280      290      300      310

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310      320      330      340      350      360
Cry1Ac NSITI-YTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQQVY
      . . . . .
gi|129 STITLFPVIGPPFGTT--TTQTLHNARINRGGISS---GLIGSSNLNQNFNIT--PIF
      320      330      340      350      360

370      380      390      400      410      420
Cry1Ac RTLSSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQNN
      . . . . .
gi|129 NPLLTPFIRSWLDSGIDREGLATTNWMGTGPFETIGLRFISFTARGNSNYFPDYFIRNI
      370      380      390      400      410      420

430      440      450      460      470      480
Cry1Ac NVPPRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVK
      . . . . .
gi|129 S-----GVRDLRNLDRKPLHFNEIRNIGTTPVSSLSVHNKRKNNIYAVHE-----
      430      440      450      460      470

490      500      510      520      530
Cry1Ac GNFLFNGSVIS-GP-GFTGGDLVRLNLSGNNIQNRGYIEVP-----IHFPSTSTRYRV
      . . . . .
gi|129 -----NGSMIHLMPKDYTGFTTISP IATHVNNQRNRTFISEKFGNQGDSLRFEQSNNTARY
      480      490      500      510      520

540      550      560      570      580
Cry1Ac RVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS-SLG
      . . . . .
gi|129 TFRGNNGSNYLYLVRVSSLGNSTIRVTINGRVYATATNVNTTND-GVNDNGAHFSDINIG
      530      540      550      560      570      580

590      600      610      620      630      640
Cry1Ac NIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDY
      . . . . .
gi|129 NVVASSNTDVPLDINVTFNFGAQLDLMNIMLVPTNISPLY
      590      600      610      620

>>gi|4239728|emb|CAA10671.1| Cry2Aa protein [Bacillus th (633 aa)
  initn: 210 initl: 171 opt: 267 Z-score: 307.7 bits: 68.0 E(): 3.2e-08
Smith-Waterman score: 273; 21.717% identity (54.714% similar) in 594 aa overlap
(45-604:56-609)

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . .
gi|423 FEHKSALDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLKK---VGSGLIKRILSELWGII
      30      40      50      60      70      80

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAISRLEGLSNLYQIYAESPREWEADPTNP
      . . . . .
gi|423 FPSSSTNLMQDILRETEQFLNQLRNLDTLARVNAELIGLQANIREFNQVQVDF-LNPTQN
      90      100      110      120      130      140

130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGRWGF
      . . . . .
gi|423 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLFSIRDVILNADEWGI
      150      160      170      180      190      200

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```

190      200      210      220      230      240
Cry1Ac DAATINSRNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLD
      . . . . .
gi|423 SAATLRTRYDRYLNRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLNVFE
      210      220      230      240      250

250      260      270      280      290      300
Cry1Ac IVSLFPNYDSRITYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKRSPLHMDILNS
      . . . . .
gi|423 YVSIWLSLFKYQSLMVSSGANL---YASGGGPQQTQSFTAQNWPPLYSLFQVNSNYILSG
      260      270      280      290      300      310

310      320      330      340      350      360
Cry1Ac IT-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . . . . .
gi|423 ISGTRLSITFPNIGLPLGPTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST--
      320      330      340      350      360

370      380      390      400      410
Cry1Ac GVRTLSSTLYRRPFNIGINNQQLSVLDG--TEFAYGTSSNLPSAVYRKSQTVDSLDEIP
      . . . . .
gi|423 -VLPLSTPFVRSWLDGSDTREGVATSTNQWTE-SFQTTLSLRCGAFSARGNSNYFPDYF
      370      380      390      400      410      420

420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFNSVSIIRAPMFSWIHRSAEFNIIASDS
      . . . . .
gi|423 IRNISGVPLVIRNEDLTRLPHYNQIRNIESPSGTPGGARAYLVS-VHNRK--NNIYAANE
      430      440      450      460      470

480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNLSGNNIQNRGYIEVP-----IHFP
      . . . . .
gi|423 -----NGTMIHLAPEDYTGFTTISP IATHVNNQRNRTFISEKFGNQGDSLRFE
      480      490      500      510      520

530      540      550      560      570      580
Cry1Ac STSTRYRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESAN
      . . . . .
gi|423 QSNNTARHTLRGNGSNYLYLVRVSSIGNSTI-RVTINGRVYTVSNVNTTNDGVDNNGA
      530      540      550      560      570      580

590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLG
      . . . . .
gi|423 RFDINIGNIVASDNTNVTLNINVTLSNGTTPFLDMNIMFVPTNLPLPLY
      590      600      610      620      630

>>gi|114848912|gb|ABI83671.1| insecticidal crystal prote (633 aa)
  initn: 233 initl: 171 opt: 267 Z-score: 307.7 bits: 68.0 E(): 3.2e-08
Smith-Waterman score: 279; 21.920% identity (54.560% similar) in 625 aa overlap
(45-637:56-628)

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . .
gi|114 FEHKSALDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLKK---VGSGLIKRILSELWGII
      30      40      50      60      70      80

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```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNP
      ::      .      :      :      :      :      :      :      :      :      :
gi|114 FPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQVQVDF--LNPTQN
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
      .      .      .      .      .      .      .      .      .      .      .
gi|114 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLFSFIRDVILNADEWGI
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIV
      :      :      :      :      :      :      :      :      :      :      :
gi|114 SAATLRITYRDYLRNYTRDYSNYCINTYQTAFR---GLNLR-LHDMSEFRTYMFLNVFEYV
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac SLFPNYSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQGIIEGSIKSPHMLDILNSIT
      .      .      .      .      .      .      .      .      .      .      .
gi|114 SIWSLFKYQSLMVSSGANL---YASGSGPQQTQSFTAQNPFLYSLFQVNSNYILSGIS
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac -----IYTDHRGEYYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
      :      :      :      :      :      :      :      :      :      :      :
gi|114 GTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST---V
      320      330      340      350      360

      370      380      390      400      410      420
Cry1Ac YRTLSSTLYRRPFNIGINNQQLSVLDG--TEFAYGTSSNLPASVYRKSQVDSLDEIPPQ
      :      :      :      :      :      :      :      :      :      :      :
gi|114 LPPLSTPFVRSWLDGSGTDREGVATSTNWQTE-SFQTTLSLRCGAFSARGNSNYFPDYFIR
      370      380      390      400      410      420

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
      :      :      :      :      :      :      :      :      :      :      :
gi|114 NISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVS-VHNRK--NNIYAANE--
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNQSVIS-GP-GFTGGDLVRLNSSGNNIQRNGYIEVP-----IHFPST
      :      :      :      :      :      :      :      :      :      :      :
gi|114 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQS
      480      490      500      510      520

      530      540      550      560      570      580
Cry1Ac STRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESANAF
      .      .      .      .      .      .      .      .      .      .      .
gi|114 NTTARYTLRGNGNSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTNNNDGVNDNGARF
      530      540      550      560      570      580

      590      600      610      620      630      640
Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTSTNQLGLK
      .      .      .      .      .      .      .      .      .      .      .
gi|114 SDINIGNIVA---SDSTNVTLTLD---INVTLSNGTTPFDL-----MNIMFVPTNLPPLY

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      590      600      610      620      630
      650      660      670      680      690      700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDINRQPE

>>gi|4239730|emb|CAA10672.1| Cry2Aa protein [Bacillus th (633 aa)
  initn: 208 initl: 168 opt: 267 Z-score: 307.7 bits: 68.0 E(): 3.2e-08
Smith-Waterman score: 273; 21.71% identity (54.20% similar) in 594 aa overlap
(45-604:56-609)

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIWGF
      :      :      :      :      :      :      :      :      :      :      :
gi|423 FEHKSLDTIQKEWMEWRRTDHSLYVAPVVGTVSSFLKK---VGSLLIKRILSELWGII
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNP
      :      .      :      :      :      :      :      :      :      :
gi|423 FPSGSTNLMQDILRETEQFLNQRLNTDTLARVNAELIGLQANIREFNQVQVDF--LNPTQN
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
      :      :      :      :      :      :      :      :      :      :      :
gi|423 A-PLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLFSFIRDVILNADEWGI
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLD
      :      :      :      :      :      :      :      :      :      :      :
gi|423 SAATLRITYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFE
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac IVSLFPNYSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQGIIEGSIKSPHMLDILNS
      :      .      .      .      .      .      .      .      .      .      .      .
gi|423 YVSIWSLFKYQSLMVSSGANL---YASGSGPQQTQSFTAQNPFLYSLFQVNSNYILSG
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac IT-----IYTDHRGEYYWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      :      :      :      :      :      :      :      :      :      :      :
gi|423 ISGTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST--
      320      330      340      350      360

      370      380      390      400      410
Cry1Ac GVYRTLSSTLYRRPFNIGINNQQLSVLDG--TEFAYGTSSNLPASVYRKSQVDSLDEIP
      :      :      :      :      :      :      :      :      :      :      :
gi|423 -VLPPLSTPFVRSWLDGSGTDREGVATSTNWQTE-SFQTTLSLRCGAFSARGNSNYFPDYF
      370      380      390      400      410      420

      420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDS
      :      :      :      :      :      :      :      :      :      :      :
gi|423 IRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGGARAYLVS-VHNRK--DNIYAANE
      430      440      450      460      470

      480      490      500      510      520

```



Regulatory Product Characterization Team

Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFRGSAQGIIEGSIRSPHLMIDILNS
gi|292 YVSIWLSLFKYQSLMVSSGANL----YASGSGPQQTSFTAQNWPFYLSLFQVNSNYILSG

Cry1Ac IT-----IYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGT--MGNAAPQQRIVAQL
gi|292 ISGTRLSITFPNIGGLPGSTTTTHSLNSARVNYSGG-VSSGLIGATNLNHNFCSTVLPPL

Cry1Ac GQGVYRT-LSSSTLYRRFPNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGETVDSLDEI
gi|292 STPFVRSWLDSDGTREGVATSTNWQTESFQTTLRLRCGASSARGNSNYFPDYFIRNISGV

Cry1Ac PPQNNVPPRQGFSHRSLHVMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
gi|292 PLVIRN---EDLTRPL-HYNQIRNIESPSGTPGGARAYLVS-VHNRK--NNIYAANE--

Cry1Ac QIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPST
gi|292 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQS

Cry1Ac STRYRVRVR-YASVTPHILNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESANAF
gi|292 NTTARYTLRNGNSSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGVNDNGARF

Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|292 PDINIGNIVASDNTNVTLIDINVTLSNGTFFDLMNIMFVPTNLPLPY

>>gi|142732|gb|AAA22335.1| P2 crystal protein (633 aa)
initn: 208 init1: 171 opt: 265 Z-score: 305.3 bits: 67.6 E(): 4.4e-08
Smith-Waterman score: 276; 21.717% identity (54.545% similar) in 594 aa overlap
(45-604:56-609)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGI
gi|142 FEHKSLDTIQKEWMEWKRTDHSYLVAPVVGTVSSPFLKK---VGSLLIGKRILSELWGII

Cry1Ac GPSQWDAFLVQI----EQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
gi|142 FPSGSTNLMQDILRETEQFLNQLRNTDLARVNAELIGLQANIREFNQVQDNF-LNPTQN

130 140 150 160 170 180

Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGF
gi|142 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQANMHLFSFIRDVILNADEWGI

Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYRQFRRELTTLVLD
gi|142 SAATLRTYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLRHDLML---EFRTYMFNLNVFE

Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFRGSAQGIIEGSIRSPHLMIDILNS
gi|142 YVSIWLSLFKYQSLMVSSGANL----YASGSGPQQTSFTAQNWPFYLSLFQVNSNYILSG

Cry1Ac IT-----IYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
gi|142 ISGTRLSITFPNIGGLPGSTTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCST--

Cry1Ac GYVRTLSSTLYRRFPNIGINNQQLSVLDG--TEFAYGTSSNLPSAVYRKSGETVDSLDEIP
gi|142 -VLPPLSTPFVRSWLDSDGTREGVATSTNWQTE-SFQTTLRLRCGAFSARGNSNYFPDYF

Cry1Ac PQN-NNVP--PRQGFSHRSLHVMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDS
gi|142 IRNISGVPLVIRNEDLTRLPLHYNQIRNIESPSGTPGGARAYLVS-VHNRK--NNIYAANE

Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
gi|142 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQS

Cry1Ac STSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESANAF
gi|142 QSNNTARYTLRNGNSSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGVNDNGARF

Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
gi|142 RPSDINIGNIVASDNTNVTLIDINVTLSNGTFFDLMNIMFVPTNLPLPY

>>gi|27447976|gb|AA013750.1|AF273218\_1 Cry2Aa [Bacillus (633 aa)
initn: 208 init1: 171 opt: 265 Z-score: 305.3 bits: 67.6 E(): 4.4e-08
Smith-Waterman score: 276; 21.717% identity (54.545% similar) in 594 aa overlap
(45-604:56-609)

20 30 40 50 60 70



```

480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|142 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFE
      480      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESAN
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|142 QSNNTARYTLRGNNGNSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGVNDNGA
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|142 RFSIDINIGNIVASDNTNVTLTDINVTLNSGTPFDLMNIMFVPTNLPLLY
      590      600      610      620      630

```

>>gi|45685586|gb|AAS75548.1| Cry2Aa [Bacillus thuringien (633 aa)  
 initn: 208 init1: 171 opt: 265 Z-score: 305.3 bits: 67.6 E(): 4.4e-08  
 Smith-Waterman score: 276; 21.717% identity (54.545% similar) in 594 aa overlap  
 (45-604:56-609)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGF
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 FEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLKK---VGLIGKRILSELWGII
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 FPSGSTNLMQDILRETEQFLNQLRNTDTLARVNAELIGLQANIREFNGQVDNF-LNPTQN
      90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGF
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 SAATLRTYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVFE
      210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac IVSLFPNYSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSIKRSRPHLMDILNS
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 YVSIWLSLFKYQSLMVSSGANL----YASGSGPQQTSFTAQNWPLFLYSLFQVNSNYILSG
      260      270      280      290      300      310

```

```

310      320      330      340      350      360
Cry1Ac IT-----IYTDahrgeyYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 ISGTRLSITFPNIGGLPGSTTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST--
      320      330      340      350      360

```

```

370      380      390      400      410
Cry1Ac GVYRTLSSSTLYRRPFNIGINNQQLSVLDG--TEFAYGTSSNLPFSAVYRKSQVDSLDEIP
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 -VLPLSTPFVRSWLDSDGTDRGVATSTNWQTE-SFQTTLSLRCGAFSARGNSNYFPDYF
      370      380      390      400      410      420

```

```

420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDS
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 IRNISGVPLVIRNEDLTRLPLHYNQIRNIESPSGTPGGARAYLVV-VHNRK--NNIYAANE
      430      440      450      460      470

```

```

480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFE
      480      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESAN
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 QSNNTARYTLRGNNGNSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGVNDNGA
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|456 RFSIDINIGNIVASDNTNVTLTDINVTLNSGTPFDLMNIMFVPTNLPLLY
      590      600      610      620      630

```

>>gi|33314185|gb|AAQ04263.1|AF433645\_3 Cry2Aa [Bacillus (633 aa)  
 initn: 208 init1: 171 opt: 265 Z-score: 305.3 bits: 67.6 E(): 4.4e-08  
 Smith-Waterman score: 276; 21.717% identity (54.545% similar) in 594 aa overlap  
 (45-604:56-609)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLG--LVDIIWGF
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 FEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLKK---VGLIGKRILSELWGII
      30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 FPSGSTNLMQDILRETEQFLNQLRNTDTLARVNAELIGLQANIREFNGQVDNF-LNPTQN
      90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGF
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQAANMHLSFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      :.:.: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .: .:
gi|333 SAATLRTYRDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVFE
      210      220      230      240      250

```



Regulatory Product Characterization Team

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . .
gi|678 FEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLLKK---VGLIGKRILSELWGII
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP
      . . . . .
gi|678 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELIGLQANIREFNQVQDNF-LNPTQN
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF
      . . . . .
gi|678 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQANMHLFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLD
      . . . . .
gi|678 SAATLRTRYRDLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFE
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHLMIDILNS
      . . . . .
gi|678 YVSIWLSLFKYQSLMVSSGANL----YASGSGPQQTQSFTAQNWPFYLSLFQVNSNYILSG
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac IT-----IYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . . . . .
gi|678 ISGTRLSITFPNIGLPGSTTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST--
      320      330      340      350      360

```

```

      370      380      390      400      410
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDG--TEFAYGTSSNLPSAVYRKSQTVDSLDEIP
      . . . . .
gi|678 -VLPPLSTPFVRSWLDSGTDREGVATSTNWQTE-SFQTTLSLRGAFSARGNSNYFPDYF
      370      380      390      400      410      420

```

```

      420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDS
      . . . . .
gi|678 IRNISGVPLVIRNEDLTRLPHYNQIRNIESPSGTPGGARAYLVS-VHNKR--NNIYAANE
      430      440      450      460      470

```

```

      480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
      . . . . .
gi|678 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFE
      480      490      500      510      520

```

```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESAN
      . . . . .
gi|678 QSNTTARYTLRGNNGSNLYLVRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGVDNNGA
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
      . . . . .
gi|678 RFSNDINIGNIVASDNTNVTLDINVTLNSGTPFDLMNIMFVPTNLPPLY
      590      600      610      620      630

```

```

>>gi|27311150|gb|AA00678.1| Sequence 12 from patent US (634 aa)
  initn: 208 initl: 171 opt: 265 Z-score: 305.3 bits: 67.6 E(): 4.4e-08
Smith-Waterman score: 276; 21.717% identity (54.545% similar) in 594 aa overlap
(45-604:57-610)

```

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
      . . . . .
gi|273 FEHKSLDTIQKEWMEWKRTDHSLYVAPVVGTVSSFLLKK---VGLIGKRILSELWGII
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP
      . . . . .
gi|273 FPSGSTNLMQDILRETEQFLNQLRLNTDTLARVNAELIGLQANIREFNQVQDNF-LNPTQN
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF
      . . . . .
gi|273 PVPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQANMHLFIRDVILNADEWGI
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLD
      . . . . .
gi|273 SAATLRTRYRDLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFE
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHLMIDILNS
      . . . . .
gi|273 YVSIWLSLFKYQSLMVSSGANL----YASGSGPQQTQSFTAQNWPFYLSLFQVNSNYILSG
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac IT-----IYTDHRGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      . . . . .
gi|273 ISGTRLSITFPNIGLPGSTTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST--
      320      330      340      350      360

```

```

      370      380      390      400      410
Cry1Ac GVYRTLSSITLYRRPFNIGINNQLSVLDG--TEFAYGTSSNLPSAVYRKSQTVDSLDEIP
      . . . . .
gi|273 -VLPPLSTPFVRSWLDSGTDREGVATSTNWQTE-SFQTTLSLRGAFSARGNSNYFPDYF
      370      380      390      400      410      420

```

```

      420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDS
      . . . . .
gi|273 IRNISGVPLVIRNEDLTRLPHYNQIRNIESPSGTPGGARAYLVS-VHNKR--NNIYAANE
      430      440      450      460      470      480

```

```

      480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
      :::::  :  ::  .  ....  :  ::  :  :
gi|273 -----NGMTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDLSLRF
      490      500      510      520

```

```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESAN
      ....  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|273 QSNTTARYTLRGNNGNSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTNNNDGVNDNGA
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
      :..  .:..:..  :  :  :  .
gi|273 RFSIDINIGNIVASDNTNVTLIDINVTLNLSGTPFDLMNIMFVPTNLPLPY
      590      600      610      620      630

```

```

>>gi|3716488|emb|CAA03661.1| unnamed protein product [Pa (706 aa)
  initn: 160 initl: 119 opt: 265 Z-score: 304.6 bits: 67.6 E(): 4.8e-08
Smith-Waterman score: 265; 27.344% identity (62.891% similar) in 256 aa overlap
(6-251:84-332)

```

```

                                10      20      30
Cry1Ac          CMQAMDNNP-NINECIPYNCLSNPEVEVLGGERIE
      :  :  :  .  .  .  :  :  :  :  :  :  :  :  :  :
gi|371 PIYNNNDNNDNAICDELGLTPIDNNTICSTDFTPINVMRTDPFRKSTQELTREWTEWKE
      60      70      80      90      100     110

```

```

      40      50      60      70      80
Cry1Ac TG---YTPIDISLSLTQFLLSEFVPGA-GFVLG-LVDIIWIGFQPSQWDAFLVQIEQLIN
      .  :  :  :  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|371 NSPSLFTPAIVGV-VTSFLLQSLKKQATSFLKLTLDLIFPNNSSLTMEIILRATEQVYVQ
      120     130     140     150     160     170

```

```

      90      100     110     120     130     140
Cry1Ac QRIEEFARNQAISRLEGLSN---LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT
      :..  .  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|371 ERLDTDANRVSQELVGLKNNLTFNDQVEDFLQNRVGISPLAII DSI----NTMQQLFV
      180     190     200     210     220

```

```

      150     160     170     180     190     200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGN
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|371 NRLPQFQVSGYQVLLPLFAQAATLHLTFLRDVIINADEWNIPTAQLNTYTRYFKEYIAE
      230     240     250     260     270     280

```

```

      210     220     230     240     250     260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIR-YNQFRRELTLTLDIVSLFPNYDSRTYPIRTVS
      :..:..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|371 YSNYALSTYDDGFRTRFYF--RNTLEDMLQFKTFMTLNALDLVSIWSLLKYVNLVYSTSA
      290     300     310     320     330     340

```

```

      270     280     290     300     310     320
Cry1Ac QLTREIYTNPVLENFDPGSRGSAQIEGSIIRSPHLMIDLNSITIIYTDahrgeyywshgqi
gi|371 NLYNIGDNKVNegaYpISyGpFFNSYIQTKSNYVLVSGVSGIGARFTYSTVTLGryLHDDLK
      350     360     370     380     390     400

```

```

>>gi|152013907|gb|ABS20060.1| dipterans toxic crystal pr (99 aa)
  initn: 236 initl: 236 opt: 254 Z-score: 304.4 bits: 64.7 E(): 4.9e-08
Smith-Waterman score: 254; 46.875% identity (71.875% similar) in 96 aa overlap
(919-1014:5-99)

```

```

      890      900      910      920      930      940
Cry1Ac KKRWDKREKLEWETNIVYKEAKESVDALFVNSQYDQLQADTNLAMIHAADKRVHSIREAY
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|152          CFIPNVQDEALQFDTTLAQIQYAEYLVQSIPIVYV
      10      20      30

```

```

      950      960      970      980      990      1000
Cry1Ac LPELSVIPGVNAAI FEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHVDVEEQNN
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|152 NDWLSVDPGMNYDIYVELDARVAQARYLYDTRNIIKNGDFTQGVMGVHWHTGNADVQ-QXD
      40      50      60      70      80      90

```

```

      1010     1020     1030     1040     1050     1060
Cry1Ac QRSVLVPEWEAEVSVQEVRCVPCGRGYILRVYAYKEGYGECVCTIHEIENNTDELKFSNCV
      :  :  :
gi|152 GVSVLV

```

```

>>gi|27447952|gb|AA013734.1|AF252262_3 insecticidal crys (633 aa)
  initn: 208 initl: 171 opt: 263 Z-score: 303.0 bits: 67.2 E(): 5.9e-08
Smith-Waterman score: 272; 21.717% identity (54.377% similar) in 594 aa overlap
(45-604:56-609)

```

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAQVFLG--LVDIIWIGIF
      .....  :  :  :  :  :  :
gi|274 FEHKSLDTIQKEWMEWKRTDHSLSYVAPVVTGVSFLLKK---VGLIGKRILSELWGII
      30      40      50      60      70      80

```

```

      80      90      100     110     120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|274 FPSGSTNLMQDILRETEQFLNQLRNTDTLARVNAELIGLQANIREFNOQVDNF-LNPTQN
      90      100     110     120     130     140

```

```

      130     140     150     160     170     180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|274 PVPLSITSSVNTMQQLFNRLPQFQIQGYQLLLLPLFAQAANMHLFSIRDVILNADEWGI
      150     160     170     180     190     200

```

```

      190     200     210     220     230     240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLD
      :..:..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|274 SAATLTRYDYLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMPFNVFE
      210     220     230     240     250

```

```

      250     260     270     280     290     300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDPGSRGSAQIEGSIIRSPHLMIDLNS
      :..:..  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
gi|274 YVSIWSLFKYQGLMVSSGANL---YASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSG
      260     270     280     290     300     310

```

```

          310      320      330      340      350      360
Cry1Ac IT-----IYTDahrgeyywSGHQIMASpVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQ
gi|274 ISGTRLSITFPNIGGLPGSTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCST--
          320      330      340      350      360

```

```

          370      380      390      400      410
Cry1Ac GvyrtLSSTLYRRPFNIGINNQQLSVLDG--TEFAYGTSSNLPSAVYRKSGTVDSLDEIP
gi|274 -VLPPLSTPFVRSWLDGSGTDREGVATSTNWQTE-SFQTTLSLRCAFSAARGNSNYFPDYP
          370      380      390      400      410      420

```

```

          420      430      440      450      460      470
Cry1Ac PQN-NNVP--PRQGFShRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDS
gi|274 IRNISGVPLVIRNEDLTRPLHYNQIRNIESPSGTPGARAYLVS-VHNrk--NNIYAANE
          430      440      450      460      470

```

```

          480      490      500      510      520
Cry1Ac ITQIPAVKGNFLFNgsvis-GP-GFTGGDLVRLNssGNniQNGYIEVP-----IHFP
gi|274 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFE
          480      490      500      510      520

```

```

          530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTPATATSLDNLQSS--DFGYFESAN
gi|274 QSNtTARyTLRNGNSYNLYLRVSSIGNSTI-RVTINGRVYTVSNVNTTTNNDGvNDNGA
          530      540      550      560      570      580

```

```

          590      600      610      620      630      640
Cry1Ac AFTS-SLGNIVGVRNfSGTAGVIIDRFEFIPVtATLEAEYNLERAQKAVNALFTSTNQLG
gi|274 RfSDINIGNIVASDNtNVTLdINVTlNSGTPFDLMNIMFVPTNLPLPY
          590      600      610      620      630

```

>>gi|3994349|gb|AAC87777.1|AR008751 Sequence 6 from pate (1257 aa)  
 initn: 744 initl: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08  
 Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap  
 (33-1058:60-1177)

```

          10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLEFVPGAGFV
gi|399 SKYDEMIKAFEKKWKKGAKGKDLLDVAWYITTGEIDPLNVIKGVLsvL--TLIPEVGTV
          30      40      50      60      70      80

```

```

          70      80      90      100      110
Cry1Ac LG----LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNAQISRLEGLSNLY
gi|399 ASAASTIVSFIFWPKIFGDKPNAKNIFEELKQIEALIQDITNYQDAINQKkFDSLQKTI
          90      100      110      120      130      140

```

```

          120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNdmNSALtTAIPLFAVQNYQVPLLSVYVQAANL
gi|399 NLYTVAI-----DNNDYV---TAKTQLENLNSILtSDISIFiPEGYETGGLPYAMVANA
          150      160      170      180      190

```

```

          180      190      200      210      220      230
Cry1Ac HlSVLRDVSvVFGQRWGFDAATINSRYNDLTRLIGNYTDHavrWYNTGLERVWGPDSRDWI
gi|399 HILLLRDAIVNAEKLGFSdKEVDTHKKYIKMTIHnhTEAVIKAFNLGLDKFKSLDVNSYN
          200      210      220      230      240      250

```

```

          240      250      260      270      280
Cry1Ac RYNQFRRELtTLVLDIVSLFPNYDSRTYPiRTVSQLTREIYT---NPVLENFDGS-----
gi|399 KKANYIKGtEMVLDLVALWPTFDpDHYQKEVEIEFTRTISSPIYQVPVKMNQNTSSSIV
          260      270      280      290      300      310

```

```

          290      300      310      320
Cry1Ac -----FRGSAQIEGSIRSPH--LMDILNSI--TIYTDahrgeyyw-----SGHQ
gi|399 PSDLFHYQGDLVKLEFSTRtDNDGLAKIftGIRNTfYKSPNthETHVDFSYNTQSSGNI
          320      330      340      350      360      370

```

```

          330      340      350      360      370      380
Cry1Ac IMAS----PVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN
gi|399 SRGSSNPiPIDLNNPIISTCIRNSfYKAIAGSSVLVNFkdG---TQGYAFaQAPTg-GAW
          380      390      400      410      420      430

```

```

          390      400      410      420
Cry1Ac NQQLSVLDGT---EFAYGTSSNLPSAVYRKSGTVDSLDEIppQNN-----NVPPRQG
gi|399 DHSFIeSDGAPEGHKLNyIYTS--PGDTLRDFINvYTLtSTPTINELStEKIKGfPAEKg
          440      450      460      470      480      490

```

```

          430      440      450      460      470      480
Cry1Ac FSHRLSHVSMF-RSGFSNSSVSII---RAPMFSWIH--RSAEFNNIIASDSITQIPAVKQ
gi|399 YIKNQGIKMYGKPEYINGAQPVNLENQQTlIFEFHASKTAQYtTIRIRYAS-TQ--GtKG
          500      510      520      530      540      550

```

```

          490      500      510      520
Cry1Ac NflFNgsVI-----SGPGFTGG-----DLVRLMS---SGNN---IQNR---GYIEV
gi|399 YFRLDNqELQTLNIPTSHNGYVtGNIGENyDLYtIGSYtITEGNHtLQIQHNDKNGMVLd
          560      570      580      590      600      610

```

```

          530      540      550
Cry1Ac PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWGNS-----
gi|399 RIEFVFKDSLQDspQDspPEVHEStIIFDKSSPTIwSSNkHSYSHIHLEGSYtSQGSYPH
          620      630      640      650      660      670

```

```

          560      570      580      590      600
Cry1Ac ---SIFSNtVPATATSL---DNLQSDfGYFESANA--FTSSLGNIVGVRNfSGTAGVI
gi|399 NLLINLfhPtdPNRnHTIHvNNGDMNVdYgKdSVADGLNfNKItATIPSDAWYSGtITSM
          680      690      700      710      720      730

```

```

          610      620      630      640      650      660
Cry1Ac --IDRFEFIPVtATLEAEYNLERAQKAVNALFTSTNQLGLKtNVtDYHIDQVSNLVtYtLS
gi|399 HLFNDNnfKtITPKfELSNELENItTQVNALFASaQDTLASNVSDYwIEQVVMKVDALS
          740      750      760      770      780      790

```

```

        670      680      690      700      710      720
Cry1Ac DEFCLDEKRELSSEKVKHAKRRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|399 DEVFVGKEKKALRKLNVQAKRRLSKIRNLLIGGNFDNLV----AWYMGKDVVKESDHELFK
        800      810      820      830      840

        730      740      750      760      770
Cry1Ac ENYVTLGSG-TFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HET
gi|399 SDHVLLPPPTF---HPSYIFQKVEESKLPNTRYTISGFIAGHGEDVELVVSRYGQEIQKV
        850      860      870      880      890      900

        780      790      800      810      820      830
Cry1Ac VNVPGTGSLLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSQRDGEKCAHSHHFFSLDIDV
gi|399 MQVPYEEAL-PLTSESN-SSC-----CVPNLLNINETLA-----DPHFFSYSIDV
        910      920      930      940

        840      850      860      870      880      890
Cry1Ac GCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
gi|399 GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
        950      960      970      980      990      1000

        900      910      920      930      940
Cry1Ac WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIIHAADKRVHSIREAYL
gi|399 TEITAIIQPVLNQINALYENEDWNGSIRSNSVYHDLQIIMPLPTLTKTEEINCNVDHPAFL
        1010      1020      1030      1040      1050      1060

        950      960      970      980      990      1000
Cry1Ac PE-----LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSVCNVKGVHDVE
gi|399 LKVYHWFMTDRIGEHTILARFQEAALDRAYTQLESRNLLHNGHFTTDTANWTIEGDAHHT
        1070      1080      1090      1100      1110      1120

        1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSLVVPWEAEVSEVVRVCP---GRGYILRVYAYKEGYEGCVTIHEIENNTDE
gi|399 ILEDGRVRLRLPDWSSNATQTIEIEDFDLDQEQYQLLIHAK---GKGSITLQHGEEENEYV
        1130      1140      1150      1160      1170      1180

        1070      1080      1090      1100      1110      1120
Cry1Ac LKFSNCVEEIYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYT
gi|399 ETHHTHTNDFITSQNIPFTFKGNQIEVHITSEDEGLDITVIEVSKTDTNTNIENSP
        1190      1200      1210      1220      1230      1240

>>gi|5972714|gb|AAE12605.1| Sequence 6 from patent US 58 (1257 aa)
  initn: 744 init1: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08
Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
(33-1058:60-1177)

        10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLEFVPGAGFV
gi|597 SKYDEMIKAFKWKKGAKGKDLLDVAWYITTGEIDPLNVKGVLSVL--TLIPEVGTV
        30      40      50      60      70      80

```

```

        70      80      90      100      110
Cry1Ac LG---LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEAFARNQAIISRLLEGLSNLY
gi|597 ASAASTIVSFIWPKIFGDKPNAKNIFEELKPKQIEALIQQDITNYQDAINQKKFDSLQKTI
        90      100      110      120      130      140

        120      130      140      150      160      170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|597 NLYTVVAI-----DNNDYV---TAKTQLENLNSILTSDISIFIFIEGYETGGLPYAMVANA
        150      160      170      180      190

        180      190      200      210      220      230
Cry1Ac HLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSRDWI
gi|597 HILLRLDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTEAVIKAFNLGLDKFKSLDVNSYN
        200      210      220      230      240      250

        240      250      260      270      280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYT---NPVLENFDGS----
gi|597 KKANYIKGTMEMVLDLVALWPTFDPDHYQKEVEIEFTRTISPIYQPVPKNQNTSSSIV
        260      270      280      290      300      310

        290      300      310      320
Cry1Ac -----FRGSAQIEGSIIRSPH--LMDILNSI--TIYTDahrGEYYW-----SGHQ
gi|597 PSDLFHYQGDVLKLEFSTRDNDGLAKIFTGIRNTFYKSPNTHETHYHVDVFSYNTQSSGNI
        320      330      340      350      360      370

        330      340      350      360      370      380
Cry1Ac IMAS---PVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLSSLYRRPFNIGIN
gi|597 SRGSSNPIPIDLNNPIISTCIRNSFYKAIAGSSSVLVNFKDG---TQGYAFAQAPTG-GAW
        380      390      400      410      420      430

        390      400      410      420
Cry1Ac NQQLSVLDGT---EFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNN-----NVPPRQG
gi|597 DHSFIESDGAPEGHKLNLIYTS--PGDTLRDFINVTLISTPTINELSTEKIKGFPAEKG
        440      450      460      470      480      490

        430      440      450      460      470      480
Cry1Ac FSHRLSHVSMF-RSGFSSNSVSI---RAPMFSWIH--RSAEFNIIASDSITQIPAVKG
gi|597 YIKNQGIKYYGKPEYINGAQPVNLENQOTLIFEFHASKTAQYTIIRIRYAS-TQ--GTRK
        500      510      520      530      540      550

        490      500      510      520
Cry1Ac NFLFNQSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
gi|597 YFRLDNQELQTLNIPSTSHNGYVTGNIGENYDLYTIGSYTITEGNHTLQIQHNDKNGMVLVD
        560      570      580      590      600      610

        530      540      550
Cry1Ac PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWGNS-----
gi|597 RIEFVFKDSLQDQSPPEVHSTIIFDKSSPTIWSNKHSHYSHIHLEBGSYTSQGSYPH

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Regulatory Product Characterization Team

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620      630      640      650      660      670
Cry1Ac ----SIFSNTVPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRNFSGTAGVI
      . . . . .
gi|597  NLLINLFHPTDPNRNHTIHVNNGDMNVYDGKDSVADGLNFNKITATIPSDAWYSGTITSM
      680      690      700      710      720      730

610      620      630      640      650      660
Cry1Ac --IDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
      . . . . .
gi|597  HLFNDNNFKTIIPKFEELSNELENIITQVNALFASSAQDTLASNVSDYWIEQVVMKVDALS
      740      750      760      770      780      790

670      680      690      700      710      720
Cry1Ac DEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
      . . . . .
gi|597  DEVFGKEKKALRKLNVQAKRLSKIRNLLIGGNFDNLV----AWYMGKDDVVKESDHELFK
      800      810      820      830      840

730      740      750      760      770
Cry1Ac ENYVTLGS-TFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQLEIYSIRYNAK-HET
      . . . . .
gi|597  SDHVLLPPPTF---HPSYIFQKVEESKLPNTRYTISGFIHGEDVELVVSRYGQEIQKV
      850      860      870      880      890      900

780      790      800      810      820      830
Cry1Ac VNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFFSLDIDV
      . . . . .
gi|597  MQVPYEEAL-PLTSESN-SSC-----CVPNLNINETLA-----DPHFFYSIDV
      910      920      930      940

840      850      860      870      880      890
Cry1Ac GCTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
      . . . . .
gi|597  GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
      950      960      970      980      990      1000

900      910      920      930      940
Cry1Ac WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIHAADKRVHSIREAYL
      . . . . .
gi|597  TEITAIIQPVLNQINALYENEDWNGSIRSNSVSYHDLEQIMLPTLLKTEEINCNYDHPAFL
      1010     1020     1030     1040     1050     1060

950      960      970      980      990      1000
Cry1Ac PE----LSVIPGVNAAFEELEGRIFTAFLSYDARNVIKNGDFNNGLSWVNVKGHVVDVE
      . . . . .
gi|597  LKVYHWFMTDRIGEHTILARFQEAALDRAYTQLESRNLLHNGHFTTDTANWTIEGDAHHT
      1070     1080     1090     1100     1110     1120

1010     1020     1030     1040     1050     1060
Cry1Ac EQNNQRSVLLVPEWEAEVSEQEVRVCP---GRGYILRVTAAYKEGYEGECVTTIHEIENNTDE
      . . . . .
gi|597  ILEDGRRVRLRPDWSNATQTEIEIEDFDLDQYQLLIHAK---GKGSITLQHGEEENEYV
      1130     1140     1150     1160     1170     1180

1070     1080     1090     1100     1110     1120
Cry1Ac LKFSNCVEEIEYPNNTVTCNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYT

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gi|597  ETHTHHTNDFITSQNIPFTFKGNQIEVHITSEDEGEFLIDHITVIEWSKTDTNTNIIENSP
      1190     1200     1210     1220     1230     1240
>>gi|142772|gb|AAA22355.1| delta-endotoxin (1257 aa)
      initt: 744 inilt: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08
Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
(33-1058:60-1177)

10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLSEFVPGAGFV
      . . . . .
gi|142  SKYDEMIKAFEKKWKKGAKGKDLLDVAWYTIITGEIDPLNVIKGVLSVL--TLIPEVGTV
      30      40      50      60      70      80

70      80      90      100     110
Cry1Ac LG----LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNQAI SRLEGLSNLY
      . . . . .
gi|142  ASAASTIVSFIWPKIFGDKPNAKNIFEELKPKQIEALIQDITNYQDAINQKKFDSLQKTI
      90      100     110     120     130     140

120     130     140     150     160     170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
      . . . . .
gi|142  NLYTVAI-----DNNDYV---TAKTQLENLNSILTSDISIFIEGYETGGLPYAMVANA
      150     160     170     180     190

180     190     200     210     220     230
Cry1Ac HLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
      . . . . .
gi|142  HILLRLDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTEAVIKAFNLGLDKFKSLDVNSYN
      200     210     220     230     240     250

240     250     260     270     280
Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYT---NPVLENFDGS-----
      . . . . .
gi|142  KKANYIKGTEMVLDLVALWPTFDPDHYQKEVEIEFTRTISSEPIYQPVKPNMQNTSSSIV
      260     270     280     290     300     310

290     300     310     320
Cry1Ac -----FRGSAQIEGSIRSPH--LMDILNSI--TIYTDARHGEYYW-----SGHQ
      . . . . .
gi|142  PSDLPHYQGDLVKLEFSTRTDNDGLAKIFTGIRNTFYKSPNTHETVHVDFSYNTQSSGNI
      320     330     340     350     360     370

330     340     350     360     370     380
Cry1Ac IMAS---PVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGIN
      . . . . .
gi|142  SRGSSNPIDILNNPIISTCIRNSFYKAIAGSSVLVNFKDG---TQGYAFAQAPTG-GAW
      380     390     400     410     420     430

390     400     410     420
Cry1Ac NQQLSVLDGT---EFAYGTSSNLPASAVYRKSGETVDSLDEIPPQNN-----NVPPRQG
      . . . . .
gi|142  DHSFIESDGAPEGHKLNLYIYTS--PGDTRLRDFINVYTLISTPTINELSTEKIKGFPAEKG
      440     450     460     470     480     490

430     440     450     460     470     480
Cry1Ac FSHRLSHVSMF-RSGFSNNSVSII---RAPMFSWIH--RSAEFNNIIASDSITQIPAVKG
      . . . . .

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gi|142 YIKNQGIMKYYGKPEYINGAQPVNLENQQTLLIFEFHASKTAQYTIRIRYAS-TQ--GTKG
      500      510      520      530      540      550
Cry1Ac 490          500          510          520
NFLFNGSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 YFRLDNQELQTLNIPSTSHNGYVTGNIGENYDLYTIGSYTITEGNHTLQIQHNDKNGMVL
      560      570      580      590      600      610
Cry1Ac 530          540          550
PIHF--PSTSTR-----YRVRVRYASVTP-----IHLNVNMGNS-----
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 RIEFVPKDSLQDSDPPEVHESTIIFDKSSPTIWSNKHYSYSHIHLEGSYTSQGSYPH
      620      630      640      650      660      670
Cry1Ac 560          570          580          590          600
----SIFSNTPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRNFSGTAGVI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 NLLINLPHPTDPNRNHTIHVNNNGDMNVDYKDSVADGLNFKNKITATIPSDAWYSGTITSM
      680      690      700      710      720      730
Cry1Ac 610          620          630          640          650          660
--IDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 HLFNDNNFKTITPKFELSNLENIITQVNALFASSAQDTLASNVSDYVIEQVVMKVDALS
      740      750      760      770      780      790
Cry1Ac 670          680          690          700          710          720
DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 DEVFGKEKALRKLNVQAKRLSKIRNLLIGGNFDNLV-----AWYMGKDVVKESDHELFK
      800      810      820      830      840
Cry1Ac 730          740          750          760          770
ENYVTLSG-TFDECYPTYLYQKIDESKCLKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HET
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 SDHVLLPPTPF---HPSYIFQKVEESKLPNTRYTISGFIAHGEDVELVVSRYGQEQIQKV
      850      860      870      880      890      900
Cry1Ac 780          790          800          810          820          830
VNVPGTGSLSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 MQVPYEEAL-PLTSESN-SSC-----CVPNLLNINETLA-----DPHFYSYSIDV
      910      920      930      940
Cry1Ac 840          850          860          870          880          890
GCTDLNEDLGVVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
      950      960      970      980      990      1000
Cry1Ac 900          910          920          930          940
WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIAHADKRVHSIREAYL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 TEITAIQPVLNQINALYENEDWNGSIRSNSVSYHDLEQIMLPTLLKTEEINCNYDHPAFL
      1010      1020      1030      1040      1050      1060
Cry1Ac 950          960          970          980          990      1000
PE-----LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSCWNVKGVHDVE

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      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 LKVYHWFMTDRIGEHGTILARFQEALDRAYTQLESRNLLHNGHFTTDTANWTTIEGDAHHT
      1070      1080      1090      1100      1110      1120
Cry1Ac 1010      1020      1030      1040      1050      1060
EQNNQRSVLVPEWEAEVSQEVVCP---GRGYILRVYAYKEGYGEGCVTIHEIENNTDE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 ILEDGRRVLRPLDWSSNATQTIEIEDFDLDQYQLLIHAK---GKGSITLQHGEEYEV
      1130      1140      1150      1160      1170      1180
Cry1Ac 1070      1080      1090      1100      1110      1120
LKFSNCVEEIIYPNNTVTNDYTVNQEEYGGAYTSRNRGYNEAPSVPADYASVYEEKSYT
gi|142 ETHTHHTNDFITSQNIPTFKGNQIEVHITSEDEGFLDITVIEVSKTDTNTNIENS
      1190      1200      1210      1220      1230      1240
>>gi|1831843|gb|AAB46297.1| Sequence 6 from patent US 55 (1257 aa)
      initn: 744 initl: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08
Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
(33-1058:60-1177)
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      10          20          30          40          50          60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLEFVPGAGFV
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 SKYDEMIKAFEKWKKGAKGKDLLDVAWYIITGEIDPLNVIKVLSVL--TLIPEVGTV
      30          40          50          60          70          80
Cry1Ac 70          80          90          100         110
LG---LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNQAIISRLGLSNLY
gi|183 ASAASTIVSFIWPKIFGDKPNKAKNIFEELKPKQIEALIQDITNYQDAINQKFKDSLQKTI
      90          100         110         120         130         140
Cry1Ac 120         130         140         150         160         170
QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|183 NLYTVAI-----DNNDYV---TAKTQLENLNSILTSDISIFIEGYETGGLPYAMVANA
      150         160         170         180         190
Cry1Ac 180         190         200         210         220         230
HLSVLRDVSVFGQWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
gi|183 HILLLRDAIVNAEKLGFSKVEVDTHKKYIKMTIHNHTEAVIKAFNLGLDKFKSLDVNSYN
      200         210         220         230         240         250
Cry1Ac 240         250         260         270         280
RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYT---NPVLENFDGS-----
gi|183 KKANYIKGTEEMVLDLVALWPTFFDPHYQKEVEIEFTRTISSEPIYQVPKNQNTSSSIV
      260         270         280         290         300         310
Cry1Ac 290         300         310         320
-----FRSQAQIEGSIRSPH--LMDILNSI--TIYTDHRGEYYW-----SGHQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 PSDLFHYQGDVLEKLEFSTRDNDGLAKIFTGIRNTFYKSPNTHETVYHVDVFSYNTQSSGNI
      320         330         340         350         360         370
Cry1Ac 330         340         350         360         370         380
IMAS----PVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSLTLYRRPFNIGIN

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gi|183 SRGSSNPPIPDLNPNPIISTCIRNSFYKALAGSSVLVNFKDG---TQGYAFAQAP*G-GAW
380 390 400 410 420 430
Cry1Ac NQQLSVLDGT---EFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN-----NVP*PRQG
390 400 410 420
gi|183 DHSFIESDGAPEGHKLNYIYTS--PGD*TLRDFINVYTLISTPTINELSTEKIKGFPAEKG
440 450 460 470 480 490
Cry1Ac FSHRLSHVSMF-RSGFSN*SSVSII--RAPMFSWIH--RSAEFNIIIASDSITQIPAVKG
430 440 450 460 470 480
gi|183 YIKNQGIMKYYGKPEYINGAQPVNLENQ*OTLIFEFHASKTAQYTIIRIRYAS-TQ--G*TKG
500 510 520 530 540 550
Cry1Ac NFLFNGSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
490 500 510 520
gi|183 YFRLDNQELQTLNIPTSHNGVVTGNIGENYDL*YITIGSYTITEGNTLQIQHNDKNGMVL
560 570 580 590 600 610
Cry1Ac PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWGNS-----
530 540 550
gi|183 RIEFV*PKDSLQD*SPD*SPPEVHESTIIIFDKSSPTI*WSSNKHSYSHIHLEGSYTSQGSYPH
620 630 640 650 660 670
Cry1Ac ----SIFSN*TVPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRN*FSGTAGVI
560 570 580 590 600
gi|183 NLLINL*FHP*TPD*PNR*NH*IHV*NN*GDM*NV*DY*GK*DS*VAD*GL*FN*KITATIPSDAWYSGTITSM
680 690 700 710 720 730
Cry1Ac --IDRFEP*IPV*ATLEAEYNLERAQKAVNAL*FTSTNQLGLKTNVTDYHIDQVSNLVTYLS
610 620 630 640 650 660
gi|183 HLFNDNNFKTITPKFELSNELENI*TTQV*NA*LFASSAQD*TLASNVSDYIEQVVMKVDALS
740 750 760 770 780 790
Cry1Ac DEFCLDEKRE*SEKVKHAKR*LSDERNLLQDSNFKDINRQPERG*WGSGTGITIQGGDDVFK
670 680 690 700 710 720
gi|183 DEVFG*EK*KA*LR*KL*LVNQAKR*LSKIRNLLIGGNFDNLV----AWYMGKDVVKESDH*ELFK
800 810 820 830 840
Cry1Ac ENYV*TL*SG-TFDE*CY*TYL*YQKID*ESK*LKAF*TRYQLR*GYIEDSQDLEIYSIRYNAK-HET
730 740 750 760 770
gi|183 SDH*VLL*PP*PT*F---HPSYIFQKVE*ESK*LPN*TRY*TI*SGFIAHG*ED*VELV*VSRY*GQ*EIQ*V
850 860 870 880 890 900
Cry1Ac VNVPGT*GSL*W*PLSAQ*SPI*GK*GEPNRCAPHLEWNPDLDC*SCR*DG*EK*CAH*SHH*FSLDIDV
780 790 800 810 820 830
gi|183 MQVPY*E*EAL-PLT*SESN-SSC-----CVP*NLNIN*ETLA-----DPHF*FYSIDV
910 920 930 940
Cry1Ac VNVPGT*GSL*W*PLSAQ*SPI*GK*GEPNRCAPHLEWNPDLDC*SCR*DG*EK*CAH*SHH*FSLDIDV
840 850 860 870 880 890

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Cry1Ac GCTDLNEDLGVVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
: . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|183 GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
950 960 970 980 990 1000
Cry1Ac WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIHAA*DKRVHSIREAYL
900 910 920 930 940
gi|183 TEITAIQ*PVLNQINALYENEDWNGSIRSNVSYHDLEQIMLPTLLKTE*INCNYDHPAFL
1010 1020 1030 1040 1050 1060
Cry1Ac PE-----LSVIPGVNA*IFEELEGRIFTAFSLYDARNVIKNGDFN*NGLSCWNVKGVHDVDE
950 960 970 980 990 1000
gi|183 LKVYHWFMTDRIGE*HGTILARFQEALDRAYTQLESRNLLHNGH*FTTDTANW*IEGDAHHT
1070 1080 1090 1100 1110 1120
Cry1Ac EQNNQR*SVL*V*PEW*EAEV*SQEVRVCP---GRGYILRV*TA*YKEGYGEGCVTIHEIEN*NTDE
1010 1020 1030 1040 1050 1060
gi|183 ILEDGRVLR*LPD*WSSNATQ*TI*EIEDFDLDQ*EYQLLIHAK---GKGSITLQHG*EENEYV
1130 1140 1150 1160 1170 1180
Cry1Ac LKFSN*CV*EE*E*E*IP*NN*TV*TCNDY*TVNQ*EEYGGAYTSRNR*GYNEAP*SPADYASVY*E*E*KS*Y*
1070 1080 1090 1100 1110 1120
gi|183 ETH*TH*HT*ND*FIT*SQ*NI*P*FT*FK*GNQIEV*HITS*ED*GE*FL*DI*HIT*VIEV*SK*TD*NT*NI*E*NSP
1190 1200 1210 1220 1230 1240
>>gi|997763|gb|AAA76064.1| Sequence 2 from patent US 543 (1257 aa)
initn: 744 initl: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08
Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
(33-1058:60-1177)
Cry1Ac QAMD*NN*PN*INECIPYNCLSNPEVEVLGG*ER*IE*TG-YTPIDISL*SL*TFLLSEFVPGAGFV
10 20 30 40 50 60
gi|997 SKYDEMIKAF*EK*W*KK*GAK*GK*DLLD*VAW*YI*IT*G*EID*PLNVIKGVLSV*--TLIPEV*G*TV
30 40 50 60 70 80
Cry1Ac LG---LVDII*WG-IFG--PSQWDA*FLV---QIEQLINQRI*E*EFARNQAI*SRLEGLSNLY
70 80 90 100 110
gi|997 ASA*ASTIVSFI*WPKIF*GDKPN*AKNIFEELK*PQIEALIQDITNYQDAIN*QK*FK*FDSLQ*KT*
90 100 110 120 130 140
Cry1Ac QIYA*ESFREWEAD*PTN*PALREEMRIQFNDMNSAL*TTAIP*LF*AVQNYQV*PLLSVYVQAANL
120 130 140 150 160 170
gi|997 NLY*TV*AI-----DNNDYV---TAKTQ*LENLNSIL*TS*DISIF*IE*G*Y*ET*GGLPY*Y*AV*NA
150 160 170 180 190
Cry1Ac HLSVLRD*VSVFGQR*W*G*FDAATINSRYNDL*TRLIGNYTDH*AVRWYNTGLER*V*W*G*P*DR*DWI
180 190 200 210 220 230
gi|997 HILL*LRDAIVNA*EK*LG*FS*DK*EVD*TH*KKYIKMTI*HN*HTEAVIK*AF*NL*GL*DK*FK*SLD*VNS*YN
200 210 220 230 240 250
Cry1Ac 240 250 260 270 280

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Cry1Ac RYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYT---NPVLENFDGS-----
gi|997 KKANYIKGMTEMLDLVALWPTFDPDHYQKEVEIEFTRTIISSPIYQPVKMNQNTSSSIV
260 270 280 290 300 310

Cry1Ac -----FRGSAQIEGSIKRSRPH--LMDILNSI--TIYTDahrgeyyw-----SGHQ
gi|997 PSDLFHYQGDVLKLEFSTRTDNDGLAKIFTGIRNTFYKSPNTHETIYHVDVFSYNTQSSGNI
320 330 340 350 360 370

Cry1Ac IMAS---PVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGQVYRSLSTLYRRPFNIGIN
gi|997 SRGSSNPIPIDLNNPIISTCIRNSFYKAIAGSSVLVNFKDG--TQGYAFAQAPTG-GAW
380 390 400 410 420 430

Cry1Ac NQQLSVLDGT---EFAYGTSSNLPSAVYRKSgtVDSLDEIPPQNN-----NVPPRQG
gi|997 DHSFIESDGAPEGHKLNIIYTS--PGDTLRDFINVTLLSTPTINELSTEKIKGFPAEKG
440 450 460 470 480 490

Cry1Ac FSHRLSHVSMF-RSGFSNSSVSII---RAPMFSWIH--RSAEFNNIIASDSITQIPAVKG
gi|997 YIKNQGIKMYGKPEYINGAQPVNLENQOTLIFEHASKTAQYTIIRIRYAS-TQ--GTKG
500 510 520 530 540 550

Cry1Ac NFLFNGSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
gi|997 YFRLDNQBLQTLNIPITSHNGYVTGNIGENYDLYTIGSYTITEGNTLQIQHNDKNGMVL
560 570 580 590 600 610

Cry1Ac PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWNNS-----
gi|997 RIEFVPKDSLQDSDPPEVHESTIIFDKSSPTIWSNKHSHYHLEGSYTSQGSYPH
620 630 640 650 660 670

Cry1Ac ---SIFSNTPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRNFGTAGVI
gi|997 NLLINLFHPTDPNRNHTIHVNNGDMNVYDGDVADGLNFKITATIPSDAWYSGTITSM
680 690 700 710 720 730

Cry1Ac --IDRFEPVPTATLEAEYNLERAQKAVNALFTSNQLGLKTNVTDYHIDQVSNLVTYLS
gi|997 HLFNDNNFKTITPKFELSNELENITTQVNALFASSAQDTLANSVSDYWIEQVVMKVDALS
740 750 760 770 780 790

Cry1Ac DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFK
gi|997 DEVFGKEKKALRKLVLNQAKRLSKIRNLLIGGNFDNLV----AWYMGKDVVKESDHELK
800 810 820 830 840

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Cry1Ac ENYVTLSG-TFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HET
gi|997 SDHVLPPPTF---HPSYIFQKVEESKLPNTRYTISGFIAHGEDVELVVSRYGQEIQKV
850 860 870 880 890 900

Cry1Ac VNVPGTGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFLSDIDV
gi|997 MQVPYEEAL-PLTSESN-SSC-----CVPNLNINETLA-----DPHFFSYSIDV
910 920 930 940

Cry1Ac GCTDLNEDLGVVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
gi|997 GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
950 960 970 980 990 1000

Cry1Ac WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIHAAADKRVHSIREAYL
gi|997 TEITAIQPVNLQINALYENEDWNGSIRSNVSYHDLEQIMLPTLLKTEEINCNDHPAPL
1010 1020 1030 1040 1050 1060

Cry1Ac PE-----LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGHVDVE
gi|997 LKVYHFMFMDRIGEHGTILARFQEQALDRAYTQLESRNLLHNGHFTTDTANWITIEGDAHHT
1070 1080 1090 1100 1110 1120

Cry1Ac EQNNQRSVLVPEWAEVSEQEVRVCP---GRGYILRVVTAYKEGYGEGCVTIHEIENNTDE
gi|997 ILEDGRRVLRLPDWSSNATQTIIEIDFDLDDQYQLLIHAK---GKGSITLQHGEEENEYV
1130 1140 1150 1160 1170 1180

Cry1Ac LKFSNCEVEEIIYPNNIVTCDNYTVNQEEYGGAYTSRNRGYNEAPSVADYASVYEEKSYT
gi|997 ETHTHHTNDFITSNIPFTFKGNQIEVHITSEDEGFLDITVIEVSKTDTNTNIIENSP
1190 1200 1210 1220 1230 1240

>>gi|12810189|gb|AAE44104.1| Sequence 6 from patent US 6 (1257 aa)
initn: 744 initl: 222 opt: 266 Z-score: 302.1 bits: 68.0 E(): 6.6e-08
Smith-Waterman score: 738; 23.222% identity (54.070% similar) in 1167 aa overlap
(33-1058:60-1177)

Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLSEFVPGAGFV
gi|128 SKYDEMIKAFKWKKKGAKGKDLLDVAWYIITTEIDPLNVIKGLSVL--TLIPEVGTV
30 40 50 60 70 80

Cry1Ac LG---LVDIIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNQAI SRLEGLSNLY
gi|128 ASAASTIVSFIWPKIFGDKPNKAKNIFEELKPKQIEALIQDDIYNYQDAINQKFKDSLQKTI
90 100 110 120 130 140

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10      20      30      40      50      60
Cry1Ac QAMDNPNINECIPYNCLSNPEVEVLGGERIETG-YTPIDISLSLTQFLLESEFVPGAGFV
gi|401 SKYDEMIKAFEKKWKKGKAGKDLLDVAWYITTGEIDPLNVIKGVLSVL--TLIPEVGTV
30      40      50      60      70      80

70      80      90      100     110
Cry1Ac LG---LVLDIWG-IFG--PSQWDAFLV---QIEQLINQRIEEFARNQAISRLEGLSNLY
gi|401 ASAASTIVSFIWPKIFGDKPNAKNIFEELKPKQIEALIQQDITNYQDAINQKKFDSLQKTI
90      100     110     120     130     140

120     130     140     150     160     170
Cry1Ac QIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|401 NLYTVAI-----DNNDYV---TAKTQLENLNSILTSDISIFPEGYETGGLPYAMVANA
150     160     170     180     190

180     190     200     210     220     230
Cry1Ac HLSVLRDVSVFQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWI
gi|401 HILLRLDAIVNAEKLGFSDKEVDTHKKYIKMTIHNHTEAVIKAFNLGLDKFKSLDVNSYN
200     210     220     230     240     250

240     250     260     270     280
Cry1Ac RYNQFRRELTLTLDIVSLFPNYDSRTYPIRTVSQLTREIYT---NPVLENFDGS-----
gi|401 KKANYIKGMTEMLDLVALWPTFFDPDHYQKEVEIEFTRTISSPIYQPVPKMNQNTSSSIV
260     270     280     290     300     310

290     300     310     320
Cry1Ac -----FRGSAQIEGSIRSPH--LMDILNSI--TIYDHAHRGEYIW-----SGHQ
gi|401 PSDLFHYQGDVLKLEFSTRTDNDGLAKIFTGIRNTFYKSPNTHETHYHVDFSYNTQSSGNI
320     330     340     350     360     370

330     340     350     360     370     380
Cry1Ac IMAS---PVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRSLSTLYRRPFNIGIN
gi|401 SRGSSNPIDLNNPIISTCIRNSFYKAIAGSSVLVNFKDG---TQGYAFAQAPTG-GAW
380     390     400     410     420     430

390     400     410     420
Cry1Ac NQQLSVLDGT----EFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNN-----NVPPRQG
gi|401 DHSFIESDGAPEGHKLNYIYTS--PGDTRLDFINVYTLISTPTINELSTEKIKGFPAEKG
440     450     460     470     480     490

430     440     450     460     470     480
Cry1Ac FSHRLSHVSMF-RSGFSNSSVSII---RAPMFSWIH--RSAEFNNIIASDSITQIPAVKG
gi|401 YIKNQGIMKYYGKPEYINGAQPVNLENQQTILIFEHASKTAQYTIIRIRYAS-TQ--GTKG
500     510     520     530     540     550

490     500     510     520
Cry1Ac NFLFNGSVI-----SGPGFTGG-----DLVRLNS---SGNN---IQNR---GYIEV
gi|401 YFRLDNQELQTLNIPTSHNGYVTGNIGENYDLYTIGSYTITBGNHTLQIQHNDKNGMVL

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560     570     580     590     600     610
Cry1Ac PIHF-PSTSTR-----YRVRVRYASVTP-----IHLNVNWGNS-----
gi|401 RIEFVFKDSLQDSDPQSPPEVHSTIIFDKSSPTIWSSNKHSYSHIHLEGSYTSQGSYPH
620     630     640     650     660     670

560     570     580     590     600
Cry1Ac ---SIFSNTVPATATSL---DNLQSSDFGYFESANA--FTSSLGNIVGVRNFSGTAGVI
gi|401 NLLINLFHPTDPNRNHTIHVNNGDMNVDYKDSVADGLNFKITATIPSDAWYSGTITSM
680     690     700     710     720     730

610     620     630     640     650     660
Cry1Ac --IDRFEPFIVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLS
gi|401 HLFNDNNFKTITPKFELSNELENITQVNALPASSAODTLASNVSQVWIEQVMKVDALS
740     750     760     770     780     790

670     680     690     700     710     720
Cry1Ac DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGGWGSGTITIQGGDDVFK
gi|401 DEVFGKEKALRKLNVQAKRLSKIRNLLIGGNFDNLV----AWYMGKDVVKESDHELFS
800     810     820     830     840

730     740     750     760     770
Cry1Ac ENYVTLGS-TFDECYPTYLYQKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAK-HET
gi|401 SDHVLPPPTF--HPSYIFQKVEESKLPNTRYTISGFIAHGEDVELVVSRYGQEIQKV
850     860     870     880     890     900

780     790     800     810     820     830
Cry1Ac VNVPGTGSWLPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDEKCAHSHHFLSDIDV
gi|401 MQVPYEEAL-PLTSEN-SSC-----CVPNLNINETLA-----DPHFFYSIDV
910     920     930     940

840     850     860     870     880     890
Cry1Ac GCTDLNEDLVGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARVKRAEKKWRDKREKLE
gi|401 GSLEMEANPGIEFGLRIVKPTGMARVSNLEIREDRPLTAKEIRQVQRAARDWKQNYEQER
950     960     970     980     990     1000

900     910     920     930     940
Cry1Ac WETNIVYKEAKESVDALFVNSQ-----YDQLQADTNIAMIAHADKRVHSIREAYL
gi|401 TBITAIQPVLNQINALYENEDWNGSIRSNVSYHDLEQIMLPTLLKTEEINCNYDHPAFL
1010    1020    1030    1040    1050    1060

950     960     970     980     990     1000
Cry1Ac PE-----LSVIPGVNAAIFFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWCWNVKGVHDVE
gi|401 LKVYHWFMTDRIGEHTILARFQEALDRAYTQLESRNLLHNGHFTTDTANWTIEGDAHHT
1070    1080    1090    1100    1110    1120

1010    1020    1030    1040    1050    1060
Cry1Ac EQNNQRSVLVVPEWEAEVSVQEVRCV---GRGYILRVTAKEYGEGCVTIHEIENNTDE

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      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 TBITAIIQPVLNQINALYENEDWNGSIRSNSVSYHDLEQIMLPTLLKTEEINCNDHPAFL
      1010      1020      1030      1040      1050      1060

      950      960      970      980      990      1000
Cry1Ac PE-----LSVIPGVNAAFEELEGRIFTAFSLYDARNVIKNGDFNNGLSWNKGVHVDVE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 LKVYHWFMTDRIGEHTILARFQEALDRAYTQLESRNLLHNGHFTTDTANWTIEGDAHHT
      1070      1080      1090      1100      1110      1120

      1010      1020      1030      1040      1050      1060
Cry1Ac EQNNQRSVLVPEWAEVSEVRCVCP---GRGYILRVYAYKEGYGECVTHIEIENNTDE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|209 ILEDGRRVRLRPDWSNATQTIEIEDFDLDQEQYQLLIHAK---GKGSITLQHGEEENEYV
      1130      1140      1150      1160      1170      1180

      1070      1080      1090      1100      1110      1120
Cry1Ac LKFSNCVEEIEYPNNTVTCDYTVNQEEYGGAYTSRNRGYNEAPSPADYASVYEEKSYT

gi|209 ETHHTHTNDFITSQNIPFTFKGNQIEVHITSEDEGLFDIHITVIEVSKTDTNTNIIENSP
      1190      1200      1210      1220      1230      1240

```

>>gi|1429252|emb|CAA67506.1| parasporal crystal protein (706 aa)  
 initn: 160 initl: 119 opt: 262 Z-score: 301.1 bits: 67.0 E(): 7.5e-08  
 Smith-Waterman score: 262; 26.953% identity (62.891% similar) in 256 aa overlap  
 (6-251:84-332)

```

      10      20      30
Cry1Ac          CMQAMDNNP-NINECIPYNCLSNPEVEVLGGERIE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142 PIYNNNDNNDNAICDELGLTPIDNNTICSTDFTPINVMRTDPFRKKSTQELTREWEKWE
      60      70      80      90      100      110

      40      50      60      70      80
Cry1Ac TG---YTPIDISLSLTQFLLSEFVPGA-GFVLG-LVDIIWGFGPSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142 NSPSLFTPAIVGV-VTSFLLQSLKKQATSFLKLTLDLFPNNSSLTMEIEILRATEQYVQ
      120      130      140      150      160      170

      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAISRLEGLSN---LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142 ERLD TDTANRVSQELVGLKNNLTTFNDQVEDFLQNRVGLSPLAII DSI---NTMQQLFV
      180      190      200      210      220

      150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142 NRLPQFQVSGYQVLLLPFAQAATLHLTFLRDVIINADEWNIPTAQLNTYTRYFKEYIAE
      230      240      250      260      270      280

      210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIR-YNQFRRELTLTVLDIVLFPNYSRTPYRTVVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|142 YSNYALSTYDDGFRTRFYF--RNTLEDMLQFKTFMTLNALDLVSIWLLKYVNLVSTSA
      290      300      310      320      330      340

      270      280      290      300      310      320
Cry1Ac QLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHLMIDLNSITIIYTDHRGEYIYWSGHQI

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gi|142 NLYNIGDNKVNNEGAYPISYGPFFNSYIQTKSNYVLSGVSGIGARFYSTVLRGRLHDDLK
      350      360      370      380      390      400

>>gi|15105505|gb|AAE66099.1| Sequence 2 from patent US 6 (706 aa)
  initn: 160 initl: 119 opt: 262 Z-score: 301.1 bits: 67.0 E(): 7.5e-08
  Smith-Waterman score: 262; 26.953% identity (62.891% similar) in 256 aa overlap
  (6-251:84-332)

      10      20      30
Cry1Ac          CMQAMDNNP-NINECIPYNCLSNPEVEVLGGERIE
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|151 PIYNNNDNNDNAICDELGLTPIDNNTICSTDFTPINVMRTDPFRKKSTQELTREWEKWE
      60      70      80      90      100      110

      40      50      60      70      80
Cry1Ac TG---YTPIDISLSLTQFLLSEFVPGA-GFVLG-LVDIIWGFGPSQWDAFLVQIEQLIN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|151 NSPSLFTPAIVGV-VTSFLLQSLKKQATSFLKLTLDLFPNNSSLTMEIEILRATEQYVQ
      120      130      140      150      160      170

      90      100      110      120      130      140
Cry1Ac QRIEEFARNQAISRLEGLSN---LYQIYAESFREWEADPTNPALREEMRIQFNDMNSALT
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|151 ERLD TDTANRVSQELVGLKNNLTTFNDQVEDFLQNRVGLSPLAII DSI---NTMQQLFV
      180      190      200      210      220

      150      160      170      180      190      200
Cry1Ac TAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQWGFDAATINSRYNDLTRLIGN
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|151 NRLPQFQVSGYQVLLLPFAQAATLHLTFLRDVIINADEWNIPTAQLNTYTRYFKEYIAE
      230      240      250      260      270      280

      210      220      230      240      250      260
Cry1Ac YTDHAVRWYNTGLERVWGPDSRDWIR-YNQFRRELTLTVLDIVLFPNYSRTPYRTVVS
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|151 YSNYALSTYDDGFRTRFYF--RNTLEDMLQFKTFMTLNALDLVSIWLLKYVNLVSTSA
      290      300      310      320      330      340

      270      280      290      300      310      320
Cry1Ac QLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHLMIDLNSITIIYTDHRGEYIYWSGHQI

```

>>gi|158478175|gb|ABW49932.1| Sequence 6 from patent US (627 aa)  
 initn: 241 initl: 140 opt: 259 Z-score: 298.3 bits: 66.3 E(): 1.1e-07  
 Smith-Waterman score: 264; 21.762% identity (55.095% similar) in 579 aa overlap  
 (45-595:56-594)

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVGLVDIIWGF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|158 FEHKS LDTIQKEWMEWKRTDHSLSYVPIVGTIASFLLKIGGLIKRILSELKNLIFPSG
      30      40      50      60      70      80

      80      90      100      110      120      130
Cry1Ac GPSQWDAFLVQIEQLINQRIEE--FARNQAISRLEGLSNLYQIYAESFREWEADPTNPAL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```





Smith-Waterman score: 245; 80.000% identity (90.000% similar) in 50 aa overlap (126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|566 SNPALREEMRTQFNVMSALIAAIPLLRVR
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|566 NYEVALLSVYVQAANLHLSV
40 50

>>gi|14103756|gb|AAE55190.1| Sequence 41 from patent US (50 aa)
initn: 245 init1: 245 opt: 245 Z-score: 298.2 bits: 62.6 E(): 1.1e-07
Smith-Waterman score: 245; 80.000% identity (90.000% similar) in 50 aa overlap (126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|141 SNPALREEMRTQFNVMSALIAAIPLLRVR
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|141 NYEVALLSVYVQAANLHLSV
40 50

>>gi|23325101|gb|AAN23801.1| Sequence 41 from patent US (50 aa)
initn: 245 init1: 245 opt: 245 Z-score: 298.2 bits: 62.6 E(): 1.1e-07
Smith-Waterman score: 245; 80.000% identity (90.000% similar) in 50 aa overlap (126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|233 SNPALREEMRTQFNVMSALIAAIPLLRVR
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|233 NYEVALLSVYVQAANLHLSV
40 50

>>gi|56664656|gb|AAW18081.1| Sequence 41 from patent US (50 aa)
initn: 245 init1: 245 opt: 245 Z-score: 298.2 bits: 62.6 E(): 1.1e-07
Smith-Waterman score: 245; 80.000% identity (90.000% similar) in 50 aa overlap (126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|566 SNPALREEMRTQFNVMSALIAAIPLLRVR
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|566 NYEVALLSVYVQAANLHLSV
40 50

>>gi|14112761|gb|AAE58176.1| Sequence 41 from patent US (50 aa)
initn: 245 init1: 245 opt: 245 Z-score: 298.2 bits: 62.6 E(): 1.1e-07
Smith-Waterman score: 245; 80.000% identity (90.000% similar) in 50 aa overlap (126-175:1-50)

100 110 120 130 140 150
Cry1Ac ARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQ
gi|141 SNPALREEMRTQFNVMSALIAAIPLLRVR
10 20 30

160 170 180 190 200 210
Cry1Ac NYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWY
gi|141 NYEVALLSVYVQAANLHLSV
40 50

>>gi|16240156|gb|AAE79611.1| Sequence 7 from patent US 6 (137 aa)
initn: 250 init1: 135 opt: 250 Z-score: 297.6 bits: 63.9 E(): 1.2e-07
Smith-Waterman score: 250; 37.324% identity (62.676% similar) in 142 aa overlap (495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|162 PGFXGGDILRRTSPXQISXLRVNITAPL--
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVYASVTPIHNLNWNWGNSSIFSNTVPATATSLDNLQSSDF---GYFESAN
gi|162 ---SQRYRVRIXXASTTXXQFHTSIXGRPINQGNFSXTMSSGNSLQSGXFRVTGPTTPXN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac AFTSSLGNIVGVRNFGTAGVIIDRFEPVPTATLAEYNLERAQKAVNALFTSTNQLGL
gi|162 FSNNGSVFTLSXHVFNNGNEVYIDRIEFVPAEVTFAEYDLERAKKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504385|gb|AAM57088.1| Sequence 7 from patent US 6 (137 aa)
initn: 250 init1: 135 opt: 250 Z-score: 297.6 bits: 63.9 E(): 1.2e-07
Smith-Waterman score: 250; 37.324% identity (62.676% similar) in 142 aa overlap (495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|215 PGFXGGDILRRTSPXQISXLRVNITAPL--

```

                10      20
Cry1Ac 530      540      550      560      570      580
PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215 ---SQRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
30      40      50      60      70      80

```

```

                590      600      610      620      630      640
Cry1Ac AFTSSLGNIVGVRNFSVSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|215 FSNSSVFTLSXHVFNFSNGNEVYIDRIEFVPAEVTFEAEYDLERAKVASLFL
90      100     110     120     130

```

```

                650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|53970012|gb|AAV19105.1| Sequence 7 from patent US 6 (137 aa)
  initn: 250 initl: 135 opt: 250 Z-score: 297.6 bits: 63.9 E(): 1.2e-07
Smith-Waterman score: 250; 37.324% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

                470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539          PGFXGGDILRRITSPXQISXLRVNIITAPL--
                10      20

```

```

                530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 ---SQRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
30      40      50      60      70      80

```

```

                590      600      610      620      630      640
Cry1Ac AFTSSLGNIVGVRNFSVSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 FSNSSVFTLSXHVFNFSNGNEVYIDRIEFVPAEVTFEAEYDLERAKVASLFL
90      100     110     120     130

```

```

                650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|33731229|gb|AAQ37292.1| Sequence 7 from patent US 6 (137 aa)
  initn: 250 initl: 135 opt: 250 Z-score: 297.6 bits: 63.9 E(): 1.2e-07
Smith-Waterman score: 250; 37.324% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

                470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337          PGFXGGDILRRITSPXQISXLRVNIITAPL--
                10      20

```

```

                530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 ---SQRYRVRVRYASVTPPIHLNVNWNSSIFSNTPVATATSLDNLQSSDF---GYFESAN
30      40      50      60      70      80

```

```

                590      600      610      620      630      640
Cry1Ac AFTSSLGNIVGVRNFSVSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
.. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 FSNSSVFTLSXHVFNFSNGNEVYIDRIEFVPAEVTFEAEYDLERAKVASLFL
90      100     110     120     130

```

```

                650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|155097691|gb|ABT00622.1| Sequence 212 from patent U (634 aa)
  initn: 181 initl: 144 opt: 257 Z-score: 295.9 bits: 65.8 E(): 1.5e-07
Smith-Waterman score: 264; 22.147% identity (52.981% similar) in 587 aa overlap
(45-595:57-601)

```

```

                20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVVLG--LVDIIWGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKK---VGLVKGKRLSELWGLI
30      40      50      60      70      80

```

```

                80      90      100     110     120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FPSGSTNLMDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNP
90      100     110     120     130

```

```

                130     140     150     160     170     180
Cry1Ac ---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NRNAVPLSITSSVNTMQQLFLSRLPQFVQGYQLLLLLPLFAQAANMHLSFIRDVVLNADE
140    150     160     170     180     190

```

```

                190     200     210     220     230     240
Cry1Ac WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 WGISAATLRTYRDYLKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLN
200    210     220     230     240     250

```

```

                250     260     270     280     290     300
Cry1Ac VLDIVSLFPNYSRTPYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSIKSPHLMDI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VFEYVSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSFLQVNSNYV
260    270     280     290     300

```

```

                310     320     330     340     350
Cry1Ac LNSIT-----IYTDARHGEYYSWGHQIMASPVGSGPEFTFPFLYGTMGNAAPQQRIVAQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 LNGFSGARLSNTFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASFPNQNFCS
310    320     330     340     350     360

```

```

                360     370     380     390     400     410
Cry1Ac LGQGVYRTLSSTLYRRFPNIGINNQL--SVLDGTEFAYGTSSNLPASAVYRKSQVDSLDSE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 T---FLPPLLPFFVRSWLDGSDREGVATVTNWTESFESTIGIRCGAFARGNSNYFPD
370    380     390     400     410     420

```

```

                420     430     440     450     460     470
Cry1Ac IPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNIIAS

```

```

      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAV
      430      440      450      460      470

```

```

      480      490      500      510      520      530
Cry1Ac DSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|155 HE-----NGSMIHLAPNDYTGFITSPIHATQVNNQTRTFISEKFGNQGDSL
      480      490      500      510      520

```

```

      540      550      560      570
Cry1Ac YR---VRVRYA----SVTPIHLNVN-WGNSSIFS--NIVPATATSLDNLQSSDFGYFES
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|155 FEQNNTTARYTLGGNGNSYNLYLRVSSIGNSTIRVTINGRVYVATNVNTTTNND-GVNDN
      530      540      550      560      570      580

```

```

      580      590      600      610      620      630
Cry1Ac ANAFTS-SLGNIVGVNRFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQ
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|155 GARFSDINMGVNVASSNSDVLPLDINVTFNSTQDFLNMIMLVPTNISPIY
      590      600      610      620      630

```

```

>>gi|33731254|gb|AAQ37317.1| Sequence 57 from patent US (137 aa)
  initn: 231 init1: 126 opt: 246 Z-score: 292.8 bits: 63.1 E(): 2.2e-07
Smith-Waterman score: 246; 38.028% identity (64.789% similar) in 142 aa overlap
(495-633:1-137)

```

```

      470      480      490      500      510      520
Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|337          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|337 PLTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|337 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVASLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|21504418|gb|AAM57113.1| Sequence 57 from patent US (137 aa)
  initn: 231 init1: 126 opt: 246 Z-score: 292.8 bits: 63.1 E(): 2.2e-07
Smith-Waterman score: 246; 38.028% identity (64.789% similar) in 142 aa overlap
(495-633:1-137)

```

```

      470      480      490      500      510      520
Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|215          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|215 PLTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|215 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVASLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|215 PLTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|215 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVASLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|16240190|gb|AAE79636.1| Sequence 57 from patent US (137 aa)
  initn: 231 init1: 126 opt: 246 Z-score: 292.8 bits: 63.1 E(): 2.2e-07
Smith-Waterman score: 246; 38.028% identity (64.789% similar) in 142 aa overlap
(495-633:1-137)

```

```

      470      480      490      500      510      520
Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|162          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|162 PLTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|162 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVASLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|53970037|gb|AAV19130.1| Sequence 57 from patent US (137 aa)
  initn: 231 init1: 126 opt: 246 Z-score: 292.8 bits: 63.1 E(): 2.2e-07
Smith-Waterman score: 246; 38.028% identity (64.789% similar) in 142 aa overlap
(495-633:1-137)

```

```

      470      480      490      500      510      520
Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|539          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|539 PLTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|539 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVASLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

      470      480      490      500      510      520
Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```

```

gi|539          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :

```



```

350      360      370      380      390      400
Cry1Ac  400      410      420      430      440      450
TSSNLPsAVYRKSGTVDLSDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
gi|155  TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPPGTPGG
410      420      430      440      450      460

```

```

460      470      480      490      500
Cry1Ac  IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNNGSVIS-GP-GFTGGDLVRLNSSG
gi|155  ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTTISP IHATR
470      480      490      500

```

```

510      520      530      540      550
Cry1Ac  NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
gi|155  VNNQTRTFISEKFGNQGDLSRFEQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTING
510      520      530      540      550      560

```

```

560      570      580      590      600      610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
gi|155  RYVTAANVNTTNNND-GVNDNGARFSDINIGNVVA---SDNSNPLD---INVTLNSG
570      580      590      600      610

```

```

620      630      640      650      660      670
Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
gi|155  TQFDL-----MNIMFVPTNLPPLY
620      630

```

>>gi|155097654|gb|ABT00585.1| Sequence 138 from patent U (634 aa)  
 initn: 184 initl: 146 opt: 252 Z-score: 290.0 bits: 64.8 E(): 3.1e-07  
 Smith-Waterman score: 269; 22.673% identity (53.469% similar) in 591 aa overlap  
 (45-595:57-601)

```

20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGIF
gi|155  FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLKK---VGSVLGKRI LSELWGLI
30      40      50      60      70      80

```

```

80      90      100     110     120
Cry1Ac  GPSQWDAFLVQI---EQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP
gi|155  FPSGSTNLMQDILRETEKFLNQLRLNTDTLARVNAEMTGL---QANVEEFNRQVDNFLNP
90      100     110     120     130

```

```

130     140     150     160     170     180
Cry1Ac  ---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQR
gi|155  NQNAVPLSITSSVNTLQQLFLNRLPQFRVQGYQLLLLPLFAQANLHLSFIRDVVLNADE
140     150     160     170     180     190

```

```

190     200     210     220     230     240
Cry1Ac  WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLT
gi|155  WGISAATLRTYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLHDHTL---EFRTYMFLN

```

```

200     210     220     230     240     250
Cry1Ac  250     260     270     280     290     300
VLDIVLSFPNYDSRTYPIRTVSQLTREIYTNVPLENFDGSGFRGSAQIEGSI RSPHLMDI
gi|155  VFEYVSIWLSLFKYQSLLVSSANL----YASGSGPQQTQSFTSQDWPFPLYSLFQVNSNYV
260     270     280     290     300

```

```

310     320     330     340     350
Cry1Ac  LNSITITYTDAHRGEYY-----WSGHQIMASPVGFGPEFTFFLYGTMGNAAPQORI
gi|155  LNG---FSGARSSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNF
310     320     330     340     350     360

```

```

360     370     380     390     400     410
Cry1Ac  VAQLQGQVYRTLSSTLYRRPFNIGINQQQL-SVLDGTEFAYGTSSNLPsAVYRKSGTVDs
gi|155  NCST---FLPPLLPFVRSWLDSGSDREGVAVTNNWQTESFETTLGLRSGAFTARGNSNY
370     380     390     400     410

```

```

420     430     440     450     460
Cry1Ac  LDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNI
gi|155  FPDYFIRNISGVPLVVKNE DLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNI
420     430     440     450     460     470

```

```

470     480     490     500     510     520
Cry1Ac  IASDSITQIPAVKGNFLFNNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----
gi|155  HAVHE-----NGSMIHLAPNDYTGFTTISP IHATQVNNQTRTFISEKFGNQGD
480     490     500     510     520

```

```

530     540     550     560     570
Cry1Ac  -IHFP--STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFG
gi|155  SLRFEQNNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVTNTNND-G
530     540     550     560     570     580

```

```

580     590     600     610     620     630
Cry1Ac  YFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFT
gi|155  VNDNGARFSDINIGNV VASSNSDVPDLINVTLNSGTQFDLMNIMLVPTNISPLY
590     600     610     620     630

```

>>gi|155097589|gb|ABT00520.1| Sequence 8 from patent US (634 aa)  
 initn: 140 initl: 140 opt: 251 Z-score: 288.8 bits: 64.5 E(): 3.6e-07  
 Smith-Waterman score: 273; 23.220% identity (52.542% similar) in 590 aa overlap  
 (81-637:95-629)

```

60      70      80      90      100     110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNL
gi|155  KVGSLVGRKRI SELSLIFPGSSTNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---
70      80      90      100     110     120

```

```

120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155  -QANVEEFNRQVDNFLNPNRNALPLSITSSVNTMQQLFLNRLPQFQIQGYQLLLLPLFAQ

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```

130      140      150      160      170      180
Cry1Ac 170      180      190      200      210      220
AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
190      200      210      220      230

230      240      250      260      270      280
Cry1Ac R--DWIRYNQFRRELTLTVLVDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
gi|155 RLHDM---EFRTYMFLNVFEYVSIWLSLFKYQSLVSSGANL---YASGSGPQQTQSFT
240      250      260      270      280      290

290      300      310      320      330
Cry1Ac GSAQGIIEGSIIRSPHMLDILNSITIIYTDahrgeyy-----wSGHQIMASPVGFSGPE
gi|155 SQDWPFLYSLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGTTTTHALLAARVNSYSGV
300      310      320      330      340

340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYG
gi|155 SS---GDIGASPFNFQFSCST---FLPPLLPFVRSWLDGSDRGVNTVITNWQTESFE
350      360      370      380      390      400

400      410      420      430      440      450
Cry1Ac TSSNLPsAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
410      420      430      440      450      460

460      470      480      490      500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
gi|155 ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
470      480      490      500

510      520      530      540      550
Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRYASVT-PIHLNVN-WGNSSIFS--NT
gi|155 VNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRNGNSYNLYLRVSSIGNSTIRVTING
510      520      530      540      550      560

560      570      580      590      600      610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
gi|155 RvyTATNVNTTNNND-GVNDNGARFSDINIGNVVA---SDNSNPLD---INVTLNSG
570      580      590      600      610

620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRElsekvk
gi|155 TQFDL-----MNIMFVPTNLPLLY
620      630

```

>>gi|155097693|gb|ABT00624.1| Sequence 216 from patent U (634 aa)  
 initn: 167 init1: 133 opt: 250 Z-score: 287.6 bits: 64.3 E(): 4.2e-07

Smith-Waterman score: 270; 22.658% identity (53.322% similar) in 587 aa overlap  
 (45-595:57-601)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWIGIF
gi|155 FQHKSLDVTQREWEWKKNNHSLYLDPIVGTVASFLLKK---VGSVLGKRILSELWNLI
30      40      50      60      70      80

80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAIISRLGLESLNYQIYAESFREWEADPTNP
gi|155 FPSGSTNLMDILRETEQFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNP
90      100      110      120      130

130      140      150      160      170      180
Cry1Ac ---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQR
gi|155 NRNAVPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLPLFAQANLHLSFIRDVILNADE
140      150      160      170      180      190

190      200      210      220      230      240
Cry1Ac WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLT
gi|155 WGISAAATLRTYRDYLKKNYTRDYSNYCINTYQSAFK---GLNTRLRHDTLTK---FRTYMFLN
200      210      220      230      240      250

250      260      270      280      290      300
Cry1Ac VLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGFSFRGSAQGIIEGSIIRSPHLM
gi|155 VFEYVSIWLSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYV
260      270      280      290      300

310      320      330      340      350
Cry1Ac LNSIT-----IYTDahrgeyywSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQ
gi|155 LNGFSGARLSNTFPNIVGLPGSTTTHALLAARVNSYSGGISS---GDIGASPFNFQFNC
310      320      330      340      350      360

360      370      380      390      400      410
Cry1Ac LGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDE
gi|155 T---FLPPLLPFVRSWLDGSDREGVATVITNWQTESFETTLGLRSGAFTARGNSNYFPD
370      380      390      400      410      420

420      430      440      450      460      470
Cry1Ac IPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIRAPMFSWIHRSAEFNIIAS
gi|155 YFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAV
430      440      450      460      470

480      490      500      510      520
Cry1Ac DSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTR
gi|155 HE-----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSL
480      490      500      510      520

```

Cry1Ac YR---VVRVRYA---SVTPIHNLV---NWGNSSIFS--NTVPATATSLDNLQSSDFGYFES



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gi|155 SS---GDIGASPFNQNFSCST---FLPPLLTPFVRSWLDSDRGGVNTVTNWQTESFE
350 360 370 380 390 400

Cry1Ac TSSNLPFAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSSNSV-SI
400 410 420 430 440 450

gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYSQIRNIESPSGTPGG
410 420 430 440 450 460

Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
460 470 480 490 500

gi|155 ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
470 480 490 500

Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
510 520 530 540 550

gi|155 VNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRNGNSYNLYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac VPATATSLDNLQSSDFGYFESANAFS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLE
560 570 580 590 600 610

gi|155 RVYTATNVTNTTND-GVNDGARFSDINIGNVVA---SDNSNVLPLD---INVTLNSG
570 580 590 600 610

Cry1Ac AEYNLERAQKAVNALFTSTNQGLKLTNVDYHIDQVSNLVYLSDEFCLDEKRELSEKVK
620 630 640 650 660 670

gi|155 TQFDL-----MNIMFVPTNLPLLY
620 630

>>gi|155097674|gb|ABT00605.1| Sequence 178 from patent U (634 aa)
initn: 178 init1: 144 opt: 249 Z-score: 286.5 bits: 64.1 E(): 4.9e-07
Smith-Waterman score: 270; 22.813% identity (53.002% similar) in 583 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIGWIF
20 30 40 50 60 70

gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGRKILLELRNLIFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEQFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFQGRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFQVQGYQLLLLPLFAQAANMHLFSIRDVVLNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTTLVLDI
190 200 210 220 230 240

gi|155 AATLRTYRDLKNYTREYSNYCINTYQSFAK---GLNTRLHDTL---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQTLREIYTNPVLENFDGSRGSAQIEGSIKRSPLMDILNSI
250 260 270 280 290 300

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNSF
260 270 280 290 300 310

Cry1Ac T-----IYTAHRGEYVWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQORIVAQLGQG
310 320 330 340 350 360

gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGSISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac VYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPFAVYRKSGTVDSLDEIPPQ
370 380 390 400 410 420

gi|155 FLPPLLTPFVRSWLDSDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N--NNVP--PRQGFSHRLSHVSMFRSGFSSNSV-SIIRAPMFSWIHRSAEFNIIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYR--
480 490 500 510 520 530

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490 500 510 520

Cry1Ac -VRVRYA-----SVTPHILNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAF
540 550 560 570 580

gi|155 NTTARYTLWGNNSYNLYLRVSSIGNSTIRVTINGRVYTATNVTNTTND-GVNDGARF
530 540 550 560 570 580

Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQGLK
590 600 610 620 630 640

gi|155 SDIKMGNVASSNSDVLINVTNFSGTQFDLMNIMLVPTNISPIY
590 600 610 620 630

>>gi|155097617|gb|ABT00548.1| Sequence 64 from patent US (634 aa)
initn: 139 init1: 139 opt: 249 Z-score: 286.5 bits: 64.1 E(): 4.9e-07
Smith-Waterman score: 270; 23.220% identity (52.373% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac LSEFVPGAGFVLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNL
60 70 80 90 100 110

gi|155 KVGSLVGRKIRLSELRSILFPGSTNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
120 130 140 150 160



Regulatory Product Characterization Team

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Cry1Ac -VRVRYA-----SVTPIHLLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAF
gi|155 NITARYTLWGNNSYNLYLRVSSIGNSTIRVTINGRVTATNVNTTNNND-GVNDNGARF
530 540 550 560 570 580

590 600 610 620 630 640
Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|155 SDIKMGVNVVASSNSDVPLDINVTFNSGTQFDLNMIMLVPTNISPIY
590 600 610 620 630

>>gi|155097614|gb|ABT00545.1| Sequence 58 from patent US (634 aa)
initn: 140 initl: 140 opt: 249 Z-score: 286.5 bits: 64.1 E(): 4.9e-07
Smith-Waterman score: 283; 22.930% identity (53.185% similar) in 628 aa overlap
(45-637:57-629)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF--VPGAGFVLGLVDIIGWIF
gi|155 FQHKSLDTVQEEWMEWKDNHSLYVDPVIGTVASFLLKKGSLVSKRILSELNLIFFPSG
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRTEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNQVDNFLNPNRRA
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLNVFEY
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFSAQIEGSIKSPHMLDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFQSDWPFYLSLQVNSNYVNLNG-
260 270 280 290 300 310

310 320 330 340 350
Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTPLYGTMGNAAPQQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTITTHALLAARVNYSGGVSS---GDIGASPFNQNFSCST
320 330 340 350 360

360 370 380 390 400 410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYKSGTVDSLDEI
gi|155 ---FLPPLLTpFVRSWLDSDRGVNTVTNWTESFETTLGLRSGAFTARGNSNHFPDY
370 380 390 400 410 420

420 430 440 450 460 470

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Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSFGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS-VHNKR--NNIYAVH
430 440 445 450 460 470

480 490 500 510 520
Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDLSLRF
480 490 500 510 520

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNITARYTLRGNNSYNLYLRVSSIGNSTIRVTINGRVYATNVNTTNNND-GVNDNG
530 540 550 560 570 580

590 600 610 620 630
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNL
590 600 610 620 630

640 650 660 670 680 690
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|21504415|gb|AAM57111.1| Sequence 53 from patent US (137 aa)
initn: 225 initl: 120 opt: 240 Z-score: 285.8 bits: 61.8 E(): 5.4e-07
Smith-Waterman score: 240; 37.324% identity (64.085% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNGYIEVPIHF
gi|215 PGFTGGDVIRRTNTGG---FGAIRVSVTG
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVN-WGNSSI--FSNTVPATATSLDNLQSSDFGYFESANA
gi|215 PLTQ-RYRIRFRYASTIDFDFFVTRGGTTINNFRFTRTMNRQGESRYESYRVEFTTPFN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|215 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDXEAACKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQP
gi|215

>>gi|53970035|gb|AAV19128.1| Sequence 53 from patent US (137 aa)
initn: 225 initl: 120 opt: 240 Z-score: 285.8 bits: 61.8 E(): 5.4e-07
Smith-Waterman score: 240; 37.324% identity (64.085% similar) in 142 aa overlap
(495-633:1-137)

```

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 PLTQ-RYRIRFRYASTIDFDFFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDXEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|16240188|gb|AAE79634.1| Sequence 53 from patent US (137 aa)  
 initn: 225 init1: 120 opt: 240 Z-score: 285.8 bits: 61.8 E(): 5.4e-07  
 Smith-Waterman score: 240; 37.324% identity (64.085% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 PLTQ-RYRIRFRYASTIDFDFFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDXEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|33731252|gb|AAQ37315.1| Sequence 53 from patent US (137 aa)  
 initn: 225 init1: 120 opt: 240 Z-score: 285.8 bits: 61.8 E(): 5.4e-07  
 Smith-Waterman score: 240; 37.324% identity (64.085% similar) in 142 aa overlap  
 (495-633:1-137)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337          PGFTGGDVIRRTNTGG---FGAIRVSVTG
                    10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANA
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 PLTQ-RYRIRFRYASTIDFDFFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFN
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSLGNI-VGVRNFGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 FTQSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDXEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|155097628|gb|ABT00559.1| Sequence 86 from patent US (634 aa)  
 initn: 174 init1: 138 opt: 248 Z-score: 285.3 bits: 63.9 E(): 5.7e-07  
 Smith-Waterman score: 271; 23.540% identity (53.650% similar) in 548 aa overlap  
 (81-595:95-601)

```

      60      70      80      90      100     110
Cry1Ac LSEFVPGAGFVLGLVDIINGIFGPSQWDAFLVQIEQLINQRIEFAFNQAIKRLSGLSNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KVGSLVVKRILSELRLSIFPGSTNMQDILRETEKFLNQLRNTDTLARVNALEGL---
      70      80      90      100     110     120

```

```

      120     130     140     150     160
Cry1Ac YQIYAESFREWEADTPN---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 -QANVEEFNRQVDNPLNPNRRAVPLSITSSVNTMQQLFLNRLPQFQMQYQLLLPLFAQ
      130     140     150     160     170     180

```

```

      170     180     190     200     210     220
Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYQNYLKNYTRDYSNYCINTYQTAFK---GLNT
      190     200     210     220     230

```

```

      230     240     250     260     270
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQL-----TREIYTNPVL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RLHDTL---EFRTYMFNLVFEYVSIWLSLFYQQLLVSSGANLYASGSGPQQRQSPFSQDW
      240     250     260     270     280     290

```

```

      280     290     300     310     320     330
Cry1Ac ENFDGSRGSAQIEGSIKIRSPHMLDILNSITITYTDAHRGEYVWSGHQIMASPVGFSGPEF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 PFLYSLFQVNSNYVNLNFGSARLSNTFPNIV---GLPGNT--TTHALLAARVNYSGGIS
      300     310     320     330     340

```

```

      340     350     360     370     380     390
Cry1Ac TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQQL--SVLDGTEFAYGT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 S----GDIGASPFNQFNFCST---FLPPLLPFVRSWLDGSDREGVATVTNWTQTESFET
      350     360     370     380     390     400

```

```

      400     410     420     430     440     450
Cry1Ac SSNLPASVYRKSQVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSV--SII
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

gi|155 TLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGA
410 420 430 440 450 460

Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGN
460 470 480 490 500 510

gi|155 RAYMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGTFTISPIHATQV
470 480 490 500

Cry1Ac NIQNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPIHLLNVN-WGNSSIFS--NT
520 530 540 550

gi|155 NNQTRTFISEKFGNQDGLRFEQNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
560 570 580 590 600 610

gi|155 RVYTATNVNTTTNND-GVNDNGARFSDINIGNVVASSNSDVLPLDINVTLSGTQDFLMMI
570 580 590 600 610 620

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK
620 630 640 650 660 670

gi|155 MLVPTNISPLY
630

>>gi|86440157|gb|ABC95997.1| Cry2Ac [Bacillus thuringien (623 aa)
initn: 201 init1: 166 opt: 247 Z-score: 284.2 bits: 63.7 E(): 6.5e-07
Smith-Waterman score: 257; 23.858% identity (54.992% similar) in 591 aa overlap
(85-637:98-618)

Cry1Ac VPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGL-SNLYQI
60 70 80 90 100 110

gi|864 LVGKRILSELQNLIFPGSIDLMQEIILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
120 130 140 150 160 170

gi|864 NRQVDNFLNPNQNPVPLAIIIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
130 140 150 160 170 180

Cry1Ac HLSVLRDVSFVGFQWRGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--D
180 190 200 210 220

gi|864 HLSFIRDVILNADEWGISAAATVRYDHLRNFTRNYSNYCINTYQTAFR---GLNTRLHD
190 200 210 220 230 240

Cry1Ac WIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQTLREIYTNVLENFDGSRGSAQ
230 240 250 260 270 280

gi|864 ML---EFRTYMFNLVFEYVSIWLSLFKYQSLVSSGANL---YASL-----GS--GPTQ
250 260 270 280

Cry1Ac GIEGSIRSPLMDILNSITIIYDHAHRGEYYWSGHQIMASPV--GFSGPE--FTFPLYGTM
290 300 310 320 330 340

gi|864 -----SFT----AQNWPFLYSLFQVNSNYVLNGLSGARTTITFPNIGGL
290 300 310 320

Cry1Ac GNAAPQ-----RIVAQLGQGVYRTLSSTLYRRPFNIG--INNQQL----SVLD-GTEF-
350 360 370 380 390

gi|864 PGSTTTQTLHFARINRVGGVSSSRIGQANL-NQNFNISTLFPNLPQTPFIRSWLDSGTRE
330 340 350 360 370 380

Cry1Ac AYGTSNLSAVYRKSGTVDSLDEIPPQNNVPPRQGFHRLSHVSMFRSGFSNSVSI
400 410 420 430 440 450

gi|864 GVATSTNWQSGAFETLLRFSIFSARGNSNFFP----DYFIRNISGVVGTISNADLA--
390 400 410 420 430

Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNS
460 470 480 490 500

gi|864 RPLYFNEI-RDI---GTTAVASLVTVHNRKNNIYDTHENGTMHILAPNDYTGTFTVPIHA
440 450 460 470 480 490

Cry1Ac SGNNIQNRGYIE-----VPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNT
510 520 530 540 550

gi|864 TQVNNQIRTFISEKYGNDGLRFEFSNTTARYTLRGNGNSYN-LYLRVSSIGSSTIRVT
500 510 520 530 540 550

Cry1Ac VPATATSLD-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATL
560 570 580 590 600 610

gi|864 INGRVYTANVNTTTNNDGVLNNGARFSDINIGNVVA---SANTNVPLD---IQVTFNG
560 570 580 590 600

Cry1Ac EAEBYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK
620 630 640 650 660 670

gi|864 NPQFEL-----MNIMFVPTNIPPLY
610 620

>>gi|120431602|gb|ABM21764.1| cry2A-type insecticidal cr (633 aa)
initn: 133 init1: 133 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.355% identity (53.925% similar) in 586 aa overlap
(45-595:56-600)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEF--VPGAGFVLGLVDIIWGF
20 30 40 50 60 70

gi|120 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVGLVKRILSELRLNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|120 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGFQWRGFD
130 140 150 160 170 180

gi|120 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 AATLRTYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQQLTR-----EIYTNPVLENFDGSGFRGSAQGIIEGSIRSPH
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 VSFWSVFKYQSLLVSSGANLNARGRGPQQAQSFSTSPGWAFNLNSLFQVNSNYVFNFRGAR
260 270 280 290 300 310

Cry1Ac LMDILNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLG
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 LFNSFPNIIGLPG-----FTTTHPLLAAKVNYKGRISS---GDIGASPVNQNFCS--
320 330 340 350 360

Cry1Ac QGVYRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEIP
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 -KFLPPLLPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSNYFPDYF
370 380 390 400 410 420

Cry1Ac PQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDS
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 IRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNKR--NNIHAVEH
430 440 450 460 470

Cry1Ac ITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRF
480 490 500 510 520

Cry1Ac --STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 QNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQ
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|120 ARFSDINIGNVVARSNSDVSLDINVSLNSRTLIDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097657|gb|ABT00588.1| Sequence 144 from patent U (634 aa)
initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 272; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGI
20 30 40 50 60 70
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FQHKSLDTVQEEWMEWKDNHSLYVDPIVGTVASFLLKKVGSVVGKRIKSELNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL----QANVEEFNRQVDNLFNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 AATLRTYRDLKKNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIRSPHMDILNSI
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VSIWLSLKFYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFVLSLQVNSNYVNLG-
260 270 280 290 300 310

Cry1Ac TIYTDHRGEYY-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 --FSGARLSQTFPNIVGLPGTTTHALLAARVNYSGGVSS---GDIGASPVNQNFSCST
320 330 340 350 360

Cry1Ac QGVYRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSQGTVDLDEI
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 ---FLPPLLPFVRSWLDGSDRGGVNTVNWQTESFETTLGLRSGAFTARGNSNYFPDYF
370 380 390 400 410 420

Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGLRAYMVS-VHNKR--NNIYAVH
430 440 450 460 470

Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRF
480 490 500 510 520

Cry1Ac PSTSTRYRVRVRYASVT-PIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 EQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQ
590 600 610 620 630

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gi|155 ARFSDINIGNVVA---SDNSNVPLD---INVTLNSGTQFEL-----MNIMFVPTNLS
590 600 610 620 630

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
640 650 660 670 680 690

gi|155 PLY

>>gi|155097671|gb|ABT00602.1| Sequence 172 from patent U (634 aa)
initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
20 30 40 50 60 70

gi|155 FQHKSLDVTQEEWMEWKDNHSLYVDPVIGTVASFLLKKVGLVSKRILSELRNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPLHMDILNSI
250 260 270 280 290 300

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLSFQVNSNYVLNG-
260 270 280 290 300 310

Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
310 320 330 340 350

gi|155 --FSGARLSQTFPNIVGLPGTTTHALLAARVNYSGGVSS---GDIGASFPNQNFSCST
320 330 340 350 360

Cry1Ac GQGVYRTLSSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPASVYRKSQVDSLDEI
360 370 380 390 400 410

gi|155 ---FLPPLLTTPFVRSWLDSDGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
420 430 440 450 460 470

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS-VHNKR--NNIYAVH
430 440 450 460 470

Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF
480 490 500 510 520

gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRF
480 490 500 510 520

Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
530 540 550 560 570 580

gi|155 EQSNTTARYTLRGNNGSNLYLRVSSIGNSTIRVTVINGRVYATATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
590 600 610 620 630

gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP
590 600 610 620 630

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
640 650 660 670 680 690

gi|155 PLY

>>gi|155097622|gb|ABT00553.1| Sequence 74 from patent US (634 aa)
initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
20 30 40 50 60 70

gi|155 FQHKSLDVTQEEWMEWKDNHSLYVDPVIGTVASFLLKKVGLVSKRILSELRNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPLHMDILNSI
250 260 270 280 290 300

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gi|155 VSIWSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNVVLNG-
260 270 280 290 300 310

Cry1Ac TIYTDAHRGEYY-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
310 320 330 340 350

gi|155 --FSGARLSQTFPNIVGLPGTTTTTHALLAARVNYSGGVSS---GDIGASPFNQNFSCST
320 330 340 350 360

Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQ-L-SVLDGTEFAYGTSSNLP-SAVYRKSGETVDSLDEI
360 370 380 390 400 410

gi|155 ---FLPPLLTFFVRSWLDSDGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASD
420 430 440 450 460 470

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS-VHNRK--NNIYAVH
430 440 450 460 470

Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNNSGNNIQNRGYIEVP-----IHF
480 490 500 510 520

gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF
480 490 500 510 520

Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
530 540 550 560 570 580

gi|155 EQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
590 600 610 620 630

gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP
590 600 610 620 630

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
640 650 660 670 680 690

gi|155 PLY

>>gi|155097646|gb|ABT00577.1| Sequence 122 from patent U (634 aa)
initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGI
80 90 100 110 120

gi|155 FQHKSLDTVQEEWMEWKKDNHSLYVDPIVGTVASFLLKKVGLSKRLSELRLNLIFFPSG
80 90 100 110 120

Cry1Ac GPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEKFLNQRINTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
190 200 210 220 230 240

gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHML---EPRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSGIRSPHMLDILNSI
250 260 270 280 290 300

gi|155 VSIWSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNVVLNG-
260 270 280 290 300 310

Cry1Ac TIYTDAHRGEYY-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
310 320 330 340 350

gi|155 --FSGARLSQTFPNIVGLPGTTTTTHALLAARVNYSGGVSS---GDIGASPFNQNFSCST
320 330 340 350 360

Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQ-L-SVLDGTEFAYGTSSNLP-SAVYRKSGETVDSLDEI
360 370 380 390 400 410

gi|155 ---FLPPLLTFFVRSWLDSDGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASD
420 430 440 450 460 470

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS-VHNRK--NNIYAVH
430 440 450 460 470

Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNNSGNNIQNRGYIEVP-----IHF
480 490 500 510 520

gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF
480 490 500 510 520

Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
530 540 550 560 570 580

gi|155 EQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
590 600 610 620 630

gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP
590 600 610 620 630

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
640 650 660 670 680 690

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Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINR

gi|155 PLY

>>gi|155097655|gb|ABT00586.1| Sequence 140 from patent U (634 aa)
initn: 167 initl: 131 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 258; 22.945% identity (53.425% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF

gi|155 FQHKSLDTVQREWTEWKKNHSLYLDPIVGTVASFLLKKVGSLSIKRILSELRNLIFFPSG
30 40 50 60 70 80

Cry1Ac 80 90 100 110 120
GPSQWDAFLVQIEQLINQRIEFARNQAISRLLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELEGL---QANVEEFNRQVDNFLNPPRRA
90 100 110 120 130 140

Cry1Ac 130 140 150 160 170 180
LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF

gi|155 VHSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNAGEWGIS
150 160 170 180 190 200

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI

gi|155 AATLRTYQDYLNKYNTRDYSNYCINTYQTAFK---GLNTRLHDTL---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac 250 260 270 280 290 300
VSLFPNYSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQIEGSIKRSPLHMDILNSI

gi|155 VSIWLSFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVNLNGF
260 270 280 290 300 310

Cry1Ac 310 320 330 340 350 360
TI--YTDahrgeyywsg---HQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG

gi|155 SGARLSNTFPNIVGLPGSTMTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac 370 380 390 400 410 420
VYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAFYGTSSNLPASVYKSGTVDSLDEIPPQ

gi|155 FLPPLLPFVRSWLDGSDREGVATVTNWTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac 430 440 450 460 470
N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

480 490 500 510 520

Cry1Ac QIPAVKGNFLFNQSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--

gi|155 -----NGSMIHLAPNDYTGFTIISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490 500 510 520

Cry1Ac 530 540 550 560 570 580
STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NIVPATATSLDNLQSSDFGYFESANA

gi|155 NTTARYTLRGNNSYN-LYLRVSSIGNSTIRVINGRVYTATNVNITTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac 590 600 610 620 630 640
FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|155 LSDINIGNVVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097663|gb|ABT00594.1| Sequence 156 from patent U (634 aa)
initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF

gi|155 FQHKSLDTVQEEWMEWKKNHSLYVDPIVGTVASFLLKKVGSLSIKRILSELRNLIFFPSG
30 40 50 60 70 80

Cry1Ac 80 90 100 110 120
GPSQWDAFLVQIEQLINQRIEFARNQAISRLLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---QANVEEFNRQVDNFLNPPRRA
90 100 110 120 130 140

Cry1Ac 130 140 150 160 170 180
LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF

gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNAGEWGIS
150 160 170 180 190 200

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI

gi|155 AATLRTYQNHRLNRYTRDYSNYCINTYQTAFR---GLNTRLHDTL---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac 250 260 270 280 290 300
VSLFPNYSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQIEGSIKRSPLHMDILNSI

gi|155 VSIWLSFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVNLNG-
260 270 280 290 300 310

Cry1Ac 310 320 330 340 350
TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL

gi|155 --FSGARLSQTFNIVGLPGTTTHALLAARVNYSGGVSS---GDIGASPFNQNFSCST
320 330 340 350 360

360 370 380 390 400 410

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Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEI
gi|155 ---FLPPLLPVFRSWLDSGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
      370      380      390      400      410      420

      420      430      440      450      460      470
Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIIASPSGTPGGLRAYMVS-VHNRK--NNIYAVH
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNIIQNRGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTIISPIHATQVNNQTRTFISEKFGNQGDSLRF
      480      490      500      510      520

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNG
      530      540      550      560      570      580

      590      600      610      620      630
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQ
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLSNGTQFDL-----MNIMFVPTNLP
      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|155097690|gb|ABT00621.1| Sequence 210 from patent U (634 aa)
  initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGI
gi|155 FQHKSLDTVQEEWMEWKKDNHSLYVDPIVGTVASFLLKKVGLVSKRILSELRLNLIFFSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAIISRLGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQRLLNTDTLARVNAELTGL---QANVEEFNRQVDNFPNRRNA
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

      190      200      210      220      230      240

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Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTLVLDI
gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDMML---EPTYMFLNVFYEY
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRVTSQTLREIYTNPVLENFDGSGFRGSAQIEGSIKSPHMLDILNSI
gi|155 VSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLFQVNSNYVLNG-
      260      270      280      290      300      310

      310      320      330      340      350
Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSPEFTFPlyGTMGNAAPQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGVSS---GDIGASPFNQFSCST
      320      330      340      350      360

      360      370      380      390      400      410
Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEI
gi|155 ---FLPPLLPVFRSWLDSGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
      370      380      390      400      410      420

      420      430      440      450      460      470
Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIIASPSGTPGGLRAYMVS-VHNRK--NNIYAVH
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNIIQNRGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTIISPIHATQVNNQTRTFISEKFGNQGDSLRF
      480      490      500      510      520

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNG
      530      540      550      560      570      580

      590      600      610      620      630
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQ
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLSNGTQFDL-----MNIMFVPTNLP
      590      600      610      620      630

      640      650      660      670      680      690
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|155097685|gb|ABT00616.1| Sequence 200 from patent U (634 aa)
  initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

      20      30      40      50      60      70

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Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
gi|155 FQHKSLDVTQEEWMEWKKDNHSLYVDPVIGTVASFLLKVKVGLKRLSELRLNLFPSG
      30          40          50          60          70          80

      80          90          100         110         120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLNTDTTLARVNAELTGL----QANVEEFNRQVDNFLNPNRRA
      90          100         110         120         130         140

      130         140         150         160         170         180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150         160         170         180         190         200

      190         200         210         220         230         240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYQNHLRNYTRDYSNYCINTYQTAFR--GLNTRLHDML--EFRTYMFLNVFEY
      210         220         230         240         250

      250         260         270         280         290         300
Cry1Ac VSLFPNYSRRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSIKIRSPHLMIDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLG-
      260         270         280         290         300         310

      310         320         330         340         350
Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGVSS---GDIGASPFNQFSCST
      320         330         340         350         360

      360         370         380         390         400         410
Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEI
gi|155 ---FLPPLLTpFVRSWLDsGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
      370         380         390         400         410         420

      420         430         440         450         460         470
Cry1Ac PPQN-NNVP--PRQGFshRLshVSMFRSGFSNSSV-SIIRAPMFswIHRSAEFNNI IASD
gi|155 FIRNISGvPLVVRNEDLRPLHYNQIRNIASpSGTpgGLRAYMVS-VHNRK--NNIYAVH
      430         440         450         460         470

      480         490         500         510         520
Cry1Ac SITQIPAVKGNFLFNgsVIS-GP-GFTGGDLVRLNSSGNNIQRNGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRF
      480         490         500         510         520

      530         540         550         560         570         580
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNTTARYTLRGNgsYNLYLRVSSIGNSTIRVtIngrvYtATNVNTTTNND-GVNDNG
      530         540         550         560         570         580

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      590         600         610         620         630
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP
      590         600         610         620         630

      640         650         660         670         680         690
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|155097588|gb|ABT00519.1| Sequence 6 from patent US (634 aa)
  initn: 140 initl: 140 opt: 246 Z-score: 282.9 bits: 63.4 E(): 7.7e-07
Smith-Waterman score: 274; 22.771% identity (53.025% similar) in 628 aa overlap
(45-637:57-629)

      20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
gi|155 FQHKSLDVTQEEWMEWKKDNHSLYVDPVIGTVASFLLKVKVGLKRLSELRLNLFPSG
      30          40          50          60          70          80

      80          90          100         110         120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLNTDTTLARVNAELTGL----QANVEEFNRQVDNFLNPNRRA
      90          100         110         120         130         140

      130         140         150         160         170         180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150         160         170         180         190         200

      190         200         210         220         230         240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYQNHLRNYTRDYSNYCINTYQTAFR--GLNTRLHDML--EFRTYMFLNVFEY
      210         220         230         240         250

      250         260         270         280         290         300
Cry1Ac VSLFPNYSRRTYPIRTVSQTLTREIYTNPVLENFDGSRGSAQIEGSIKIRSPHLMIDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLG-
      260         270         280         290         300         310

      310         320         330         340         350
Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGVSS---GDIGASPFNQFSCST
      320         330         340         350         360

      360         370         380         390         400         410
Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPsAVYRKSgtVDSLDEI
gi|155 ---FLPPLLTpFVRSWLDsGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
      370         380         390         400         410         420

      420         430         440         450         460         470
Cry1Ac PPQN-NNVP--PRQGFshRLshVSMFRSGFSNSSV-SIIRAPMFswIHRSAEFNNI IASD
gi|155 FIRNISGvPLVVRNEDLRPLHYNQIRNIASpSGTpgGLRAYMVS-VHNRK--NNIYAVH
      430         440         450         460         470

      480         490         500         510         520
Cry1Ac SITQIPAVKGNFLFNgsVIS-GP-GFTGGDLVRLNSSGNNIQRNGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRF
      480         490         500         510         520

      530         540         550         560         570         580
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNTTARYTLRGNgsYNLYLRVSSIGNSTIRVtIngrvYtATNVNTTTNND-GVNDNG
      530         540         550         560         570         580

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Cry1Ac 420 430 440 450 460 470
PPQN--NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNNIIASD
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS--VHNKR--NNIYAVH

Cry1Ac 480 490 500 510 520
SITQIPAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQSNNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTATNVNNTTNNND--GVNDNG

Cry1Ac 590 600 610 620 630
NAFTS--SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQL
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP

Cry1Ac 640 650 660 670 680 690
GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|155097666|gb|ABT00597.1| Sequence 162 from patent U (634 aa)
initn: 140 initl: 140 opt: 245 Z-score: 281.7 bits: 63.2 E(): 9e-07
Smith-Waterman score: 273; 23.052% identity (52.941% similar) in 629 aa overlap
(45-637:57-629)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
gi|155 FQHKSLDTVQEEWMEWKKDNHSLYVDPVIGTVASFLLRKGSLVSKRILSELRNLIFFPSG

Cry1Ac 80 90 100 110 120
GPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQRLNTDTTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA

Cry1Ac 130 140 150 160 170 180
LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLNVFEY

Cry1Ac 250 260 270 280 290 300
VSLFFPYDSDRTYPIRTVSQTLREIYTNPLENFDDGSGFRGSAQGIIEGSIRSPHMLDILNSI
gi|155 VSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLG-

Cry1Ac 310 320 330 340 350
TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGVSS---GDIGASPFQDNFSCST

Cry1Ac 360 370 380 390 400 410
GQGVYRTLSTLYRRPFNIGINNQQL--SVLDGTEFAYGTSNNLPSAVYRKSQGTVDLDEI
gi|155 ---FLPPLLTPFVRSWLDGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY

Cry1Ac 420 430 440 450 460 470
PPQN--NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNNIIASD
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS--VHNKR--NNIYAVH

Cry1Ac 480 490 500 510 520
SITQIPAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF
gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF

Cry1Ac 530 540 550 560 570
--PSTSTRYRVRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFES
gi|155 GQSNNTTARYTLRGNNGNSYN--LYLRVSSIGNSTIRVTINGRVYTATNVNNTTNNND--GVNDN

Cry1Ac 580 590 600 610 620 630
ANAFTS--SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQ
gi|155 GARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP

Cry1Ac 640 650 660 670 680 690
LGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDIN
gi|155 PPLY

>>gi|155097680|gb|ABT00611.1| Sequence 190 from patent U (634 aa)
initn: 162 initl: 131 opt: 245 Z-score: 281.7 bits: 63.2 E(): 9e-07
Smith-Waterman score: 258; 22.871% identity (53.422% similar) in 599 aa overlap
(45-595:57-601)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIIWGIF
gi|155 FQHKSLDTVQREWEWKKNNHSLYLDPIVGTVASFLLK---VGLVSKRILSELWGLI

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      80          90          100          110          120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP
      ::      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 FPSGSTNLMQDILRETEKFLNQRLNTDTLARVNAELTGLRANVEEFNRQVDNF-LNPNRN
      90          100          110          120          130          140

      130          140          150          160          170          180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGF
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 AVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANMHLFIRDVILNADEWGI
      150          160          170          180          190          200

      190          200          210          220          230          240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLD
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 SAATLRTRYRDLKKNYTREYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFE
      210          220          230          240          250

      250          260          270          280          290          300
Cry1Ac IVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRFGSAQIEGSIKRSRPHLMDILNS
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 YVSIWLSFKYQSLLVSSGANL---YAS-----GS--GPQQ-----TQS
      260          270          280

      310          320          330          340          350          360
Cry1Ac ITIYDHRGEYYWSGHQIMASPV--GFSGPEF--TFPLYGTM-GNAAPQQRIVAQLGQ-
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 FT---SQDWPFLYSLFQVNSNYVLNFGFSGARLSNTFPNIGGLPGSTTTALLAARVNPY
      290          300          310          320          330          340

      370          380          390          400
Cry1Ac -GVYRTLSTLYRRPFNIGINNQL-----SVLD-GTEF-AYGTSSNLPSAVYRK
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 GGIS--SGDIGASPFNQNFNCSTFLPPLLTPFVRSWLDGSDRGVATVTNWNQTESFES
      350          360          370          380          390          400

      410          420          430          440          450          460
Cry1Ac SGTVDSLDEIPPQNNVPPRQGFSHRLSHVSM-----FRSGFNSSSVSIIRAPMFSWIH
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 TIGIRSGAFTARGNSNYFPDY-FIRNISGVPLVVRNEDLRRPLHYNEIRNIASP--SGTP
      410          420          430          440          450

      470          480          490          500          510
Cry1Ac RSAEFNNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIE
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 GGARAYMVSVHNKRNNIHAVH---ENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFIS
      460          470          480          490          500          510

      520          530          540          550          560
Cry1Ac VP-----IHFP--STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLD
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 EKFGNQGDSLRFEQNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVN
      520          530          540          550          560          570

      570          580          590          600          610          620
Cry1Ac NLQSSDFGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQ
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 TTTNND-GVNDNGARFSDINMGNVVASSNSDVPLDINVTLNLSGTQFDLMNIMLVPTNISP
      580          590          600          610          620          630

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>>gi|155097620[gb|ABT00551.1| Sequence 70 from patent US (634 aa)
  initn: 141 initl: 141 opt: 245 Z-score: 281.7 bits: 63.2 E(): 9e-07
  Smith-Waterman score: 266; 23.220% identity (52.203% similar) in 590 aa overlap
  (81-637:95-629)

      60          70          80          90          100          110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNL
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 KVGSLVGRKILSELRSIFPSGSTNLMQDILRETEKFLNQRLNTDTLARVNAELTGL---
      70          80          90          100          110          120

      120          130          140          150          160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 -QANVEEFNRQVDNFNLPNRRNAVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQ
      130          140          150          160          170          180

      170          180          190          200          210          220
Cry1Ac AANLHLSVLRDVSFVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 AANLHLSFIRDVILSADEWGISAATLRTRYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
      190          200          210          220          230

      230          240          250          260          270          280
Cry1Ac R--DWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSR
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 RLHDM---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFT
      240          250          260          270          280          290

      290          300          310          320          330
Cry1Ac GSAQIEGSIKRSRPHLMDILNSITIYDHRGEYY-----WSGHQIMASPVGFSGPE
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 SQDWPFLYSLFQVNSNYVLNFGFSGARLSQTFPNIVGLPGSTTTALLAARVNSGGV
      300          310          320          330          340

      340          350          360          370          380          390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYG
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 SS---GDIGASPFNQNFNCST--FLPPLLTPFVRSWLDGSDRGVNTVTNWNQTESFE
      350          360          370          380          390          400

      400          410          420          430          440          450
Cry1Ac TSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFNSSSV-SI
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 TTLGLRSGAFTARGNSNYFPDYFIQNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
      410          420          430          440          450          460

      460          470          480          490          500
Cry1Ac IRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDHTGFTISPIHATQ
      470          480          490          500

      510          520          530          540          550
Cry1Ac NNIQNRGYIEVPE-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
      .:      .:      .:      .:      .:      .:      .:      .:      .:      .:
gi|155 VNNQTRTFISEKFGNQGDSLRFEQNNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
      510          520          530          540          550          560

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          290      300      310      320      330      340
Cry1Ac  SFRGSAQIEGSIKSPHMLDIL--NSITIIYTDahrgeyywSGHQIMASVGFSGPEFTFP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  S--GPTQSFtaQ-NWPFLYSLFQVNSNYVLNGLSGARTITFPNIGGLPGSTTTQTLHFA
      280      290      300      310      320      330

```

```

          350      360      370      380      390      400
Cry1Ac  LYGTMGNAAPQQRIVAQLGQGVYRtLSSTLYRRPFNIGINNQQLSVLDGTEFAyGTSSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  RINYRGGVSSSRIGQANLNQNFN---ISTLfn-PLQTFPIRSWLDs-DTDRegvatSTNW
      340      350      360      370      380      390

```

```

          410      420      430      440      450      460
Cry1Ac  PSAVYRKSGTVDSLDEIPpQNNVPPRQGFShRLSHVSMFRSGFSNSVSIIRAPMFSWI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  QSGAFETLLRFSIFsARGNSNFFP----DYfIRNISGVVGTISNADLA--RPLHfNEI
      400      410      420      430      440

```

```

          470      480      490      500      510
Cry1Ac  HRSAEFNIIASDSITQIPAVKGNfL---FNGSVIS-GPG-FTGGDLVRLNssGNIIQNR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  -RDI---GTTAVASLVTVHNRKNNIYDThENGtMIHLAPNDYtGFTVSPiHATQVNNQIR
      450      460      470      480      490      500

```

```

          520      530      540      550      560
Cry1Ac  GYIE-----VPIHFPSTSTRYVRVRYASVtPIHLNVNWGNSSIFsNTVPATATSL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  TFISEKYGNQGDsLRFELSNtTARyTLRGNGNSYN-LYLRVSSIGSStIRVtINGRVYTA
      510      520      530      540      550

```

```

          570      580      590      600      610      620
Cry1Ac  D-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVtATLEAEYNLER
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  NVNTTTNDGVLdNGARFSDINIGNVVA---SANTNVPLD---IQVtFNGNPQfEL--
      560      570      580      590      600

```

```

          630      640      650      660      670      680
Cry1Ac  AQKAVNALFTSTNQLGLKtNVTdYHIDQVSNLVtYLSDFECLDEKRElSEKVKHAKRLSD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|124  ---MNIMFVPTNLpPLY
      610      620

```

>>gi|155097687|gb|ABT00618.1| Sequence 204 from patent U (634 aa)  
 initn: 140 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06  
 Smith-Waterman score: 266; 23.051% identity (52.542% similar) in 590 aa overlap  
 (81-637:95-629)

```

          60      70      80      90      100      110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGIgFPGSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  KVGSLVgKRILSELsRLIFPGSTNLmQDILREtEKfLNQRlNTDTLARVNAEltGL---
      70      80      90      100      110      120

```

```

          120      130      140      150      160
Cry1Ac  YQIYAESFREWEADPTNP---ALREEMRIQFNdMNSALtTAIPLFAVQNYQVPLLSVYVQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -QANVEEFNRQVDnFLNPNRNNAVPLsITSSVNTMQQLFLNRLPQfMQGyQLLLPLPFAQ
      130      140      150      160      170      180

```

```

          170      180      190      200      210      220
Cry1Ac  AANLHLSVLRDVSvFQWRGFDAAtINSRYNDLTRLIGNyTDHAvRWYNTGLERvWGPDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  AANLHLSfIRDvILNADEWGIaATLRtYRNHLRNyTRDYSnYCINTYQTAfR---GLNT
      190      200      210      220      230

```

```

          230      240      250      260      270      280
Cry1Ac  R--DWIRYnQFRRELtLTvLDIVSLFPNyDSRtYPIRtVtSQtLREIYtNPVLEnFDGSSFR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RLHdML---EFRTYmFLNVfEYvSIWslfKYQsLLVSSGANL----YASGSGPQqQTSfT
      240      250      260      270      280      290

```

```

          290      300      310      320      330
Cry1Ac  GSAQLEGSIKSPHMLDILNSITIIYTDahrgeyy-----wSGHQIMASVGFSGPE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SQDWPFlySLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGtTTtHALLAARvNYSGGV
      300      310      320      330      340

```

```

          340      350      360      370      380      390
Cry1Ac  FTfPLYGTMGNAAPQQRIVAQLGQGVYRtLSSTLYRRPFNIGINNQQL-SVLDGTEFAyG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SS----GDIGASPFfNQfNfSCST--FLPpLLtPFVRSWLDsSGDRGgVNTVtVNWQTESfE
      350      360      370      380      390      400

```

```

          400      410      420      430      440      450
Cry1Ac  TSSNLPSAVYRKSGTVDSLDEIPpQNNVPPRQGFShRLSHVSMFRSGFSNSVSIIRAPMFSWI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  TTLGLRSGAftARGNSNYFPDYfIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGtPGG
      410      420      430      440      450      460

```

```

          460      470      480      490      500
Cry1Ac  IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNfLNGSVIS-GP-GFTGGDLVRLNssGNIIQNR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  ARAYMVS-VHNRK--NNIYAVHE-----NGtMIHLAPEDYtGFTTSPiHATQ
      470      480      490      500

```

```

          510      520      530      540      550
Cry1Ac  NNIQNRgyIEVP-----IHFPSTSTRYVRVRYASVtPIHLNVN-WGNSSIFs--NT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VNNQTRtFISEKfGNQGDsLRFEQSNtTARyTLRGNGNSYNLYLRVSSIGNStIRVtING
      510      520      530      540      550      560

```

```

          560      570      580      590      600      610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVtATLEAEYNLER
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RVYtATNVNTTTnND-GVNDNGARFSDINIGNVVA---SDNSNVPLD---INvtLNSG
      570      580      590      600      610

```

```

          620      630      640      650      660      670
Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKtNVTdYHIDQVSNLVtYLSDFECLDEKRElSEKVKHAKRLSD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  TQFDL-----MNIMFVPTNLpPLY
      620      630

```

>>gi|155097658|gb|ABT00589.1| Sequence 146 from patent U (634 aa)  
 initn: 140 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06  
 Smith-Waterman score: 266; 23.051% identity (52.542% similar) in 590 aa overlap  
 (81-637:95-629)



```

          470          480          490          500
Cry1Ac  510    520          530    540    550
NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
510          520          530          540          550          560

```

```

          560          570          580          590          600          610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RVYTATNVNTTTNND-GVNDNGARFSDINIGNVVA---SDNSVPLD---INVTLNSG
570          580          590          600          610

```

```

          620          630          640          650          660          670
Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  TQFDL-----MNIMFVPTNLPLY
620          630

```

>>gi|155097625|gb|ABT00556.1| Sequence 80 from patent US (634 aa)  
 initn: 140 init1: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06  
 Smith-Waterman score: 265; 24.252% identity (52.283% similar) in 635 aa overlap  
 (45-637:57-629)

```

          20          30          40          50          60          70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  FQHKSLDTVQEEWMEWKDNHSLYVDPVIGTVASFLKKGVLGKRLSELNLIFFPSG
30          40          50          60          70          80

```

```

          80          90          100          110          120
Cry1Ac  GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90          100          110          120          130          140

```

```

          130          140          150          160          170          180
Cry1Ac  LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150          160          170          180          190          200

```

```

          190          200          210          220          230          240
Cry1Ac  AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTLTVLDI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  AATLRTYQNHRLNRHTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVFEY
210          220          230          240          250

```

```

          250          260          270          280          290
Cry1Ac  VSLFPNYSRSTYPIRTVSQLE-----TREIYTN---PVLEN-FDGSFRGSAQGIIEGSI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VSIWLSFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFVLYSLFQVNSVYLVNGFSGAR
260          270          280          290          300          310

```

```

          300          310          320          330          340
Cry1Ac  RS---PHLMDILNSITIYTD-AHRGEYY--WSGHQIMASVPG--FSGPEFTFPLYGTGMN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  LSQTFPNIVGLPGTTTTALLAARVNYSSGSDIGASPFNQNSFCSTFLPPLL-----

```

```

          320          330          340          350          360          370
Cry1Ac  350    360    370    380    390    400
AAPQQRIVAQLGGQVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRK
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -TPFVVR--SWLDSGSDRGGVNTVTN--WQTESFETTLGLRSGAFTARGNSNYFPDYFIR-
380          390          400          410          420

```

```

          410          420          430          440          450          460
Cry1Ac  SGTVDLSDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  ----NISGVPLVVRNEDLR----RPLHYNQIRNIASPSGTPGGLRAYMVS-VHNRK--
430          440          450          460          470

```

```

          470          480          490          500          510          520
Cry1Ac  NNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP---
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  NNIYAVHE-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGN
480          490          500          510

```

```

          530          540          550          560          570
Cry1Ac  ----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTPATATSLDNLQSSD
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  QGDSLRFEQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYATNVNTTTNND
520          530          540          550          560          570

```

```

          580          590          600          610          620          630
Cry1Ac  FGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNAL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -GVNDNGARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIM
580          590          600          610          620

```

```

          640          650          660          670          680          690
Cry1Ac  FTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDS
: : : :
gi|155  FVPTNLSPLY
630

```

>>gi|155097648|gb|ABT00579.1| Sequence 126 from patent U (634 aa)  
 initn: 140 init1: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06  
 Smith-Waterman score: 266; 23.350% identity (52.623% similar) in 591 aa overlap  
 (81-637:95-629)

```

          60          70          80          90          100          110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGIQFNSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  KVGSLVGRILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70          80          90          100          110          120

```

```

          120          130          140          150          160
Cry1Ac  YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -QANVEEFNRQVDNFLNPNRNVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ
130          140          150          160          170          180

```

```

          170          180          190          200          210          220
Cry1Ac  AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT

```





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gi|155 ---FLPPLLTPFVRSWLDGSDRGGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

Cry1Ac 420 430 440 450 460 470
PPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNIIASD

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS--VHNKR--NNIYAVH
430 440 450 460 470

Cry1Ac 480 490 500 510 520
SITQIPAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF

gi|155 E-----NGSMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQDGLRF
480 490 500 510 520

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVT--PIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA

gi|155 EQSNVTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYATNVNNTTND--GVNDNG
530 540 550 560 570 580

Cry1Ac 590 600 610 620 630
NAFTS--SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL

gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGAQFDL-----MNIMFVPTNLP
590 600 610 620 630

Cry1Ac 640 650 660 670 680 690
GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINR

gi|155 PLY

>>gi|155097656|gb|ABT00587.1| Sequence 142 from patent U (634 aa)
initn: 140 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06
Smith-Waterman score: 266; 23.051% identity (52.542% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac 60 70 80 90 100 110
LSEFVPGAGFVLGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNL

gi|155 KVGSLVGKRIKILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ

gi|155 -QANVEEFNRQVDNLFNPNRNVPLSITSSVNTMQQLFLNRLPQFQMQYQLLLPLFAQ
130 140 150 160 170 180

Cry1Ac 170 180 190 200 210 220
AANLHLSVLRDVSFVGRWQFPAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS

gi|155 AANLHLSFIRDVILNADEWGISAAATLRYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
190 200 210 220 230

Cry1Ac 230 240 250 260 270 280
R--DWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLENFDGSFR

gi|155 RLHDM---EFRTYMFNLVFEYVSIWLSLFKYQSLLVSSGANL----YASGSGPQQTSQFT
240 250 260 270 280 290

Cry1Ac 290 300 310 320 330
GSAQGIIEGSIIRSPHLMILNSITIIYTDHRGEYY-----WSGHQIMASPVGFSGPE

gi|155 SQDWPFYLSLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGTTTTALLAARVNYSGGV
300 310 320 330 340

Cry1Ac 340 350 360 370 380 390
FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQ--SVLDGTEFAYG

gi|155 SS---GDIGASPFNFQFCST--FLPPLLTPFVRSWLDGSDRGGVNTVTNWQTESFE
350 360 370 380 390 400

Cry1Ac 400 410 420 430 440 450
TSSNLPASAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SI

gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
410 420 430 440 450 460

Cry1Ac 460 470 480 490 500
IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSG

gi|155 ARAYMVS--VHNKR--NNIYAVHE-----NGTMIHLAPEDYTGFTTISPIHATQ
470 480 490 500

Cry1Ac 510 520 530 540 550
NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT--PIHLNVN--WGNSSIFS--NT

gi|155 VNNQTRTFISEKFGNQDGLRFQSNVTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac 560 570 580 590 600 610
VPATATSLDNLQSSDFGYFESANAFTS--SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE

gi|155 RVYATNVNNTTND--GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
570 580 590 600 610

Cry1Ac 620 630 640 650 660 670
AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVK

gi|155 TQFDL-----MNIMFVPTNLPPLY
620 630

>>gi|155097697|gb|ABT00628.1| Sequence 224 from patent U (634 aa)
initn: 170 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06
Smith-Waterman score: 267; 23.559% identity (53.051% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac 60 70 80 90 100 110
LSEFVPGAGFVLGLVDIIWGFIFGPSQWDAFLVQIEQLINQRIEERFARNQAISRLEGLSNL

gi|155 KVGSLVGKRIKILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ

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gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQ
      130      140      150      160      170      180

      170      180      190      200      210      220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      :::::  ::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::  :::::
gi|155 AANLHLSFIRDVILNADEWEGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
      190      200      210      220      230

      230      240      250      260      270      280
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFR
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 RLHDM---EFRTYMLNFVFEVSIWSLFKYQSLVSSGANL---YASGSGPQQTQSFT
      240      250      260      270      280      290

      290      300      310      320      330
Cry1Ac GSAQGIEGSIRSPHMLDILNSITTYTDAHRGEYYWS--G-----HQIMASPVGFSGPE
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 SQDWPFYLSLFQVNSNYVLNG---FSGARLSQTFPSIVLPGTTTTHALLAARVNYSGGV
      300      310      320      330      340

      340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYG
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 SS---GDIGASPFNQFSCST---FLPPLLTPFVRSWLDGSDRGVNTVINWQTESFE
      350      360      370      380      390      400

      400      410      420      430      440      450
Cry1Ac TSSNLPSAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
      410      420      430      440      450      460

      460      470      480      490      500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 ARAYMVS-VHNRK--NNIY-----AVREN---GTMIHLAPEDYTGFTISPIHATQ
      470      480      490      500

      510      520      530      540      550
Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 VNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNNGSNYLYLRVSSIGNSTIRVTING
      510      520      530      540      550      560

      560      570      580      590      600      610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 RYVTATNVNTTNTND-GVNDGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
      570      580      590      600      610

      620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTINQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSKVK
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 TQFDL-----MNIMFVPTNLPLY
      620      630

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>>gi|155097638|gb|ABT00569.1| Sequence 106 from patent U (634 aa)  
 initn: 160 init1: 124 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06

Smith-Waterman score: 268; 22.432% identity (53.938% similar) in 584 aa overlap  
 (45-595:57-601)

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      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIWIWIF
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 FQHKSLDVTQREWEWKKNNHSLYLDPIVGTVASFLLKK---VGLVSKRILSELWGLI
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAIISREGLSNLYQIYAESFREWEADPTNP
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 FPSGSTNMQDLIRETEQFLNQLRLNTDTLARVNAELTGLRANVEEFNRQVDNF-LNPQNQ
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 AVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQANLHLGFIRDVVLNADEWGI
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNT---GLE-RVWGP-DSRDWIRYNQFRRELTLT
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 SAAALRTYRDYLNKNYTRDYSNYCINTYQSAFKGLNTRLHGTLEFRTYMFLNFVFEVSIWS
      210      220      230      240      250      260

      250      260      270      280      290      300
Cry1Ac VLDIVSLFPNYDSRTYPIRTVSQLTREIYTN--PVLENFDGSGFRGSAQGIEGSIRSPHLM
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 LFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFYLSL---FQVNSNYVLSGFSGARLS
      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac DILNSITTYTDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 NTFPNIVGLPGST-----TTHALLAARVNYSGGISS---GDIGASPFNQFNCST---
      320      330      340      350      360

      370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 FLPPLLTPFVRSWLDGSDREGVATVINWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

      430      440      450      460      470
Cry1Ac N--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNINQNRGYIEVP-----IHFP--
      : : : : :  : : : : :  : : : : :  : : : : :  : : : : :  : : : : :
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
      490      500      510      520

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTPATATSLDNLQSSDFGYFESANA

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          : . . . . . : . . . . . :
gi|155  KVGSLV GKRI LSEL RSLIFPSGSTNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---
          70      80      90      100     110     120

          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQ
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ
          130     140     150     160     170     180

          170     180     190     200     210     220
Cry1Ac  AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
          190     200     210     220     230

          230     240     250     260     270     280
Cry1Ac  R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  RLHDM---EFRTYMFNLFVFEVSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFT
          240     250     260     270     280     290

          290     300     310     320     330
Cry1Ac  GSAQGI EGSIRSPHLM DILNSIT IYTD AHRGEY Y-----WSGHQIMASPVGFSGPE
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  SQDWPF LYSLFQVNS NYVLNG ---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGV
          300     310     320     330     340

          340     350     360     370     380     390
Cry1Ac  FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL-SVLDGTEFAYG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  SS----GDIGASPFNFQNFSCST---FLPPLLTPFVRSWLDGSDRGGVNTVNWQTESFE
          350     360     370     380     390     400

          400     410     420     430     440     450
Cry1Ac  TSSNLPSAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSTPGG
          410     420     430     440     450     460

          460     470     480     490     500
Cry1Ac  IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
          470     480     490     500

          510     520     530     540     550
Cry1Ac  NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  VNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNNGSNYLYLRVSSIGNSTIRVTING
          510     520     530     540     550     560

          560     570     580     590     600     610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLE
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  RvyTATNVNTTTNND-GVNDGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
          570     580     590     600     610

          620     630     640     650     660     670

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Cry1Ac  AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
          . . . . . : . . . . . :
gi|155  TQFDL-----MNIMFVPTNLPPLY
          620     630

>>gi|155097678|gb|ABT00609.1| Sequence 186 from patent U (634 aa)
  initn: 140 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06
Smith-Waterman score: 266; 23.350% identity (52.623% similar) in 591 aa overlap
(81-637:95-629)

          60      70      80      90      100     110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  KVGSLV GKRI LSEL RSLIFPSGSTNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---
          70      80      90      100     110     120

          120     130     140     150     160
Cry1Ac  YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQ
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ
          130     140     150     160     170     180

          170     180     190     200     210     220
Cry1Ac  AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
          190     200     210     220     230

          230     240     250     260     270     280
Cry1Ac  R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  RLHDM---EFRTYMFNLFVFEVSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFT
          240     250     260     270     280     290

          290     300     310     320     330
Cry1Ac  GSAQGI EGSIRSPHLM DILNSIT IYTD AHRGEY Y-----WSGHQIMASPVGFSGPE
          . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  SQDWPF LYSLFQVNS NYVLNG ---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGV
          300     310     320     330     340

          340     350     360     370     380     390
Cry1Ac  FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL-SVLDGTEFAYG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  SS----GDIGASPFNFQNFSCST---FLPPLLTPFVRSWLDGSDRGGVNTVNWQTESFE
          350     360     370     380     390     400

          400     410     420     430     440     450
Cry1Ac  TSSNLPSAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSTPGG
          410     420     430     440     450     460

          460     470     480     490     500
Cry1Ac  IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
          470     480     490     500

          510     520     530     540     550
Cry1Ac  NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  VNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNNGSNYLYLRVSSIGNSTIRVTING
          510     520     530     540     550     560

          560     570     580     590     600     610
Cry1Ac  VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLE
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . :
gi|155  RvyTATNVNTTTNND-GVNDGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
          570     580     590     600     610

          620     630     640     650     660     670

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Regulatory Product Characterization Team

Cry1Ac NNIQNRGYIEVP-----IHF--PSTSTRYRVRVRYASVTP IHLNVN-WGNSSIFS--N
gi|155 VNNQTRTFIASEKFGNQDGLRFGQSNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTIN

Cry1Ac TVPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATL
gi|155 GRVYTATNVNNTTNNND-GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLNS

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDEFCLDEKRELSEKV
gi|155 GTQFDL-----MNIMFVPTNLPLPLY

>>gi|155097621|gb|ABT00552.1| Sequence 72 from patent US (634 aa)
initn: 140 initl: 140 opt: 244 Z-score: 280.6 bits: 63.0 E(): 1e-06
Smith-Waterman score: 260; 24.456% identity (51.926% similar) in 597 aa overlap
(81-637:95-629)

Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNL
gi|155 KVGSLVKGKRISELRSIFPSGSTNMQDILRETEKFLNQLRNTDTLARVNAELTGL---

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNFLNPNRNNAVPLSITSSVNTMQQLFLNRLPQFQMQYQLLLPLFAQ

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCISTYQTAFR---GLNT

Cry1Ac R--DWIRYNQFRRELTLTVLVDIVSLFPNYDSRTYP IRTVSQL-----TREIYTN---
gi|155 RLHDM L---EFRTYMF LNVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDW

Cry1Ac PVLEN-FDGSFRGSAQIEGSIRS---PHLMDILNSITITYTD-AHRGEYYW--SGHQIMA
gi|155 PFLYSLFQVNSNYVLNFGSGARLSQTFPNIVGLPGTTTTALLAARVNYSGVSSSDIGA

Cry1Ac SPVG--FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS
gi|155 SPFNQNFSCSTFLPPLL-----TPFV R--SWLDSGSDRGVNTVTN--WQTESFETTLG

Cry1Ac SPVG--FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS
gi|155 SPFNQNFSCSTFLPPLL-----TPFV R--SWLDSGSDRGVNTVTN--WQTESFETTLG

Cry1Ac VLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSS
gi|155 LRSGATARGNSNYFPDYFIR-----NISGVPLVVRNEDLRRPL-----HYNQIRNIBES

Cry1Ac NSSV-SIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNNGSVIS-GP-GFTGGDL
gi|155 PSGTPGGARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTI

Cry1Ac VRLNSSGNNIQNRGYIEVP-----IHF PSTSTRYRVRVRYASVT-PIHLNVN-WGNSS
gi|155 SPIHATQVNNQTRTFIASEKFGNQDGLRFEQSNNTTARYTLRGNNGNSYNLYLRVSSIGNST

Cry1Ac IFS--NTPPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFI
gi|155 IRVTINGRVYATNVNNTTNNND-GVNDNGARFSDINIGNVVA---SDNSNVPLD---I

Cry1Ac PVTATLAEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDDEFCLDEKR
gi|155 NVTLNSGTQFDL-----MNIMFVPTNLPLPLY

>>gi|155097618|gb|ABT00549.1| Sequence 66 from patent US (634 aa)
initn: 128 initl: 128 opt: 243 Z-score: 279.4 bits: 62.8 E(): 1.2e-06
Smith-Waterman score: 264; 23.051% identity (52.881% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLSNL
gi|155 KVGSLVKGKRISELRSIFPSGSTNMQDILRETEKFLNQLRNTDTLARVNAELTGL---

Cry1Ac YQIYAESF-REWEA--DPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNFLNPNRTQTATRLSITSSVNTMQQLFLNRLPQFLHGRQLLLPLFAQ

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT

Cry1Ac R--DWIRYNQFRRELTLTVLVDIVSLFPNYDSRTYP IRTVSQLTREIYTNVLENFDGSRF
gi|155 RLHDM L---EFRTYMF LNVFEYVSIWLSFKYQSLVSSGANL---YASGSGPQQTQSFT

Cry1Ac R--DWIRYNQFRRELTLTVLVDIVSLFPNYDSRTYP IRTVSQLTREIYTNVLENFDGSRF
gi|155 RLHDM L---EFRTYMF LNVFEYVSIWLSFKYQSLVSSGANL---YASGSGPQQTQSFT

Cry1Ac GSAQGIIEGSIKRSPLHMDILNSITIIYTDHRGEYY-----WSGHQIMASPVGFSGPE

gi|155 SQDWPFYLSLQVNSNYVING--FSGARLSQTFPNIVGLPGTTTHALLAARVNYSGGV
300 310 320 330 340

Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS-VLDGTEFAYG

gi|155 SS---GDIGASPFNFQNFSCST---FLPPLLTFFVRSWLDGSDRGGVNAVNTWQTESFE
350 360 370 380 390 400

Cry1Ac TSSNLPSAVYRKSQVTVSLDEIPPQN-NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SI

gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
410 420 430 440 450 460

Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLNGSVIS-GP-GFTGGDLVRLNSSG

gi|155 ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
470 480 490 500

Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVYASVT-PIHLNVN-WGNSSIFS--NT

gi|155 VNNQTRTFISEKFGNQDLSRFEQSNNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLE

gi|155 RYVYATNVNTTNDN-GVNDNGARFSDINIGNVVA---SDNSNPLD---INVTLNSG
570 580 590 600 610

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK

gi|155 TQFDL-----MNIMFVPTNLPLLY
620 630

>>gi|155097630|gb|ABT00561.1| Sequence 90 from patent US (634 aa)
initn: 138 init1: 138 opt: 243 Z-score: 279.4 bits: 62.8 E(): 1.2e-06
Smith-Waterman score: 261; 22.945% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGI

gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVRTVASPFLKVKVGLGKRILSELNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL----QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

130 140 150 160 170 180

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADRWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLDI

gi|155 AATLRTYRNYLRNYTRDYSNYCINTYQTAFK---GLNTRLHDTL---EPRTYMFLNVFBEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQTLREIYTNPVLNFDGSGFRGSAQGIIEGSIKRSPLHMDILNSI

gi|155 VSIWSLFKYQSLLVSSGANL---YASGSGVTNTQSFTSQDWPFYLSLQVNSNYVINGF
260 270 280 290 300 310

Cry1Ac T-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ

gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNFQNFSCST---
320 330 340 350 360

Cry1Ac VYRTLSSTLYRRPFNIGINNQQLS-SVLDGTEFAYGTSNLPSAVYRKSQVTVSLDEIPPQ

gi|155 FLPPLLTFFVRSWLDGSDREGVATVNTWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT

gi|155 NISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGARAYMVS-VHNRK--NNIYAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNIIQNRGYIEVP-----IHFP--

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFEQN
480 490 500 510 520

Cry1Ac STSTRYRVRVYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

gi|155 NNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTNDN-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|155 FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|72117495|gb|AAZ59758.1| Twin-arginine translocation (493 aa)
initn: 123 init1: 123 opt: 241 Z-score: 278.7 bits: 62.3 E(): 1.3e-06
Smith-Waterman score: 241; 24.586% identity (52.210% similar) in 362 aa overlap
(39-377:39-368)

10 20 30 40 50 60

Cry1Ac PNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVLG-LVDI

gi|721 RSIPSAALMAMGPAFFAHADGALGKLPVTDPMEDLKTILEVVLAE-VPVVGAMASLVGL
10 20 30 40 50 60

Cry1Ac IWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTN

gi|721 LWPVEPADVWEEIRQKVEALIEQKINDAVYSLLKSKLDGIGNTLKLYLNA--AATGDTSN
70 80 90 100 110 120

Cry1Ac PALREEMRIQFNDMNSALTTAIPLFAVQNYQ---VPLLSVYVQAANLHLSVLRDVSVFGQ

gi|721 -----MRMQFIATNTQMTLAASEFRNPDFQWVLAPLFAIFSQ---LHAVLLRDCVLHGR
130 140 150 160 170 180

Cry1Ac RWGFDAATINSRY---NDLTRLIGNYTDHAVRWYNTGLERVW--GPDSRDWIRYN---QF

gi|721 DWGWNATAYEGYVRLASDTINEYHAYLDAVVRKEQDRLEPAAPTSPGKHYTAIYNWQSF
180 190 200 210 220 230

Cry1Ac RRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDSFRGSAQGIE----

gi|721 SQKKQVLFQDYMLLLNALD---PIRNPGQ---VKTIPFPDVFSAAV--GTADDWDATCR
240 250 260 270 280

Cry1Ac ---GSIRSPHLMIDILNSITIIYTDHRGEYYWSGHQIMAS-PVGFSGPEFTFPLYGTMGNA

gi|721 AWAGAVATPFLSPAANISEIYIEL---FNFTPRIVDVSYVAG--SGPK---VWG--GNR
290 300 310 320 330

Cry1Ac APQQRIVAQLGQGV-YRTLS--STLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVY

gi|721 QDRTGIIADRVSGVEQKTISIPRSTDGKTFNFIAGASIRAGSIPTAVSLVMDGKSIALWD
340 350 360 370 380 390

Cry1Ac RKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFSWIHRSAE

gi|721 RRDLGGQQFYVSVPRKRLTTLNMWSRSRFDNDLGCIIIFGSRDPSDIPPAVREALYVTA
400 410 420 430 440 450

>>gi|66734543|gb|AA53629.1| Cry2Ac [Bacillus thuringien (623 aa)
initn: 172 init1: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 251; 23.689% identity (54.822% similar) in 591 aa overlap
(85-637:98-618)

Cry1Ac VPGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGL-SNLYQI

gi|667 LVGKRILSELQNLIFPSPSIDLMQEIILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

120 130 140 150 160 170

Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL

gi|667 NRQVDNFLNPNQNPVPLAIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
130 140 150 160 170 180

Cry1Ac HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D

gi|667 HLSFIRDVILNADEWGISAATVTRTYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
190 200 210 220 230 240

Cry1Ac WIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDSFRGSAQ

gi|667 ML---EFRTYMFVFLNVEFYVSIWLSLFKYQSLLVSSGANL---YAS-----GS--GPTQ
230 240 250 260 270 280

Cry1Ac GIEGSIKSPHLMIDILNSITIIYTDHRGEYYWSGHQIMASPV--GFSGPE--FTFPLYGTM

gi|667 -----SFT----AQNWPFYLSLQVNSNYVNLNGLSGARTITTFPNIGGL
290 300 310 320 330 340

Cry1Ac GNAAPQ-----RIVAQLGQGVYRTLSSTLYRRPFNIG--INNQL---SVLD-GTEF-

gi|667 PGSTTTQTLHFARINRYRGGVSSSRIGQANL-NQNFNISTLFLNPLQTPFIRSWLDSGTDRE
330 340 350 360 370 380

Cry1Ac AYTSSNLPASVYRKSQGVSDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNNSVSI

gi|667 GVATSNWQSGAFETTLRLRFISFARGNSNFFP-----DYFIRNISGVVGTISNADLA--
390 400 410 420 430

Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNS

gi|667 RPLHFNEI-RDI---GTTAVASLVTVHNRKNNIYDTHENGTMHPLAPNDYTGFTVSPHA
440 450 460 470 480 490

Cry1Ac SGNNIQNRGYIE-----VPIHFPSTSTRYRVRVYASVPIHLNVNWNSSIFSNT

gi|667 TQVNNQIRTFISEKYGNGQDSLRFELSNTTARYTLRGNGNSYN-LYLRVSSIGSSTIRVT
500 510 520 530 540 550

Cry1Ac VPATATSLD-NLQSSDFGYFESANAFTS-SLGNIVGVNRFSGTAGVIIDRFEFIPVTATL

gi|667 INGRVYANVNTTTNNDGVLDNGARFSDINIGNVVA---SANTNVPLD---IQVTFNG
560 570 580 590 600 610

Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTVLSDEFCLDEKRELSKV

gi|667 NPQFEL-----MNIMFVPTNLPLPLY
610 620

>>gi|37540131|gb|AAG35410.1| insecticidal crystal protei (623 aa)
initn: 172 initl: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 254; 22.696% identity (54.096% similar) in 586 aa overlap
(85-637:98-618)

60 70 80 90 100 110
Cry1Ac VPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGL-SNLYQI
gi|375 LVGKRILSELQNLIFPSPGIDLMQIEILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

120 130 140 150 160 170
Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|375 NRQVDNFLNPNQNPVPLAIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
130 140 150 160 170 180

180 190 200 210 220
Cry1Ac HLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
gi|375 HLSFIRDVILNADEWGISAAATVRYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
190 200 210 220 230 240

230 240 250 260 270
Cry1Ac WIRYNQFRRELTLTVDIVSLFPNYDSRTYPIRTVSQLE-----TREIYTN---PVLEN-
gi|375 ML---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANLYASGSGPTQSFTAQNWPFYLSL
250 260 270 280 290

280 290 300 310 320 330
Cry1Ac FDGSRFRGSAQIGEG---SIRSPHLMIDILNSITITYTDAHRGEYIWSGHQIMASPVGFSGPE
gi|375 FQVNSNYVLNGLSGARTTITFPNIGGLPGSTTTQT-LHFARINRYGG-VSSSRIGQANLN
300 310 320 330 340 350

340 350 360 370 380 390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQLSVLDGTEF-AYG
gi|375 QNFNI-STLFLNPLQTPFIRSWLDSGTDRREGVAT---STNWQSGAFETLLRFSIFSARG
360 370 380 390 400 410

400 410 420 430 440 450
Cry1Ac TSSNLPSAVYRK-SGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRA
gi|375 NSNFFPDYFIRNIGSVVGTI-----SNADLA-----RPLHFNEIRDIGTTAVASLV--
420 430 440 450

460 470 480 490 500 510
Cry1Ac PMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNI
gi|375 P---VHNRK--NNIYATHE-----NGMTIHLAPNDYTGFTVSPIHATQVNN
460 470 480 490

520 530 540 550 560
Cry1Ac QNRGYIE-----VPIHFPSTSTRYRVRYASVTPIHLLNVNWNSSIFSNTVPATA
gi|375 QIRTFISEKYGNQGDLSRFLSNTTARYTLRGNNGNSYN-LYLRVSSIGSSTIRVINGRV
500 510 520 530 540 550

570 580 590 600 610 620
Cry1Ac TSLD-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYN
gi|375 YTANVNTTTNNNDGVLDNGARFSDINIGNVVA---SANTNVPLD---IQVTFNGNPQFE
560 570 580 590 600

630 640 650 660 670 680
Cry1Ac LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKR
gi|375 L-----MNIMFVPTNLPPLY
610 620

>>gi|85700968|gb|ABC74793.1| insecticidal crystal protei (623 aa)
initn: 172 initl: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 251; 23.689% identity (54.822% similar) in 591 aa overlap
(85-637:98-618)

60 70 80 90 100 110
Cry1Ac VPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGL-SNLYQI
gi|857 LVGKRILSELQNLIFPSPGIDLMQIEILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

120 130 140 150 160 170
Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|857 NRQVDNFLNPNQNPVPLAIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
130 140 150 160 170 180

180 190 200 210 220
Cry1Ac HLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
gi|857 HLSFIRDVILNADEWGISAAATVRYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
190 200 210 220 230 240

230 240 250 260 270 280
Cry1Ac WIRYNQFRRELTLTVDIVSLFPNYDSRTYPIRTVSQLE-----TREIYTN---PVLEN-
gi|857 ML---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANL-----YAS-----GS--GPTQ
250 260 270 280

290 300 310 320 330 340
Cry1Ac GIEGSIRSPHLMIDILNSITITYTDAHRGEYIWSGHQIMASPV--GFSGPE--FTFPLYGTM
gi|857 -----SFT----AQNWPFYLSLQVNSNYVLNGLSGARTTITFPNIGGL
290 300 310 320

350 360 370 380 390
Cry1Ac GNAAPQQ----RIVAQLGQGVYRTLSSSTLYRRPFNIG--INNQQLE----SVLD-GTEF-
gi|857 PGSTTTQTLHFARINRYGGVSSSRIGQANL-NQNFNISTLFLNPLQTPFIRSWLDSGTDR
330 340 350 360 370 380

400 410 420 430 440 450
Cry1Ac AYTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRSLSHVSMFRSGFSNSSVSIIRA
gi|857 GVATSTNWQSGAFETLLRFSIFSARGNSNFFP-----DYFIRNIGSVVGTIISNADLA--
390 400 410 420 430

```

          460      470      480      490      500
Cry1Ac  RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|857  RPLHFNEI-RDI---GTTAVASLVTVHNRKNNIYDTHENGMTMIHLAPNDYTGFTVSPPIHA
          440      450      460      470      480      490

```

```

          510      520      530      540      550
Cry1Ac  SGNNIQNRGYIE-----VPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|857  TQVNNQIRTFISEKYGNQGDLSLRFELSNTTARYTLRGNGNSYN-LYLRVSSIGSSTIRVT
          500      510      520      530      540      550

```

```

          560      570      580      590      600      610
Cry1Ac  VPATATSLD-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|857  INGRVYTANVNTTTNNDGVLDNGARFSDINIGNVVA---SANTNVPLD---IQVTFNG
          560      570      580      590      600

```

```

          620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|857  NPQFEL-----MNIMFVPTNLPPLY
          610      620

```

>>gi|12822554|gb|AAE48995.1| Sequence 6 from patent US 6 (623 aa)  
 initn: 172 init1: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06  
 Smith-Waterman score: 249; 23.689% identity (54.653% similar) in 591 aa overlap  
 (85-637:98-618)

```

          60      70      80      90      100      110
Cry1Ac  VPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGL-SNLYQI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  LVGKRILSELQNLIFPGSIDLMQEIILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
          70      80      90      100      110      120

```

```

          120      130      140      150      160      170
Cry1Ac  --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  NRQVDNFLNPNQNPVPLAIIIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
          130      140      150      160      170      180

```

```

          180      190      200      210      220
Cry1Ac  HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  HLSFIRDVILNADEWGISAAATVRYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
          190      200      210      220      230      240

```

```

          230      240      250      260      270      280
Cry1Ac  WIRYNQFRRELTLTVDIVSLFPNYSRTYPIRTVSQLTREIYTNVLENFDGSRGSAQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  ML---EFRTYMFNLNVEYVSIWLSLFKYQSLLVSSGANL---YASL-----GS--GPTQ
          250      260      270      280

```

```

          290      300      310      320      330      340
Cry1Ac  GIEGSIRSPhLMDILNSITIIYTDHRGEYYWSGHQIMASPV--GFSGPE--FTFPLYGTM
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  -----SFT---AHNWPFLYSLFQVNSNYVLNGLSGARTTTITFSNIGGL
          290      300      310      320

```

```

          350      360      370      380      390
Cry1Ac  GNAAPQQ-----RIVAQLGQGVYRTLSSTLYRRPFNIG--INNQQ-----SVLD-GTEF-
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  PGSTTTQTLLHFARINRVGGVSSSRIGQANL-NQNFNISTLFLNPLQTPFIRSWLDSGTDRE
          330      340      350      360      370      380

```

```

          400      410      420      430      440      450
Cry1Ac  AYTSSNLPSAVYRKSGTVDSLDEIPPQNNVPPRQGFSHRLSHVSMFRSGFSNSVSI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  GVATSTNWQSGAFETLLRFSIFSARGNSNFFP-----DYFIRNISGVVGTISNADLA--
          390      400      410      420      430

```

```

          460      470      480      490      500
Cry1Ac  RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNS
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  RPLHFNEI-RDI---GTTAVASLVTVHNRKNNIYDTHENGMTMIHLAPNDYTGFTVSPPIHA
          440      450      460      470      480      490

```

```

          510      520      530      540      550
Cry1Ac  SGNNIQNRGYIE-----VPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  TQVNNQIRTFISEKYGNQGDLSLRFELSNTTARYTLRGNGNSYN-LYLRVSSIGSSTIRVT
          500      510      520      530      540      550

```

```

          560      570      580      590      600      610
Cry1Ac  VPATATSLD-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  INGRVYTANVNTTTNNDGVLDNGARFSDINIGNVVA---SANTNVPLD---IQVTFNG
          560      570      580      590      600

```

```

          620      630      640      650      660      670
Cry1Ac  EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKV
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|128  NPQFEL-----MNIMFVPTNPSPLY
          610      620

```

>>gi|112088062|gb|ABI06966.1| Sequence 48 from patent US (625 aa)  
 initn: 172 init1: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06  
 Smith-Waterman score: 249; 23.679% identity (54.827% similar) in 549 aa overlap  
 (85-595:98-590)

```

          60      70      80      90      100      110
Cry1Ac  VPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGL-SNLYQI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112  LVGKRILSELQNLIFPGSIDLMQEIILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
          70      80      90      100      110      120

```

```

          120      130      140      150      160      170
Cry1Ac  --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112  NRQVDNFLNPNQNPVPLAIIIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
          130      140      150      160      170      180

```

```

          180      190      200      210      220
Cry1Ac  HLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112  HLSFIRDVILNADEWGISAAATVRYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
          190      200      210      220      230      240

```



Regulatory Product Characterization Team

>>gi|13537921|emb|CAC35769.1| unnamed protein product [B (625 aa)
initn: 172 initl: 137 opt: 242 Z-score: 278.3 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 249; 23.679% identity (54.827% similar) in 549 aa overlap
(85-595:98-590)

60 70 80 90 100 110
Cry1Ac VPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGL-SNLYQI
gi|135 LVGKRILSELQNLIFPGSIDLMQEIILRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

120 130 140 150 160 170
Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|135 NRQVDNFLNPNQNPVPLAIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANL
130 140 150 160 170 180

180 190 200 210 220
Cry1Ac HLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
gi|135 HLSFIRDVILNADEWGISAATVRYRDHLRNFTRDYSNYCINTYQTAFR---GLNTRLHD
190 200 210 220 230 240

230 240 250 260 270 280
Cry1Ac WIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQ
gi|135 ML---EFRTYMFNLFVFEVYSIWSLPHYQSLVSSGANL---YAS-----GS--GPTQ
250 260 270 280

290 300 310 320 330 340
Cry1Ac GIEGSI RSPHLM DILNSIT IYTD AHRGEY YWGHQ IMA SPV--GFSGPE--FTFP LYGT M
gi|135 -----SFT---AQNWPFLYSLFQVNSNYVLNGLSGARTITTFPNI GGL
290 300 310 320

350 360 370 380 390
Cry1Ac GNAAPQQ----RIVAQLGQGVYRTLSTLYRRPFNIG--INNQQQL---SVLD-GTEF-
gi|135 PGSTTTQTLHFARINRYGGVSSSRIGQANL-NQNFNISTLFNPLQTPFIRSWLDSGT DRE
330 340 350 360 370 380

400 410 420 430 440 450
Cry1Ac AYGTSNLP S AVYRKSGTVDLSLDEIPPQNNVPPRQGF SHRLSHVSMFRSGFSNSSVSII
gi|135 GVATSTNWQSGAFETLLRFSIFSARGNSNFPP----DYFIRNISGVVGTISNADLA--
390 400 410 420 430

460 470 480 490 500
Cry1Ac RAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNS
gi|135 RPLHFNEI-RDI---GTTAVASLVTVHNRKNNIYDTHENGMIHLAPNDYTGFVSPPIHA
440 450 460 470 480 490

510 520 530 540 550
Cry1Ac SGNNIQNRGYIE-----VPIHFPSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNT
gi|135 TQVNNQIRTFISEKYNGQDLSRFELSNTTARYTLRGNNSYN-LYLRVSSIGSSTIRVT
500 510 520 530 540 550

560 570 580 590 600 610
Cry1Ac VPATATSLD-NLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATL
gi|135 INGRVYTANVNTTTTNDGVDLNGARFSDINIGNVVASANTNVPLDIQVTFNDNPFQELMN
560 570 580 590 600 610

620 630 640 650 660 670
Cry1Ac EAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKV
gi|135 IMLFQLIFHHFIKV
620

>>gi|155097707|gb|ABT00638.1| Sequence 244 from patent U (634 aa)
initn: 145 initl: 145 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 268; 22.920% identity (53.650% similar) in 589 aa overlap
(45-595:57-601)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGFVLG--LVDIIWGIF
gi|155 FQHKSLDVTQREWEWKNNHSLYLDPIVGTVASFLLKK---VGSVLGKRILSELWNLI
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD---
gi|155 FPSGSTNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNR-QVDNFLY
90 100 110 120 130

130 140 150 160 170 180
Cry1Ac PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQ
gi|155 PNRNAVPLSITSSVNTMQQLFLNRLPQFQVQGYQLLLLPLFAQAANLHLSFIRDVILNAD
140 150 160 170 180 190

190 200 210 220 230 240
Cry1Ac RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTL
gi|155 EWGISAATLRTYRDYLYKNYTRDYSNYCINTYQSAFK---GLNARLHDTL---EFRTYMFN
200 210 220 230 240 250

250 260 270 280 290 300
Cry1Ac TVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSI RSPHLM D
gi|155 NVFEVYSIWSLPHYQSLVSSGANL---YASGSGPQQTSQFSTQDWPFLYSLFQVNSNY
260 270 280 290 300

310 320 330 340 350
Cry1Ac ILSNIT-----IYTD AHRGEY YWGHQ IMA SPVGFSGPEFTFP LYGTMGNAAPQQRIVA
gi|155 VLNGFSGARLSNTFPNIGGLPGSTTTTHALLAARVNYSGGISS---GDIGASFPNQFNFC
310 320 330 340 350 360

360 370 380 390 400 410
Cry1Ac QLQGGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSNLP S AVYRKSGTVDLSL
gi|155 ST---FLPPLLTPFVRSWLDSGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFP
370 380 390 400 410 420

```

          420          430          440          450          460          470
Cry1Ac EIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNNIIA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS--VHNKR--NNIHA
          430          440          450          460          470

```

```

          480          490          500          510          520
Cry1Ac SDSITQIPAVKGNFLFNGSVIS--GPG--FTGGDLVRLNSSGNNIQNRGYIEVP-----I
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VHE-----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSL
          480          490          500          510          520

```

```

          530          540          550          560          570
Cry1Ac HFP--STSTRYRVRVRYASVTPPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RFEQNNTTARVYTLRGNNGNSYN--LYLRVSSIGNSTRATINGRVYTATNVNTTTNND--GVN
          530          540          550          560          570          580

```

```

          580          590          600          610          620          630
Cry1Ac ESANAFTS--SLGNIVGVRNFGTAGVIIDRFEPVVTATLEAEYNLERAQKAVNALFTST
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 DNGARFSDINMGNVVSSNSDVPDLINVTFNSTQFDLMNIMLVPTNISPLY
          590          600          610          620          630

```

>>gi|155097626|gb|ABT00557.1| Sequence 82 from patent US (634 aa)  
 initn: 140 initl: 140 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06  
 Smith-Waterman score: 261; 23.051% identity (52.373% similar) in 590 aa overlap  
 (81-637:95-629)

```

          60          70          80          90          100          110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KVGSLVGRKRISELRLIFPSGSTNMQDILRETEKFLNQLRLNTDTLARVNAELTGL---
          70          80          90          100          110          120

```

```

          120          130          140          150          160
Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFQVERYQLLLLPLFAQ
          130          140          150          160          170          180

```

```

          170          180          190          200          210          220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
          190          200          210          220          230

```

```

          230          240          250          260          270          280
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RLHDMLE--EFRTYMFLNVFEYVSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFT
          240          250          260          270          280          290

```

```

          290          300          310          320          330
Cry1Ac GSAQGIEGSIRSPHLMILNSITIIYTDHRGEYY-----WSGHQIMASPVFGFSGPE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SQDWPFLYSLFQVNSDYVLNG---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGV
          300          310          320          330          340

```

```

          340          350          360          370          380          390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQQLGGQVYRTLSSSTLYRRFPNIGINNQL--SVLDGTEFAYG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SS---GDIGASPFDDQNFSCST---FLPPLLTPFVRSWLDSDGSDRGVNTVTNWQTESFE
          350          360          370          380          390          400

```

```

          400          410          420          430          440          450
Cry1Ac TSSNLPSAVYRKGSTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPG
          410          420          430          440          450          460

```

```

          460          470          480          490          500
Cry1Ac IRAPMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVIS--GP--GFTGGDLVRLNSSG
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 ARAYMVS--VHNKR--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATR
          470          480          490          500

```

```

          510          520          530          540          550
Cry1Ac NNIQNRGYIEVP-----IHPFSTSTRYRVRVRYASVTPPIHLNVN--WGNSSIFS--NT
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VNNQTRTFISEKFGNQGDSLRFQSNNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
          510          520          530          540          550          560

```

```

          560          570          580          590          600          610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS--SLGNIVGVRNFGTAGVIIDRFEPVVTATLE
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 QVYTATNVNTTTNND--GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
          570          580          590          600          610

```

```

          620          630          640          650          660          670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDFECLDEKRELSEKVK
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TQFDL-----MNIMFVPTNLPPLY
          620          630

```

>>gi|155097683|gb|ABT00614.1| Sequence 196 from patent U (634 aa)  
 initn: 145 initl: 145 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06  
 Smith-Waterman score: 268; 22.920% identity (53.650% similar) in 589 aa overlap  
 (45-595:57-601)

```

          20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDIIWGF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLKK---VGSVLVGRKRISELWNLI
          30          40          50          60          70          80

```

```

          80          90          100          110          120
Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD---
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FPSGSTNMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNR--QVDNPLY
          90          100          110          120          130

```

```

          130          140          150          160          170          180
Cry1Ac PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 PNRNAVPLSITSSVNTMQQLFLNRLPQFQVQGYQLLLLPLFAQAANLHLSFIRDVILNAD
          140          150          160          170          180          190

```

```

      190      200      210      220      230      240
Cry1Ac  RMGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTL
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  EWGISAAATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNARLHDTL---EFRTYMFL
      200      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac  TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHLM
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  NVFEYVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNY
      260      270      280      290      300

      310      320      330      340      350
Cry1Ac  LLNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVA
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  VLNGFSGARLSNTFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNC
      310      320      330      340      350      360

      360      370      380      390      400      410
Cry1Ac  QLQGQVYRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSDL
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  ST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFP
      370      380      390      400      410      420

      420      430      440      450      460      470
Cry1Ac  EIPPQN-NNVP--PRQGFshrlshvsmFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIA
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  DYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHA
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac  SDSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----I
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  VHE-----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSL
      480      490      500      510      520

      530      540      550      560      570
Cry1Ac  HFP--STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYF
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  RFEQNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRATINGRVYATNVNTTTNND-GVN
      530      540      550      560      570      580

      580      590      600      610      620      630
Cry1Ac  ESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  DNGARFSDINMGNVVASSNSDVPLDINVTFNSTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

>>gi|155097703|gb|ABT00634.1| Sequence 236 from patent U (634 aa)
  initn: 145 initl: 145 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 268; 22.920% identity (53.650% similar) in 589 aa overlap
(45-595:57-601)

      20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEFVPGAGFVLG--LVDIIWGI
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  FQHKSLDTVQREWTEWKNNHSLYLDPIVGTVASFLKK---VGSVLGKRILSELWNLI
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac  GPSQWDAFLVQI----EQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEAD----
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  FPSGSTNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNK-QVDNFLY
      90      100      110      120      130

      130      140      150      160      170      180
Cry1Ac  PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQ
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  PNRNAVPLSITSSVNTMQQLFLNRLPQFVQVQYQLLLPLFAQAANLHLSFIRDVILNAD
      140      150      160      170      180      190

      190      200      210      220      230      240
Cry1Ac  RMGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTL
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  EWGISAAATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNARLHDTL---EFRTYMFL
      200      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac  TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIIRSPHLM
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  NVFEYVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNY
      260      270      280      290      300

      310      320      330      340      350
Cry1Ac  LLNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPlygTMGNAAPQQRIVA
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  VLNGFSGARLSNTFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNC
      310      320      330      340      350      360

      360      370      380      390      400      410
Cry1Ac  QLQGQVYRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSDL
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  ST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFP
      370      380      390      400      410      420

      420      430      440      450      460      470
Cry1Ac  EIPPQN-NNVP--PRQGFshrlshvsmFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIA
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  DYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHA
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac  SDSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----I
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  VHE-----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSL
      480      490      500      510      520

      530      540      550      560      570
Cry1Ac  HFP--STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYF
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  RFEQNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRATINGRVYATNVNTTTNND-GVN
      530      540      550      560      570      580

      580      590      600      610      620      630
Cry1Ac  ESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  DNGARFSDINMGNVVASSNSDVPLDINVTFNSTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

      630      640      650      660      670      680
Cry1Ac  HFP--STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYF
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  RFEQNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRATINGRVYATNVNTTTNND-GVN
      630      640      650      660      670      680

      680      690      700      710      720      730
Cry1Ac  ESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
      .:.....:.....:.....:.....:.....:.....:.....:.....:.....:.....:
gi|155  DNGARFSDINMGNVVASSNSDVPLDINVTFNSTQFDLMNIMLVPTNISPLY
      680      690      700      710      720      730

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Regulatory Product Characterization Team

>>gi|155097715|gb|ABT00646.1| Sequence 260 from patent U (634 aa)
initn: 171 initl: 131 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 258; 23.119% identity (52.477% similar) in 545 aa overlap
(81-595:95-601)

Cry1Ac LSEFVPGAGFVLGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISREGLSNL
gi|155 KVGSLVGRKILSELRLSIFPSGSTNLMQDILRETEKLLNQRLLNTDTLARVNAELEG---

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNFLNPNRNNAVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQ

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDS
gi|155 AANLHLSFIRDVILNAGEWGISAAATLRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNT

Cry1Ac R--DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLENFDGSR
gi|155 RLHDTL---EFRTYMFNLVFEYVSIWSLFKYQSLVSSGANL---YASGSGPQQTQSFT

Cry1Ac GSAQGIEGSIRSPHMLDILNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTF
gi|155 SQDWPFLYSLFQVNSNYVLNFGFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISS-

Cry1Ac PLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQ--SVLDGTEFAYGTSS
gi|155 ---GDIGASPFNQNFNCST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTL

Cry1Ac NLPsAVYRKSgTVDsLDEIPpQN--NVP--PRQGFShRLSHVSMFRSGFSNSsV--SIIRA
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPGTGGARA

Cry1Ac PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNssGNNI
gi|155 YMVS-VHNRK--NNIHAVHE-----NGSMIHLAENDYTGFTISPIHATQVNN

Cry1Ac QNRGYIEVPIHFPSTSTRYR---VRVRYA----SVTPiHLNVN-WGNSSIFs--NTVPA
gi|155 QTRTFISEKFGNQGDSLRFEQNNTTARYTLKGNNGSYNLVLRVSSIGNSTIRVTINGRVY

Cry1Ac TATSLDNLQSSDFGYFESANAFTS--SLGNIVGVRNFSGTAGVVIDRFEFIPVTATLEAEY
gi|155 TATNVNTTTNND--GVNDNGARFSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLV

Cry1Ac NLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAK
gi|155 PTNISPLY

630

>>gi|155097689|gb|ABT00620.1| Sequence 208 from patent U (634 aa)
initn: 145 initl: 145 opt: 242 Z-score: 278.2 bits: 62.6 E(): 1.4e-06
Smith-Waterman score: 268; 22.920% identity (53.650% similar) in 589 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIWIWGI
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLKK---VGSVLVGRKILSELWNLII

Cry1Ac GPSQWDAFLVQI---EQLINQRIEEFARNQAIISREGLSNLYQIYAESFREWEAD---
gi|155 FPSGSTNLMQDILRETEKFLNQRLLNTDTLARVNAELTGL---QANVEEFNR-QVDNFLY

Cry1Ac PTPNALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQ
gi|155 PNRNAVPLSITSSVNTMQQLFLNRLPQFQVQGYQLLLLPLFAQAANLHLSFIRDVILNAD

Cry1Ac RWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRRELT
gi|155 EWGISAAATLRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNARLHDTL---EFRTYMF

Cry1Ac TVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPLENFDGSRFGSAQGIEGSIRSPHLM
gi|155 NVFEYVSIWSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNY

Cry1Ac ILNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTTFPLYGTMGNAAPQQRIVA
gi|155 VLNFGFSGARLSNTFPNIGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQNFNC

Cry1Ac QLGGQGVYRTLSTLYRRPFNIGINNQQ--SVLDGTEFAYGTSSNLPSAVYRKSgTVDsL
gi|155 ST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFP



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140      150      160      170      180      190
Cry1Ac 190      200      210      220      230      240
RWGFDAAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTL
gi|155 EWGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNARLHDTL---EFRTYMFL
200      210      220      230      240      250

250      260      270      280      290      300
Cry1Ac TVLDIVSLFPPNYDSRITYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQGIIEGSIIRSPHMLD
gi|155 NVFEYVSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFYLSLFQVNSNY
260      270      280      290      300

310      320      330      340      350
Cry1Ac ILNSIT-----IYTDahrgeyywSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVA
gi|155 VLNGFSGARLSNTFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNC
310      320      330      340      350      360

360      370      380      390      400      410
Cry1Ac QLGQGVYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYGTSNNLPSAVYRKSGTVDSLD
gi|155 ST---FLPPLLPFVRSWLDGSDREGVATVNWQTESFETLGLRSGAFTARGNSNYFP
370      380      390      400      410      420

420      430      440      450      460      470
Cry1Ac EIPPQN-NNVP--PRQGFshrlshvsmFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIIA
gi|155 DYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPGTGGARAYMVS-VHNRK--NNIHA
430      440      450      460      470

480      490      500      510      520
Cry1Ac SDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----I
gi|155 VHE-----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSL
480      490      500      510      520

530      540      550      560      570
Cry1Ac HFP--STSTRYRVRVRYASVTPiHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYF
gi|155 RFEQNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRATINGRVYTATNVNTTTNND-GVN
530      540      550      560      570      580

580      590      600      610      620      630
Cry1Ac ESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
gi|155 DNGARFSDINMGNVVASSNSDVPLDINVTFNSTQFDLNMIMLVPTNISPLY
590      600      610      620      630

>>gi|155097591|gb|ABT00522.1| Sequence 12 from patent US (634 aa)
initn: 140 init1: 140 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06
Smith-Waterman score: 263; 22.810% identity (52.555% similar) in 548 aa overlap
(81-595:95-601)

60      70      80      90      100      110
Cry1Ac LSEFVPGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIIEFARNQAIIRLEGLSNI
gi|155 KVGSLVgKRILSELRLSIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVAELTGL---

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70      80      90      100      110      120
Cry1Ac 120      130      140      150      160
YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ
130      140      150      160      170      180

170      180      190      200      210      220
Cry1Ac AANLHLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQSAFR---GLNT
190      200      210      220      230

230      240      250      260      270      280
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPPNYDSRITYPIRTVSQLTREIYTNPVLENFDGSGFR
gi|155 RLHDM---EFRTYMFNLNVFEYVSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFT
240      250      260      270      280      290

290      300      310      320      330
Cry1Ac GSAQGIIEGSIIRSPHMLDILNSITITYTDahrgeyy-----WSGHQIMASPVGFSGPE
gi|155 SQDWPFYLSLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGV
300      310      320      330      340

340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYG
gi|155 SS---GDIGASPFNQNFSCST---FLPPLLPFVRSWLDGSDRGGVNTVNWQTESFE
350      360      370      380      390      400

400      410      420      430      440      450
Cry1Ac TSSNLPsAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFshrlshvsmFRSGFSNSSV-SI
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIASPGTGG
410      420      430      440      450      460

460      470      480      490      500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
gi|155 LRAYMVS-VHNRK--NNIYAVHE-----NGSMIHLAPEDYTGFTISPIHATQ
470      480      490      500

510      520      530      540      550
Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
gi|155 VNNQTRTFISEKFGNQGDSLRFEQSNNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVING
510      520      530      540      550      560

560      570      580      590      600      610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLE
gi|155 RVYASNVNTTTNND-GVNDNGARFSDINIGNVVASSNSDVPLDINVTLNSTQGFELMNI
570      580      590      600      610      620

620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK

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gi|155 MFVPTNLSPLY  
630

>>gi|155097623|gb|ABT00554.1| Sequence 76 from patent US (634 aa)  
initn: 135 init1: 135 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06  
Smith-Waterman score: 269; 22.611% identity (53.025% similar) in 628 aa overlap  
(45-637:57-629)

20 30 40 50 60 70  
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGF  
..... : : : : :  
gi|155 FQHKSLDTVQEEWMEWKKDNHSLYVDPVIGTVASFLKKVGSLSLGRKRLSELRNLIFFPSG  
30 40 50 60 70 80  
80 90 100 110 120  
Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A  
..... : : : : :  
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA  
90 100 110 120 130 140

130 140 150 160 170 180  
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF  
..... : : : : :  
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDAILNADEWGIS  
150 160 170 180 190 200

190 200 210 220 230 240  
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI  
..... : : : : :  
gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLNVFEY  
210 220 230 240 250

250 260 270 280 290 300  
Cry1Ac VSLFPNYDSRITYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSIKRSRPHLMDILNSI  
..... : : : : :  
gi|155 VSIWLSFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYLVNG-  
260 270 280 290 300 310

310 320 330 340 350  
Cry1Ac TIYTDAHRGEYY-----WSGHQIMASPVGFGPEFTFPLYGTMGNAAPQQRIVAQL  
..... : : : : :  
gi|155 --FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGVSS---GDIGASPFNQNFSCST  
320 330 340 350 360

360 370 380 390 400 410  
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQQL-SVLGDGTEFAYGTSSNLPsAVYKSGTVDLSDEI  
..... : : : : :  
gi|155 ---FLPPLLTPFVRSWLDSDGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY  
370 380 390 400 410 420

420 430 440 450 460 470  
Cry1Ac PPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASD  
..... : : : : :  
gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGGLRAYMVS-VHNRK--NNIYAVH  
430 440 450 460 470

480 490 500 510 520  
Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHF  
..... : : : : :  
..... : : : : :  
..... : : : : :

gi|155 E-----NGSMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRF  
480 490 500 510 520

530 540 550 560 570 580  
Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA  
..... : : : : :  
gi|155 EQSNTTARYTLRGNNGSNYLYLRVSSIGNSTIRVTINGRVYTATNVTNTTND-GVNDNG  
530 540 550 560 570 580

590 600 610 620 630  
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQL  
..... : : : : :  
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP  
590 600 610 620 630

640 650 660 670 680 690  
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINR

gi|155 PLY

>>gi|155097684|gb|ABT00615.1| Sequence 198 from patent U (634 aa)  
initn: 140 init1: 140 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06  
Smith-Waterman score: 263; 22.603% identity (52.226% similar) in 584 aa overlap  
(81-637:95-629)

60 70 80 90 100 110  
Cry1Ac LSEFVPGAGFVLGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNL  
..... : : : : :  
gi|155 KVGSLVGRKILSELRLIFPSGSTNMQDILRETEKFLNQLRNTDTLARVNAELTGL---  
70 80 90 100 110 120

120 130 140 150 160  
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ  
..... : : : : :  
gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ  
130 140 150 160 170 180

170 180 190 200 210 220  
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS  
..... : : : : :  
gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT  
190 200 210 220 230

230 240 250 260 270 280  
Cry1Ac R--DWIRYNQFRRELTTLVLDIVSLFPNYDSRITYPIRTVSQLTREIYTNVLENFDGSR  
..... : : : : :  
gi|155 RLHDML---EFRTYMFNLNVFEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDW  
240 250 260 270 280 290

290 300 310 320 330 340  
Cry1Ac GSAQIEGSIKRSRPHLMDILNSITI---YTDHRGEYYWSGHQIMASPVGFGPEFTFPLY  
..... : : : : :  
gi|155 PSLYSLF-QVNSNYLVNGFSGVRLSQTFFPNIVGLPGTTTTHALLAARVNYSGGVSS---  
300 310 320 330 340

350 360 370 380 390 400  
Cry1Ac GTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQQL-SVLGDGTEFAYGTSSNLP  
..... : : : : :  
..... : : : : :  
..... : : : : :

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gi|155 GDIGARTAGQNFNCST---FLPPLSPFVRSWLDGSDRGGVNTVTNWQTESFETTLGLR
350 360 370 380 390 400

Cry1Ac SAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMF
410 420 430 440 450

gi|155 SGAFRTARGNSNYFPDYFIRNISGVPLVARNEDLRRPLHYNQIRNIESPSGTPGARAYMV
410 420 430 440 450 460

Cry1Ac SWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNNSGNNIQNR
460 470 480 490 500 510

gi|155 S-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQVNNQTR
470 480 490 500 510

Cry1Ac GYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATAT
520 530 540 550 560

gi|155 TFISEKFGNQGDSLRFEQSNNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVTAT
520 530 540 550 560 570

Cry1Ac SLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLE
570 580 590 600 610 620

gi|155 NVNTTTNND-GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLSGQIFDL-
580 590 600 610 620

Cry1Ac RAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLS
630 640 650 660 670 680

gi|155 -----MNIMFVPTNLPPLY
630

>>gi|155097592|gb|ABT00523.1| Sequence 14 from patent US (634 aa)
initn: 140 initl: 140 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06
Smith-Waterman score: 260; 22.628% identity (52.555% similar) in 548 aa overlap
(81-595:95-601)

Cry1Ac LSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEERFARNQAIISREGLSNL
60 70 80 90 100 110

gi|155 KVGSLVGRKILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQ
120 130 140 150 160

gi|155 -QANVEEFNRQVDNFLNPNRNVPLSITSSVNTMQQLFLNRLPQFQMQYQLLLPLFAQ
130 140 150 160 170 180

Cry1Ac AANLHLSVLRDVSFVGRQWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
170 180 190 200 210 220

gi|155 AANLHLSFIRDVILNADEWGISAAATLRYQNHLRNYTRDYSNYCINTYQSAFR---GLNT
190 200 210 220 230

Cry1Ac R--DWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLENFDGSFR
230 240 250 260 270 280

gi|155 R--DWIRYNQFRRELTTLVLDIVSLFPNYSRTYPIRTVSQLTREIYTNPLENFDGSFR
230 240 250 260 270 280

gi|155 RLHDM---EFRTYMFNLVFEYVSIWLSFKYQSLLVSSGANL----YASGSGPQQTSQFT
240 250 260 270 280 290

Cry1Ac GSAQGIIEGSIIRSPHLMILNSITIIYTDHRGEYY-----WSGHQIMASPVGFSGPE
290 300 310 320 330

gi|155 SQDWPFYLSLFQVNSNYVLNG--FSGARLSQTFPNIVGLPGTTTTALLAARVNYSGGV
300 310 320 330 340

Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQ-L-SVLDGTEFAYG
340 350 360 370 380 390

gi|155 SS---GDIGASPFQNFNCST---FLPPLTPFVRSWLDGSDRGGVNTVTNWQTESFE
350 360 370 380 390 400

Cry1Ac TSSNLSAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
400 410 420 430 440 450

gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGG
410 420 430 440 450 460

Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNNSG
460 470 480 490 500

gi|155 LRAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
470 480 490 500

Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
510 520 530 540 550

gi|155 VNNQTRTFISEKFGNQGDSLRFEQSNNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
560 570 580 590 600 610

gi|155 RVYTASNVTNTTND-GVNDNGARFSDINIGNVVASNSDVPLDINVTLSNGTQFELMNI
570 580 590 600 610 620

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK
620 630 640 650 660 670

gi|155 MFVPTNLSPLY
630

>>gi|155097593|gb|ABT00524.1| Sequence 16 from patent US (634 aa)
initn: 140 initl: 140 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06
Smith-Waterman score: 260; 22.712% identity (52.542% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac LSEFVPGAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEERFARNQAIISREGLSNL
60 70 80 90 100 110

gi|155 KVGSLVGRKILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQ
120 130 140 150 160

gi|155 YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTAIPLFAVQNYQVPLLSVYVQ
120 130 140 150 160

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gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQ
      130      140      150      160      170      180

      170      180      190      200      210      220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      :::::  :::  . . . . .  : : : : :  : . . . . .  : . . . . .  : . .
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQSAFR---GLNT
      190      200      210      220      230

      230      240      250      260      270      280
Cry1Ac R--DWIRYNQFRELTLTVLDIVSLFPPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFR
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : :
gi|155 RLHDM---EFRTYMLNVFEYVSIWLSLFKYQSLVSSGANL---YASGSGPQQTQSFT
      240      250      260      270      280      290

      290      300      310      320      330
Cry1Ac GSAQIEGSIRSPHLMILNSITTYDAHRGEYY-----WSGHQIMASPVGFSGPE
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 SQDWPFLYSLFQVNSNYVLNG---FSGARLSQTFPNIVLPGTTTTHALLAARVNYSGGV
      300      310      320      330      340

      340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYG
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 SS---GDIGASPFNQFSCST---FLPPLLPFVRSWLDGSDRGVATVNWQTESFE
      350      360      370      380      390      400

      400      410      420      430      440      450
Cry1Ac TSSNLPSAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIASPSGTPGG
      410      420      430      440      450      460

      460      470      480      490      500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 ARAYMVS-VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
      470      480      490      500

      510      520      530      540      550
Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NT
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 VNNQTRTFISEKFGNQDGLRFEQSNNTTARYTLRGNNGSYNLYLRVSSIGNSTIRVTING
      510      520      530      540      550      560

      560      570      580      590      600      610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 RYVTASNVTNTTND-GVNDGARFSDINIGNVVA---SSNSDVPLD---INVTLNSG
      570      580      590      600      610

      620      630      640      650      660      670
Cry1Ac AEYNLERAQKAVNALFTSTINQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 TQFDL-----MNIMFVPTNLPLY
      620      630

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>>gi|155097603|gb|ABT00534.1| Sequence 36 from patent US (634 aa)
  initn: 133 init1: 133 opt: 241 Z-score: 277.0 bits: 62.4 E(): 1.6e-06

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Smith-Waterman score: 256; 22.603% identity (53.082% similar) in 584 aa overlap
(45-595:57-601)

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      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 FQHKSLDVTQREWEWKNNHSLYLDPIVGTVASFLLKKVGSVGVKRIKLSLRNLIFFPSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNP---A
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 STNLMQDILRETEKFLNQLRSLDSTLARVNAELRGL---QANVEEFNHQVDNFLNPNRNA
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 VPLSITSSVNTMQQLFLNRLPMPFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLDI
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 AATLRTYRDYLKEYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMLNVFEY
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac VSLFPPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSFRGSAQIEGS---IRSPHLMIL
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 VSIWLSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLDGF
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac NSITI---YDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 SGARLSNTFPNIVLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNFCST---
      320      330      340      350      360

      370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 FLPPLLPFVRSWLDGSDREGVATVNWQTESLETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNINQNRGYIEVP-----IHFP--
      : : : : :  : : : : :  : . . . . .  : . . . . .  : . . . . .  : . .
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQ
      490      500      510      520

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTPATATSLDNLQSSDFGYFESANA

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gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac VYRTLSSSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
370 380 390 400 410 420

gi|155 FLPLLLTPFVRSWLDSGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490 500 510 520

Cry1Ac STSTRYRVRVRYASVTPIHNLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|155 NTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|155 FSDINIGNVVASNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097669|gb|ABT00600.1| Sequence 168 from patent U (634 aa)
initn: 144 initl: 144 opt: 240 Z-score: 275.8 bits: 62.1 E(): 1.9e-06
Smith-Waterman score: 264; 22.603% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIGWIF
20 30 40 50 60 70

gi|155 FRHKSOLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGRKRLSELNRLFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADTPN---A
80 90 100 110 120

gi|155 STNLMQDILLRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNQVDNFLNPNRRA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFQGRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFVQGYQLLLLPLFAQAANMHSFIRDVVLNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTTLVLDI
190 200 210 220 230 240

gi|155 AATLRTYRDLKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQTLREIYTNPVLENFDGSRGSAQIEGSIKRSPLMDILNSI
250 260 270 280 290 300

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF
260 270 280 290 300 310

Cry1Ac T-----IYTDahrgeyYwSGHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVaQLGQG
310 320 330 340 350 360

gi|155 SGARLSNTFPNIGGLPGSTTHALLAARVNYSGGVSS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac VYRTLSSSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
370 380 390 400 410 420

gi|155 FLPLLLTPFVRSWLDSGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490 500 510 520

Cry1Ac STSTRYRVRVRYASVTPIHNLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|155 NTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|155 FSDINIGNVVASNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097637|gb|ABT00568.1| Sequence 104 from patent U (634 aa)
initn: 180 initl: 180 opt: 240 Z-score: 275.8 bits: 62.1 E(): 1.9e-06
Smith-Waterman score: 264; 23.038% identity (53.584% similar) in 586 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIGWIF
20 30 40 50 60 70

gi|155 FQHKSOLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLK---VGSVLVGRKRLSELRLGI
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAISRLEGLSNLYQIYAESF--REWEA--DP
80 90 100 110 120

gi|155 FPSGNTNLMQDILRETEKFLNQRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNP
90 100 110 120 130

Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQR
130 140 150 160 170 180

gi|155 TQNAVPLSITSSVNTMQQLFLNRLPQFQVQGYQLLLPLFAQAANLHLSFIRDVILNADE
140 150 160 170 180 190

Cry1Ac WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLTVL
190 200 210 220 230 240

gi|155 WGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAF-KALNTRLHDTL---EFPTYMFLNVF
200 210 220 230 240 250

Cry1Ac DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILN
250 260 270 280 290 300

gi|155 EYVSIWSLFKYQSLLVSSGANL---YTSGSGPQQAQSFQSDWPFLYSLFQVNSNYVLN
260 270 280 290 300 310

Cry1Ac SIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLG
310 320 330 340 350

gi|155 GFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST-
320 330 340 350 360

Cry1Ac QGVYRTLSTLYRRPFNIGINNQQ-LVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIP
360 370 380 390 400 410

gi|155 --FLPPLLPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSNYFPDYF
370 380 390 400 410 420

Cry1Ac PQN-NNPV--PRQGFshrlshvsmfRSGFSNssV-SIIrAPMFSWIHRSAEFNNIIASDS
420 430 440 450 460 470

gi|155 IRNISGVPLVVRNEDLRRPLHYNEIRNIASPGTGGARAYMVS-VHNRK--NNIHAVHE
430 440 450 460 470 480

Cry1Ac ITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNNIQRGYIEVP-----IHFP
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
490 500 510 520

Cry1Ac --STSTRYRVRVRYASVTPIHlNVN-WGNSSIFs--NTVPATATSLDNLQSSDFGYFESA
530 540 550 560 570 580

gi|155 QNNTTARYTLRGNNGNSYN-LYLRVSSSTGRSTIRVTINGRVYATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQ
590 600 610 620 630

gi|155 ARFSDINIGNVASSNSDVPLDINVTFNSGTQFDLMNIMLVPTNISPIY
590 600 610 620 630

>>gi|155097660|gb|ABT00591.1| Sequence 150 from patent U (634 aa)

initn: 167 initl: 133 opt: 240 Z-score: 275.8 bits: 62.1 E(): 1.9e-06
Smith-Waterman score: 260; 22.774% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVGLVDIIWGIF
20 30 40 50 60 70

gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASPFLKVKVGSVGLKRIKLSLRNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEKFLNQRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNR
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
130 140 150 160 170 180

gi|155 VLLSITSSVNTMQQLFLNRLPQFQVQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFPTYMFLNVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILNSI
250 260 270 280 290 300

gi|155 VSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFQSDWPFLYSLFQVNSNYVLNGF
260 270 280 290 300 310

Cry1Ac T-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
310 320 330 340 350 360

gi|155 SGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac VYRTLSTLYRRPFNIGINNQQ-LVLDGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPQ
370 380 390 400 410 420

gi|155 FLPPLLPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNPV--PRQGFshrlshvsmfRSGFSNssV-SIIrAPMFSWIHRSAEFNNIIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPGTGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNNIQRGYIEVP-----IHFP--
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
490 500 510 520

530 540 550 560 570 580

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Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTNNND-GVNDNGAR
530 540 550 560 570 580

590 600 610 620 630 640
Cry1Ac FTS-SLGNIVGVRNFGSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|155 FSDINIGNVVASNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

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>>gi|155097652|gb|ABT00583.1| Sequence 134 from patent U (634 aa)  
 initn: 169 initl: 133 opt: 240 Z-score: 275.8 bits: 62.1 E(): 1.9e-06  
 Smith-Waterman score: 262; 22.680% identity (52.749% similar) in 582 aa overlap  
 (45-595:57-601)

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20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDI IWGIF
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGVSGLVKRILSELRNLI FPSG
30 40 50 60 70 80

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80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEQFLNQRDLTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

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130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

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190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVS
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHGTL--EFRTYMFLNVFEYVS
210 220 230 240 250

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250 260 270 280 290 300
Cry1Ac LFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSI RSPHLMIDILNSIT-
gi|155 IWSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGFSG
260 270 280 290 300 310

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310 320 330 340 350 360
Cry1Ac -----IYTDahrGEYyWShGHQIMASpVGFSGPEFTFPlyGTMGNAAPQRiVAQLGQGVY
gi|155 ARLSNTFPNIGGLPGSTTHALLAARVNYSSGGISS---GDIGASPFNQFNcST---FL
320 330 340 350 360

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370 380 390 400 410 420
Cry1Ac RtlSStlyRRPFNIGInnQQL-SVldGTEfAYGtSSnLpSAVYrKSGTVdSLdeIPpQn-
gi|155 PPLLTPFVRSWLDsgSDREGVATVtNWQTEsFETTLGLrSGaFTARGNSNYFDYfIRNI
370 380 390 400 410 420

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430 440 450 460 470

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Cry1Ac NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQI
gi|155 SGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE----
430 440 450 460 470 480

480 490 500 510 520
Cry1Ac PAVKGNFLFNNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--ST
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNT
490 500 510 520 530

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530 540 550 560 570 580
Cry1Ac STRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
gi|155 TARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTNNND-GVNDNGARFS
540 550 560 570 580

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590 600 610 620 630 640
Cry1Ac S-SLGNIVGVRNFGSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKT
gi|155 DINIGNVVASNSDVPLDINVTFNSGTQFDLMNTMLVPTNISPLY
590 600 610 620 630

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>>gi|155097659|gb|ABT00590.1| Sequence 148 from patent U (634 aa)  
 initn: 169 initl: 133 opt: 240 Z-score: 275.8 bits: 62.1 E(): 1.9e-06  
 Smith-Waterman score: 262; 22.680% identity (52.749% similar) in 582 aa overlap  
 (45-595:57-601)

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20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDI IWGIF
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGVSGLVKRILSELRNLI FPSG
30 40 50 60 70 80

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80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEQFLNQRDLTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

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130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

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190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTVLDIVS
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHGTL--EFRTYMFLNVFEYVS
210 220 230 240 250

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250 260 270 280 290 300
Cry1Ac LFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSI RSPHLMIDILNSIT-
gi|155 IWSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGFSG
260 270 280 290 300 310

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310 320 330 340 350 360

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Cry1Ac -----IYTDahrGEYyWSGHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQLGQGVY

gi|155 ARLSNTFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQFNCSST---FL
320 330 340 350 360

Cry1Ac 370 380 390 400 410 420
RTLSSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDLSLDEIPPQN-

gi|155 PPLLTPFVRSWLDSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRNI
370 380 390 400 410 420

Cry1Ac 430 440 450 460 470
NNVP--PQGFShRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSITQI

gi|155 SGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE----
430 440 450 460 470 480

Cry1Ac 480 490 500 510 520
PAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--ST

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNT
490 500 510 520 530

Cry1Ac 530 540 550 560 570 580
STRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT

gi|155 TARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVTTTNN-DGVNDNGARFS
540 550 560 570 580

Cry1Ac 590 600 610 620 630 640
S-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT

gi|155 DINIGNVVASNSDVPLDINVTFNSTQFDLMNTMLVPTNISPLY
590 600 610 620 630

>>gi|33731242|gb|AAQ37305.1| Sequence 33 from patent US (136 aa)
initn: 221 initl: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

Cry1Ac 470 480 490 500 510 520
EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF

gi|337 PGFIGGALLQRTDhGSLGVLR--VQFPLHL
10 20

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANA

gi|337 ---RQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSAFAIREFNTSIR
30 40 50 60 70 80

Cry1Ac 590 600 610 620 630 640
FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|337 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRElseKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731250|gb|AAQ37313.1| Sequence 49 from patent US (136 aa)
initn: 221 initl: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

Cry1Ac 470 480 490 500 510 520
EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF

gi|337 PGFIGGALLQRTDhGSLGVLR--VQFPLHL
10 20

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANA

gi|337 ---RQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSAFAIREFNTSIR
30 40 50 60 70 80

Cry1Ac 590 600 610 620 630 640
FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|337 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRElseKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504402|gb|AAM57101.1| Sequence 33 from patent US (136 aa)
initn: 221 initl: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

Cry1Ac 470 480 490 500 510 520
EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF

gi|215 PGFIGGALLQRTDhGSLGVLR--VQFPLHL
10 20

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANA

gi|215 ---RQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSAFAIREFNTSIR
30 40 50 60 70 80

Cry1Ac 590 600 610 620 630 640
FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|215 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRElseKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731256|gb|AAQ37319.1| Sequence 61 from patent US (136 aa)
initn: 221 initl: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

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      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                        10      20

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      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIR
      30      40      50      60      70      80

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      590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      :. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
      90      100     110     120     130

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      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

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>>gi|16240172|gb|AAE79622.1| Sequence 29 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

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```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                        10      20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      :. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|33731240|gb|AAQ37303.1| Sequence 29 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

```

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                        10      20

```

```

      530      540      550      560      570      580

```

```

Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      :. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

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>>gi|53970033|gb|AAV19126.1| Sequence 49 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

```

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|539          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                        10      20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|539 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      :. : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|539 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAAKAVASLF
      90      100     110     120     130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

```

>>gi|53970023|gb|AAV19116.1| Sequence 29 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

```

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|539          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                        10      20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
      ::::: . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|539 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPTMRLGEDLRYGSFAIREFNTSIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

```



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gi|215          ::: :: :.. .. . : .. :..
                PGFIGGALLQRTDHGSLGVLR--VQFPLHL
                10      20

          530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANA
          .....: :.:.: :. . :.:.: :. . :.:.: :. . :.:.: :. . :.:.:
gi|215 ---RQQYRIRVRYASTTNIRLSVN-GSPGTISQNLPSMRLGEDLRYGSAFAIREFNTSIR
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
          :. : . : . . : : : : : : : : : : : : : : : : : : : : : :
gi|215 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAEKEDLEAAKKAVASLF
          90      100     110     120     130

          650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|53970039|gb|AAV19132.1| Sequence 61 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

          470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
          :. : : . : . . : . : : . : . . : . : : . : . . : . : : . : . .
gi|539          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
          10      20

          530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANA
          .....: :.:.: :. . :.:.: :. . :.:.: :. . :.:.: :. . :.:.:
gi|539 ---RQQYRIRVRYASTTNIRLSVN-GSPGTISQNLPSMRLGEDLRYGSAFAIREFNTSIR
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
          :. : . : . . : : : : : : : : : : : : : : : : : : : : : :
gi|539 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAEKEDLEAAKKAVASLF
          90      100     110     120     130

          650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|16240184|gb|AAE79632.1| Sequence 49 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

          470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
          :. : : . : . . : . : : . : . . : . : : . : . . : . : : . : . .
gi|162          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
          10      20

          530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANA
          .....: :.:.: :. . :.:.: :. . :.:.: :. . :.:.: :. . :.:.:

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gi|162 ---RQQYRIRVRYASTTNIRLSVN-GSPGTISQNLPSMRLGEDLRYGSAFAIREFNTSIR
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
          :. : . : . . : : : : : : : : : : : : : : : : : : : : : :
gi|162 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAEKEDLEAAKKAVASLF
          90      100     110     120     130

          650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|16240192|gb|AAE79638.1| Sequence 61 from patent US (136 aa)
  initn: 221 init1: 115 opt: 231 Z-score: 275.2 bits: 59.8 E(): 2.1e-06
Smith-Waterman score: 231; 36.620% identity (66.197% similar) in 142 aa overlap
(495-633:1-136)

          470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
          :. : : . : . . : . : : . : . . : . : : . : . . : . : : . : . .
gi|162          PGFIGGALLQRTDHGSLGVLR--VQFPLHL
          10      20

          530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLNVNWGNSSIFSNTVPATATSLDNLQSSDFGY--FESANA
          .....: :.:.: :. . :.:.: :. . :.:.: :. . :.:.: :. . :.:.:
gi|162 ---RQQYRIRVRYASTTNIRLSVN-GSPGTISQNLPSMRLGEDLRYGSAFAIREFNTSIR
          30      40      50      60      70      80

          590      600      610      620      630      640
Cry1Ac FTSSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGL
          :. : . : . . : : ~ : : ~ : : ~ : : ~ : : ~ : : ~ : : ~ :
gi|162 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAEKEDLEAAKKAVASLF
          90      100     110     120     130

          650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|155097590|gb|ABT00521.1| Sequence 10 from patent US (634 aa)
  initn: 140 init1: 140 opt: 239 Z-score: 274.7 bits: 61.9 E(): 2.2e-06
Smith-Waterman score: 260; 22.881% identity (52.373% similar) in 590 aa overlap
(81-637:95-629)

          60      70      80      90      100     110
Cry1Ac LSEFVPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
          : . : . : . : . : . : . : . : . : . : . : . : . : . : . :
gi|155 KVGSLVGKRISELRLSIFPSGSTNLMQDILRETEKFLNQLRNTDLARVNAELTGL---
          70      80      90      100     110     120

          120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
          : . : . : . : : : : . : . : . : . : . : . : . : . : . :
gi|155 -QANVEEFNRQVDNFLNPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ
          130     140     150     160     170     180

          170     180     190     200     210     220
Cry1Ac AANLHLSVLRDVSVFQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQSAFR---GLNT

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gi|155 RFS... 590 600 610 620 630
>>gi|155097610|gb|ABT00541.1| Sequence 50 from patent US (634 aa)
initn: 140 init1: 140 opt: 239 Z-score: 274.7 bits: 61.9 E(): 2.2e-06
Smith-Waterman score: 267; 22.611% identity (53.981% similar) in 628 aa overlap
(45-637:57-629)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGF
gi|155 SQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLKVKVSLGKRLSELRNLIFFSPG
30 40 50 60 70 80
Cry1Ac GPSQWDAFLVQIEQLINQRI--EEFAR-NQAI SRLEGLSNLYQIYAESFREWEADPTNPA
gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGLQANVGEFNRQVDNF----LNPNRNA
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNOFRRELTTLVLDI
gi|155 AATLRTYQHLRNYTRDYSNYCINTYQTAFR--GLNTRLHDTL--EFRTYMFNLNVFEY
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac VSLFPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSRFGSAQIEGSI RSPHLMIDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFYLSLQVNSNYLVNG-
260 270 280 290 300 310

310 320 330 340 350
Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQL
gi|155 --FSGARLSQTFPNIVGLPGTTHALLAARVNYSGGISS----GDIGASPFNQNFNCST
320 330 340 350 360

360 370 380 390 400 410
Cry1Ac GQGVYRTLSSTLYRRPFNIGINNQQ-L-SVLDGTEFAYGTSSNLPsAVYRKSgTVDSLDEI
gi|155 ---FLPPLLTPFVRswLDSGSDRGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

420 430 440 450 460 470
Cry1Ac PPQN-NNVP--PRQGFshRLSHVSMFRSGFSNSSV-SIIRAPMFswIHRSAEFNNIIASD
gi|155 FIRNISGvPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVH
430 440 450 460 470

480 490 500 510 520 530
Cry1Ac SITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNNIQRNGYIEVPIHFPSTSTRY
::: .: .: . . . . . : .: .: . . . . .

gi|155 E-----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRF
480 490 500 510 520
540 550 560 570 580
Cry1Ac R---VRVRYA---SVTP--IHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
gi|155 EQNNTTARYTLRGNNGNPYDLVLRVSSIGNSTIRATINGRVYATATNVTNTTND-GVYDNG
530 540 550 560 570 580
590 600 610 620 630
Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQL
gi|155 ARFSDINIGNVVA---SSNSDVPLD---INVTLNSGTQFDL-----MNIMFVPTNIS
590 600 610 620 630
640 650 660 670 680 690
Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINR
gi|155 PLY

>>gi|21504391|gb|AAM57093.1| Sequence 17 from patent US (136 aa)
initn: 211 init1: 107 opt: 230 Z-score: 274.0 bits: 59.6 E(): 2.4e-06
Smith-Waterman score: 230; 34.507% identity (69.014% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNssGNNIQRNGYIEVPIHF
gi|215 PGFXGGDILR-RTDGGAV--GTIRANVNA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPihLNVNwGNSSIFsNTVPATATSLDNLQSSDFGYFESANAFT
gi|215 PLTQ-QYRIRRLRYASTTSFVNL-FVNNSAAGFTLPSTMAQNGSLTYESFNTLEVHTIR
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac SSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|215 FSQSDITLRLNIFPSISGQEVYVDKLEIVPINPTREAEEDLEDAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQP
>>gi|16240164|gb|AAE79616.1| Sequence 17 from patent US (136 aa)
initn: 211 init1: 107 opt: 230 Z-score: 274.0 bits: 59.6 E(): 2.4e-06
Smith-Waterman score: 230; 34.507% identity (69.014% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNssGNNIQRNGYIEVPIHF
gi|162 PGFXGGDILR-RTDGGAV--GTIRANVNA
10 20

530 540 550 560 570 580

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Cry1Ac PSTSTRYRVRVRYASVTPIH...
gi|162 PLTQ-QYRIRLRYASTTSFV...
30 40 50 60 70 80

Cry1Ac SSLGNIVGVRN-FSGTAG--VI...
gi|162 FSQSDTTLRNLNIFP...
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLV...
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEF--VPGAGFVLGLVDIIWGIF

>>gi|33731234|gb|AAQ37297.1| Sequence 17 from patent US (136 aa)
initn: 211 init1: 107 opt: 230 Z-score: 274.0 bits: 59.6 E(): 2.4e-06
Smith-Waterman score: 230; 34.507% identity (69.014% similar) in 142 aa overlap (495-633:1-136)

Cry1Ac EFNIIASDSTIQIPAVKGNFLNGSVISGPGFTGGDLVRLN...
gi|337 PGFXGGDILR-RTDGGAV---GTIRANVNA
10 20

Cry1Ac PSTSTRYRVRVRYASVTPIH...
gi|337 PLTQ-QYRIRLRYASTTSFV...
30 40 50 60 70 80

Cry1Ac SSLGNIVGVRN-FSGTAG--VI...
gi|337 FSQSDTTLRNLNIFP...
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLV...
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRELTLTVLDI

>>gi|53970017|gb|AAV19110.1| Sequence 17 from patent US (136 aa)
initn: 211 init1: 107 opt: 230 Z-score: 274.0 bits: 59.6 E(): 2.4e-06
Smith-Waterman score: 230; 34.507% identity (69.014% similar) in 142 aa overlap (495-633:1-136)

Cry1Ac EFNIIASDSTIQIPAVKGNFLNGSVISGPGFTGGDLVRLN...
gi|539 PGFXGGDILR-RTDGGAV---GTIRANVNA
10 20

Cry1Ac PSTSTRYRVRVRYASVTPIH...
gi|539 PLTQ-QYRIRLRYASTTSFV...
30 40 50 60 70 80

Cry1Ac SSLGNIVGVRN-FSGTAG--VI...
Cry1Ac GVYR-TLSSTLYRRPFNIGINNQLSV-----LD-GTEF-AYGTSSNLPSAVYRKS...
350 360 370 380 390 400

gi|539 FSQSDTTLRNLNIFP...
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLV...
Cry1Ac KTNVTDYHIDQVSNLV...
650 660 670 680 690 700

>>gi|86161588|gb|ABC86927.1| crystal protein Cry2Ad [Bac (633 aa)
initn: 142 init1: 142 opt: 238 Z-score: 273.5 bits: 61.7 E(): 2.6e-06
Smith-Waterman score: 258; 22.054% identity (53.367% similar) in 594 aa overlap (45-595:56-600)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEF--VPGAGFVLGLVDIIWGIF
gi|861 FQHKSLDTIQKEWMEWKD...
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAI...
gi|861 STNLMEDI...
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIP...
gi|861 VPLSITSSVNTMQQLFLN...
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRELTLTVLDI
gi|861 AATLRTYQNH...
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENF...
gi|861 VSIWS-----L...
260 270 280 290

Cry1Ac TIYTDahrgeyywsgHQIMASPV--GFSGPEF--TFPLYGTM-GNAAPQQRIVAQLQG--
gi|861 -----QDWPFLYSLFQVNSNYVLSGFSGASLFTT...
300 310 320 330 340

Cry1Ac GVYR-TLSSTLYRRPFNIGINNQLSV-----LD-GTEF-AYGTSSNLPSAVYRKS...
gi|861 GITSIGSGPNFNQNCNTIS...
350 360 370 380 390 400

Cry1Ac DSLDEIPPQNNVPPRQGF...
gi|861 RCGAFTPRGN...
410 420 430 440 450

```

          480          490          500          510          520
Cry1Ac SDSITQIPAV--KGNFLF----NGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP--
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|861 GGARAYMVSVHNKNNIYAVHENGTMIHLPEDNTGFTISP IHA TQVNNQTRTFISEKFG
          460          470          480          490          500          510

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          530          540          550          560          570
Cry1Ac -----IHFPESTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|861 NQGDSLRFEQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTNN
          520          530          540          550          560          570

```

```

          580          590          600          610          620          630
Cry1Ac DFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|861 D-GVNDNGARFSDINIGNVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNLPLLY
          580          590          600          610          620          630

```

>>gi|81051716|gb|ABB55273.1| crystal protein Cry2Ad2 [Ba (633 aa)  
 initn: 142 init1: 142 opt: 238 Z-score: 273.5 bits: 61.7 E(): 2.6e-06  
 Smith-Waterman score: 261; 22.054% identity (53.535% similar) in 594 aa overlap  
 (45-595:56-600)

```

          20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGIF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 FQHKSLDTIQEKWMEWKKDNHSLYVDPVIGTVASFLKLGSLIGKRILSELRNLIFFPSG
          30          40          50          60          70          80

```

```

          80          90          100          110          120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 STNLMEDILRETEKFLNQKLNLTDTLSRVNAELTGL---QANVEEFNRQVDNFLNPNRRA
          90          100          110          120          130          140

```

```

          130          140          150          160          170          180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 VPLSITSSVNTMQQLFLNRLSQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNAEEWGIS
          150          160          170          180          190          200

```

```

          190          200          210          220          230          240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 AATLRTYQNHRLRNYTRDYSNYCIDTYQTAFR---GLNTRLHDML--EFRTYMFNLVFEY
          210          220          230          240          250

```

```

          250          260          270          280          290          300
Cry1Ac VSLFPNYDSRITYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSIRSPHLMIDLNSI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 VSIWS-----LFKYQSLLVSSGANLYASGSGPQQTQLFTS-
          260          270          280          290

```

```

          310          320          330          340          350          360
Cry1Ac TIYTDHRGEYYWSGHQIMASPV--FSGPEF--TFPLYGTM-GNAAPQRIVAQLGQ--
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 -----QDWPFYLSLQVNSNYVLVSGFSGASLFTTFPNIGGLPGSTTTQALLAARVNYSG
          300          310          320          330          340

```

```

          370          380          390          400          410
Cry1Ac GVYR-TLSSSTLYRRPFNIGINNQQLSV-----LD-GTEF-AYGTSSNLPsAVYRKSGTV
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 GITSGSIGGSNPNQNFNCNTISPPLSTSFVRSWLDSGSDRQGVNTVTNWTQTESFETTSGL
          350          360          370          380          390          400

```

```

          420          430          440          450          460          470
Cry1Ac DSLDEIPPQNNVPPRQGFSHRLSHVSMFRSFGFSNCSVSIIRAPMFSWIHRSAEFNNIIA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 RCGAFTPRGNSNYYPGY-FIRNISGVSLV---LRNED---LKRPLYNEKRNIESPSTGTP
          410          420          430          440          450

```

```

          480          490          500          510          520
Cry1Ac SDSITQIPAV--KGNFLF----NGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP--
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 GGARAYMVSVHNKNNIYAVHENGTMIHLPEDNTGFTISP IHA TQVNNQTRTFISEKFG
          460          470          480          490          500          510

```

```

          530          540          550          560          570
Cry1Ac -----IHFPESTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSS
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 NQGDSLRFEQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTNN
          520          530          540          550          560          570

```

```

          580          590          600          610          620          630
Cry1Ac DFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAKAVNA
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|810 D-GVNDNGARFSDINIGNVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
          580          590          600          610          620          630

```

>>gi|6457578|gb|AAF09583.1|AF200816\_1 crystal protein [B (633 aa)  
 initn: 142 init1: 142 opt: 238 Z-score: 273.5 bits: 61.7 E(): 2.6e-06  
 Smith-Waterman score: 261; 22.054% identity (53.535% similar) in 594 aa overlap  
 (45-595:56-600)

```

          20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGIF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|645 FQHKSLDTIQEKWMEWKKDNHSLYVDPVIGTVASFLKLGSLIGKRILSELRNLIFFPSG
          30          40          50          60          70          80

```

```

          80          90          100          110          120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|645 STNLMEDILRETEKFLNQKLNLTDTLSRVNAELTGL---QANVEEFNRQVDNFLNPNRRA
          90          100          110          120          130          140

```

```

          130          140          150          160          170          180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|645 VPLSITSSVNTMQQLFLNRLSQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNAEEWGIS
          150          160          170          180          190          200

```

```

          190          200          210          220          230          240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
          : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|645 AATLRTYQNHRLRNYTRDYSNYCIDTYQTAFR---GLNTRLHDML--EFRTYMFNLVFEY
          210          220          230          240          250

```



```

                20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF--VPGAGFVLGLVDIIWGIF
gi|118 FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGSVGLVKRILSELRNLIFFPSG
                30      40      50      60      70      80

                80      90      100     110     120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|118 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
                90      100     110     120     130     140

                130     140     150     160     170     180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|118 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
                150     160     170     180     190     200

                190     200     210     220     230     240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|118 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
                210     220     230     240     250

                250     260     270     280     290     300
Cry1Ac VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILNSI
gi|118 VSIWLFKYQSLIVSSGANL----YASGSGPQQTQSFTAQNWPFLYSLFQVNSNYILSGI
                260     270     280     290     300     310

                310     320     330     340     350     360
Cry1Ac T-----IYTDahrgeyywshqimaspvgfsgpeftfplygtmgnaapqqrivAQLGQG
gi|118 SGTRLSITFPNIGLPGSTTTHSLNSARVNYSGGVSS---GLIGATNLNHNFCNST---
                320     330     340     350     360

                370     380     390     400     410     420
Cry1Ac VYRTLSTLYRRPFNIGINNQLSVDLG--TEFAYGTSSNLPSAVYRKSQTVDSLDEIPP
gi|118 VLPLSTPFPVRSWLDSDGREGVATSTNWQTE-SFQTTLSLRCGAFSARGNSNYFPDYFI
                370     380     390     400     410     420

                420     430     440     450     460     470
Cry1Ac QN-NNVP--PRQGFshrlshvsmfrsgfSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSI
gi|118 RNISGVPLVIRNEDLRLPHYNQIRNIESPSGTPGGARAYLVS-VHNRK--NNIYAANE-
                430     440     450     460     470

                480     490     500     510     520
Cry1Ac TQIPAVKGNFLNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP
gi|118 -----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQDLSLRFEQ
                480     490     500     510     520

                530     540     550     560     570     580
Cry1Ac TSTRYRVRVRYASVT-PIHLNVN-WGNSSIFSNTVPATATSLDNLQSS--DFGYFESANA
gi|118 SNTTARYTLRGNNGSNLYLRVSSIGNSTI-RVTINGRVTYVSNVNTTTNNDGVNDNGAR

```

```

                530     540     550     560     570     580
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
                590     600     610     620     630     640
gi|118 FSDINIGNIVASDNTNVTLDINVTLNSGTPFDLMNIMFVPTNLPPLLY
                590     600     610     620     630

>>gi|155097704|gb|ABT00635.1| Sequence 238 from patent U (634 aa)
  initn: 165 init1: 133 opt: 238 Z-score: 273.5 bits: 61.7 E(): 2.6e-06
Smith-Waterman score: 252; 22.735% identity (53.333% similar) in 585 aa overlap
(45-595:57-601)

                20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF--VPGAGFVLGLVDIIWGIF
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLKKVGSVGLVKRILSELRNLIFFPSG
                30      40      50      60      70      80

                80      90      100     110     120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
                90      100     110     120     130     140

                130     140     150     160     170     180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
                150     160     170     180     190     200

                190     200     210     220     230     240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYQDYLNKYNTRDYSNYCINTYQTAFAK---GLNTRLHDLT---EFRTYMFLNVFEY
                210     220     230     240     250

                250     260     270     280     290     300
Cry1Ac VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILNSI
gi|155 VSIWLFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
                260     270     280     290     300     310

                310     320     330     340     350     360
Cry1Ac T-----IYTDahrgeyywshqimaspvgfsgpeftfplygtmgnaapqqrivAQLGQG
gi|155 SGARLSNTFPNIVGLPGSTTTHALLARVNYSGGISS---GDIGASPPNQNFNCST---
                320     330     340     350     360

                370     380     390     400     410     420
Cry1Ac VYRTLSTLYRRPFNIGINNQLSVDLGTEFAYGTSSNLPSAVYRKSQTVDSLDEIPPQ
gi|155 FLPLSTPFPVRSWLDSDGREGVATVTNWQTESFETTLGLRSGAFARGNSNYFPDYFIR
                370     380     390     400     410     420

                430     440     450     460     470
Cry1Ac N-NNVP--PRQGFshrlshvsmfrsgfSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
gi|155 NISGVPLVVRNEDLRLPHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--

```



```

190      200      210      220      230
Cry1Ac  230      240      250      260      270      280
R--DWIRYNQFRRELTLTVLDDIVSLFPPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RLHDTL---EFRTYMFNLVFEYVSIWLSLFKYQSLLVSSGANL----YASGSGPQQTQSFT
240      250      260      270      280      290

```

```

290      300      310      320      330
Cry1Ac  GSAQGIIEGSIIRSPHMLDILNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SQDWPFlySLFQVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTThALLAARVnYSGGISS-
300      310      320      330      340

```

```

340      350      360      370      380      390
Cry1Ac  PLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  ---GDIGASPPFNQNFNCST---FLPPLLPFVRSWLDsgsdREGVATVnWQTEsFETTL
350      360      370      380      390      400

```

```

400      410      420      430      440      450
Cry1Ac  NLPsAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFShRLshVSMFRSGFSnSSV-SIIRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASpSGTPGGARA
410      420      430      440      450      460

```

```

460      470      480      490      500      510
Cry1Ac  PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNssGNNI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  YMVSVHNRK---NNIHAVHE-----NGSMIHlAPNDYtGFTISPIHATQVNN
470      480      490      500

```

```

520      530      540      550      560
Cry1Ac  QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPiHLNVN-WGNSSIFs--NTVP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  QTRTFISEKfGNQGDsLRFEQNNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRV
510      520      530      540      550      560

```

```

570      580      590      600      610
Cry1Ac  ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNfSGTAGVIIDRFEFIPVTATLEAE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  YTATNVNTTTNND-GVNDNGARFSDINMGNVVSSNSDvPLDINvTLNsgTQFDLMNIML
570      580      590      600      610      620

```

```

620      630      640      650      660      670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
gi|155  VPTNISPIY
630

```

>>gi|155097688|gb|ABT00619.1| Sequence 206 from patent U (634 aa)  
 initn: 167 init1: 133 opt: 238 Z-score: 273.5 bits: 61.7 E(): 2.6e-06  
 Smith-Waterman score: 255; 23.247% identity (52.768% similar) in 542 aa overlap  
 (81-591:95-597)

```

60      70      80      90      100      110
Cry1Ac  LSEFVPGAGFVLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARNQAIrSLEGLSnl
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  KVGSLVgKRILSElKSLIFpSGSTnlMQDILRETEQFLNQRlNTDTLARVNAELTGL---

```

```

70      80      90      100      110      120
Cry1Ac  120      130      140      150      160
YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFVQNYQVPLLSVYVQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -QANVEEFNRQVDNfLNPnRnAVPLSITSSVNTMQQLfLNLRLPQfMQGYQLLLLPLfFAQ
130      140      150      160      170      180

```

```

170      180      190      200      210      220
Cry1Ac  AANLHLsVLrDVsVfGQRWGFDAATINsRYNDLTRLIGNYTDHAvRWYNTGLERVWGPDS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  AANLHLsFIRdVILNADEWGISAAATLrTYRDYlKNYTRDYsNYCINTYQsAFK---GLNT
190      200      210      220      230

```

```

230      240      250      260      270      280
Cry1Ac  R--DWIRYNQFRRELTLTVLDDIVSLFPPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RLHDTL---EFRTYMFNLVFEYVSIWLSLFKYQSLLVSSGANL----YASGSGPQQTQSFT
240      250      260      270      280      290

```

```

290      300      310      320      330
Cry1Ac  GSAQGIIEGSIIRSPHMLDILNSIT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SQDWPFlySLFQVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTThALLAARVnYSGGISS-
300      310      320      330      340

```

```

340      350      360      370      380      390
Cry1Ac  PLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  ---GDIGASPPFNQNFNCST---FLPPLLPFVRSWLDsgsdREGVATVnWQTEsFETTL
350      360      370      380      390      400

```

```

400      410      420      430      440      450
Cry1Ac  NLPsAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFShRLshVSMFRSGFSnSSV-SIIRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASpSGTPGGARA
410      420      430      440      450      460

```

```

460      470      480      490      500      510
Cry1Ac  PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNssGNNI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  YMVSVHNRK---NNIHAVHE-----NGSMIHlAPNDYtGFTISPIHATQVNN
470      480      490      500

```

```

520      530      540      550      560
Cry1Ac  QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPiHLNVN-WGNSSIFs--NTVP
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  QTRTFISEKfGNQGDsLRFEQNNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRV
510      520      530      540      550      560

```

```

570      580      590      600      610
Cry1Ac  ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNfSGTAGVIIDRFEFIPVTATLEAE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  YTATNVNTTTNND-GVNDNGARFSDINMGNVVSSNSDvPLDINvTLNsgTQFDLMNIML
570      580      590      600      610      620

```

```

620      630      640      650      660      670
Cry1Ac  YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

```

gi|155 VPTNISPIY  
630

>>gi|21504398|gb|AAM57098.1| Sequence 27 from patent US (136 aa)  
initn: 216 init1: 126 opt: 229 Z-score: 272.8 bits: 59.4 E(): 2.8e-06  
Smith-Waterman score: 229; 36.879% identity (63.830% similar) in 141 aa overlap  
(496-633:1-136)

```

470      480      490      500      510      520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP
gi|215          GFXGGDVIRRTNTGG----FGAIRVSVTGP
                        10          20

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLLNWNWGNSSI--FSNTVPATATSLDNLQSSDFGYFESANAF
gi|215 LTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNF
          30          40          50          60          70          80

```

```

590      600      610      620      630      640
Cry1Ac TSSLGNI-VGVRNFGSTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|215 TQSQDIIRTXIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVALSF
          90          100         110         120         130

```

```

650      660      670      680      690      700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPE

```

>>gi|53970022|gb|AAV19115.1| Sequence 27 from patent US (136 aa)  
initn: 216 init1: 126 opt: 229 Z-score: 272.8 bits: 59.4 E(): 2.8e-06  
Smith-Waterman score: 229; 36.879% identity (63.830% similar) in 141 aa overlap  
(496-633:1-136)

```

470      480      490      500      510      520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP
gi|539          GFXGGDVIRRTNTGG----FGAIRVSVTGP
                        10          20

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLLNWNWGNSSI--FSNTVPATATSLDNLQSSDFGYFESANAF
gi|539 LTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNF
          30          40          50          60          70          80

```

```

590      600      610      620      630      640
Cry1Ac TSSLGNI-VGVRNFGSTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|539 TQSQDIIRTXIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVALSF
          90          100         110         120         130

```

```

650      660      670      680      690      700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPE

```

>>gi|16240170|gb|AAE79621.1| Sequence 27 from patent US (136 aa)  
initn: 216 init1: 126 opt: 229 Z-score: 272.8 bits: 59.4 E(): 2.8e-06  
Smith-Waterman score: 229; 36.879% identity (63.830% similar) in 141 aa overlap  
(496-633:1-136)

```

470      480      490      500      510      520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP
gi|162          GFXGGDVIRRTNTGG----FGAIRVSVTGP
                        10          20

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLLNWNWGNSSI--FSNTVPATATSLDNLQSSDFGYFESANAF
gi|162 LTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNF
          30          40          50          60          70          80

```

```

590      600      610      620      630      640
Cry1Ac TSSLGNI-VGVRNFGSTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|162 TQSQDIIRTXIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVALSF
          90          100         110         120         130

```

```

650      660      670      680      690      700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPE

```

>>gi|33731239|gb|AAQ37302.1| Sequence 27 from patent US (136 aa)  
initn: 216 init1: 126 opt: 229 Z-score: 272.8 bits: 59.4 E(): 2.8e-06  
Smith-Waterman score: 229; 36.879% identity (63.830% similar) in 141 aa overlap  
(496-633:1-136)

```

470      480      490      500      510      520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFP
gi|337          GFXGGDVIRRTNTGG----FGAIRVSVTGP
                        10          20

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLLNWNWGNSSI--FSNTVPATATSLDNLQSSDFGYFESANAF
gi|337 LTQ-RYRIRFRYASTIDFDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNF
          30          40          50          60          70          80

```

```

590      600      610      620      630      640
Cry1Ac TSSLGNI-VGVRNFGSTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|337 TQSQDIIRTXIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKKAVALSF
          90          100         110         120         130

```

```

650      660      670      680      690      700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPE

```

>>gi|72133015|gb|AAZ66347.1| delta endotoxin [Bacillus t (633 aa)  
initn: 163 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
Smith-Waterman score: 250; 22.432% identity (52.568% similar) in 584 aa overlap  
(45-595:56-600)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLQFLLSEF--VPGAGFVLGLVDIIWGIF
gi|721 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVGLVKRILSELNRLIFPSG
          30          40          50          60          70          80

```



```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|142 FSDINIGNVWASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

```

>>gi|86440155|gb|ABC95996.1| Cry2Ab [Bacillus thuringien (633 aa)  
 initn: 133 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:56-600)

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKGVLGKRIKSELNLIFFPSG
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGLS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 AATLRTYRDYLNKNTYRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIRSPHLMIDLNSI
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLNGF
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac T-----IYTDARHGEYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
      320      330      340      350      360

```

```

      370      380      390      400      410      420
Cry1Ac VYRTLSSITLYRRPFNIGINNQL--SVLDGTEFAYGTSSNLPASAVYRKSQVDSLDEIPPQ
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 FLPPLLTFFVRSWLDSDREGVATVTNQTESFETTLGLRSGAFTVRGNSNYFPDYFIR
      370      380      390      400      410      420

```

```

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 NISGVLPLVRNEDLRRLPHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470

```

```

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQN
      480      490      500      510      520

```

```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|864 FSDINIGNVWASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNLPLLY
      590      600      610      620      630

```

>>gi|11526737|gb|AAG36762.1| Cry2Ab [Bacillus thuringien (633 aa)  
 initn: 133 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 257; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:56-600)

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKGVLGKRIKSELNLIFFPSG
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|115 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|115 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGLS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|115 AATLRTYRDYLNKNTYRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIRSPHLMIDLNSI
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~
gi|115 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLNGF
      260      270      280      290      300      310

```

```

          310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyYwSGHQIMASpVgFSGPEFTfPlyGtMgNAAPQRiVAQLGQG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 SGARLSNTfPnIVGLPGStTThALLAARVnYSGGISS----GDIGASpFNQnFNCST---
          320      330      340      350      360

```

```

          370      380      390      400      410      420
Cry1Ac VYrTLSStLYRRPFnIGInNQQL-SVLDGTEfAYGTSSnLpSAVYRkSGTVDSLDEIPpQ
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 FLpPLLTfPvRswLDSGSDREGvATvTnWQTEsFETTLGLRSGAfTARgNSNYfPDyFIR
          370      380      390      400      410      420

```

```

          430      440      450      460      470
Cry1Ac N-NNVp--PRQGFShRLShVSMFRSGfSNSSV-SIIRAPMfSwIHRSAEfNNIIASDSIT
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 NISGvPLvVRNEDLRRPLHyNEIRNIASpSGTPGGARAYMvS-VHNRK--NNIHAVHE--
          430      440      450      460      470

```

```

          480      490      500      510      520
Cry1Ac QIPAVKGNfLfnGsvIS-GPG-FTGGDLvRLnSSGnNIQRgyIEVP-----IHFP--
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 -----NGSMIHlAPNDyTGfTISPIHATQvNNQTRfISeKfGNQGDsLRFEQN
          480      490      500      510      520

```

```

          530      540      550      560      570      580
Cry1Ac STSTRyRvRVRYASvTPIHLNvN-WGNSSIFs--NTVPATATsLDNLQSSDFGyFESANA
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 NTTARyTLRGNGNSYN-LyLRvSSIGNStIRvTINGRvYtATnVnTTTnND-GVNDNGAR
          530      540      550      560      570      580

```

```

          590      600      610      620      630      640
Cry1Ac FTs-SLGNIVGvRNfSGTAGvIIDRFEPvTATLEAEyNLERAKAVNALFTSTnQLGL
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|115 FSDINIGNvVASSNsDvPLDINvTLnSGTQFDLMnIMLVPTNISPLy
          590      600      610      620      630

```

>>gi|27311151|gb|AAO00679.1| Sequence 18 from patent US (633 aa)  
 initn: 133 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 257; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:56-600)

```

          20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQfLLSEf--VPGAGfVLGLVDIIWGI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 FQHKSLDTVQKEWTEwKkNNHsLYLDPIVGTvASfLLKkVGSvLgKRILsELRNLIffPSG
          30      40      50      60      70      80

```

```

          80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAIrSLREGLsNLyQIYAESfREWEDPTNP---A
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 STNLMQDILRETEKfLNLQRLNTDTLARvNAELTGL---QANVEfENRQVDNfLNPnRNA
          90      100      110      120      130      140

```

```

          130      140      150      160      170      180
Cry1Ac LREEMRIQfNDMNSALtTAIPLFAVQNYQvPLLSvYyQAANLHLsVLRdVSVfGQRWGF
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 VPLsITSSvNTMQQLfLNLRLPQfMQGYQLLLLPLFAQAANLHLsFIRdVILNADeWGI
          150      160      170      180      190      200

```

```

          190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNyTDHAvRWYNTGLERvWGPDSR--DWIRYNQfRRELTTLVLDI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 AATLrTYRDLKnyTRDySNyCINTyQSafK---GLNTRLHdML---EFRTyMfLNVfEY
          210      220      230      240      250

```

```

          250      260      270      280      290      300
Cry1Ac VSLfPNyDSRTyPIrTVsQLTREIyTNPvLENfDGSfRGSaQIEGSIRsPHLMdILNSI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 VSIWslfKYQsLLvSSGANL---YASGSgPQQTQsFTsQDwPFlySLfQvNSvNvLNGf
          260      270      280      290      300      310

```

```

          310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyYwSGHQIMASpVgFSGPEFTfPlyGtMgNAAPQRiVAQLGQG
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 SGARLSNTfPnIVGLPGStTThALLAARVnYSGGISS----GDIGASpFNQnFNCST---
          320      330      340      350      360

```

```

          370      380      390      400      410      420
Cry1Ac VYrTLSStLYRRPFnIGInNQQL-SVLDGTEfAYGTSSnLpSAVYRkSGTVDSLDEIPpQ
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 FLpPLLTfPvRswLDSGSDREGvATvTnWQTEsFETTLGLRSGAfTARgNSNYfPDyFIR
          370      380      390      400      410      420

```

```

          430      440      450      460      470
Cry1Ac N-NNVp--PRQGFShRLShVSMFRSGfSNSSV-SIIRAPMfSwIHRSAEfNNIIASDSIT
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 NISGvPLvVRNEDLRRPLHyNEIRNIASpSGTPGGARAYMvS-VHNRK--NNIHAVHE--
          430      440      450      460      470

```

```

          480      490      500      510      520
Cry1Ac QIPAVKGNfLfnGsvIS-GPG-FTGGDLvRLnSSGnNIQRgyIEVP-----IHFP--
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 -----NGSMIHlAPNDyTGfTISPIHATQvNNQTRfISeKfGNQGDsLRFEQN
          480      490      500      510      520

```

```

          530      540      550      560      570      580
Cry1Ac STSTRyRvRVRYASvTPIHLNvN-WGNSSIFs--NTVPATATsLDNLQSSDFGyFESANA
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 NTTARyTLRGNGNSYN-LyLRvSSIGNStIRvTINGRvYtATnVnTTTnND-GVNDNGAR
          530      540      550      560      570      580

```

```

          590      600      610      620      630      640
Cry1Ac FTs-SLGNIVGvRNfSGTAGvIIDRFEPvTATLEAEyNLERAKAVNALFTSTnQLGL
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|273 FSDINIGNvVASSNsDvPLDINvTLnSGTQFDLMnIMLVPTNISPLy
          590      600      610      620      630

```

>>gi|40312|emb|CAA39075.1| crystal protein CryIIB [Bacil (633 aa)  
 initn: 133 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 257; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:56-600)

```

          20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQfLLSEf--VPGAGfVLGLVDIIWGI
          : . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403 FQHKSLDTVQKEWTEwKkNNHsLYLDPIVGTvASfLLKkVGSvLgKRILsELRNLIffPSG
          30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
gi|403 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|403 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI
gi|403 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHLM DILNSI
gi|403 VSIWLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLSFQVNSNYVLNGF
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywshqimaspvgfsgpeftfplygtmgnaapqqriv aqlgqg
gi|403 SGARLSNTFPNIVLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNCS T---
      320      330      340      350      360

```

```

      370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQQ-L-SVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIP PQ
gi|403 FLPPLLT PPFVRSWLD SGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

```

```

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
gi|403 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470

```

```

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNNGSVIS-GPG-FTGGDLVRLNSSGNNIQRNGYIEVP-----IHFP--
gi|403 -----NGSMIHLAPNDYTGFTTISP I HATQVNNQTRTFISEKFGNQD SLRFEQN
      480      490      500      510      520

```

```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTP IHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|403 NTTARTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTNNND-GVNDNGAR
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFGTAGVIIDRFEPVATLEAEYNLERAQKAVNALFTSTNQLGL
gi|403 FSDINIGNVVASSNSDVP L DINVTLNSGTQFDLMNIMLVPTNISPLY

```

```

      590      600      610      620      630
>>gi|31872007|gb|AAP59457.1| crystal delta-endotoxin Cry (633 aa)
      initn: 133 initl: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 258; 22.603% identity (53.082% similar) in 584 aa overlap
(45-595:56-600)

```

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDI IWGIF
gi|318 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASPFLKVKVSLVGRKILSELRNLI FPSG
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
gi|318 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|318 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI
gi|318 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFNPYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHLM DILNSI
gi|318 VSIWLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLSFQVNSNYVLNGF
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywshqimaspvgfsgpeftfplygtmgnaapqqriv aqlgqg
gi|318 SGARLSNTFPNIVLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNCS T---
      320      330      340      350      360

```

```

      370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQQ-L-SVLDGTEFAYGTSSNLPSAVYRKS GTVDSLDEIP PQ
gi|318 FLPPLLT PPFVRSWLD SGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

```

```

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
gi|318 NISGVPLVVRNEDLRRPLHYNGIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470

```

```

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNNGSVIS-GPG-FTGGDLVRLNSSGNNIQRNGYIEVP-----IHFP--
gi|318 -----NGSMIHLAPNDYTGFTTILPIHATQVNNQTRTFISEKFGNQD SLRFEQN

```

```

          480      490      500      510      520
Cry1Ac  530      540      550      560      570      580
STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
...:..: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|318  NNTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
530      540      550      560      570      580

          590      600      610      620      630      640
Cry1Ac  FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|318  FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590      600      610      620      630

>>gi|27436036|gb|AAO13296.1|AF336115_1 crystal delta-end (633 aa)
  initn: 133 initl: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 256; 22.603% identity (52.740% similar) in 584 aa overlap
(45-595:56-600)

```

```

          20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDI IWGIF
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVKGKRI LSELRNLI FPSG
30      40      50      60      70      80

          80      90      100     110     120
Cry1Ac  GPSQWDAFLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  STNLMQDILRETEKFLNQLRLDITVARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90      100     110     120     130     140

```

```

          130     140     150     160     170     180
Cry1Ac  LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQRWGF
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150     160     170     180     190     200

```

```

          190     200     210     220     230     240
Cry1Ac  AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  AATLRTYRDYLNKNTDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
210     220     230     240     250

```

```

          250     260     270     280     290     300
Cry1Ac  VSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHLMIDLNSI
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260     270     280     290     300     310

```

```

          310     320     330     340     350     360
Cry1Ac  T-----IYTDHAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIV AQLGQG
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  SGARLSNTFFPNIVGLPGSTTTALLAARVNYSSGGISS---GDIGASFPNQNFNCST---
320     330     340     350     360

```

```

          370     380     390     400     410     420
Cry1Ac  VYRTLSSLYRRFPNIGINNQQ-LSVLDGTEFAYGTSSNLP SAVA YRKS GTVDSLDEIPPQ
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  FLPPLLTPFVRSWLDSGSDREGVATVTNWQTESFETTLGLRSGAFTARGISNYFPDYFIR

```

```

          370     380     390     400     410     420
Cry1Ac  N-NNVP--PRQGFSHRLSHVSMFRSFGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430     440     450     460     470

          480     490     500     510     520
Cry1Ac  QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
480     490     500     510     520

```

```

          530     540     550     560     570     580
Cry1Ac  STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  NNTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
530     540     550     560     570     580

          590     600     610     620     630     640
Cry1Ac  FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|274  FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590     600     610     620     630

```

```

>>gi|155097708|gb|ABT00639.1| Sequence 246 from patent U (634 aa)
  initn: 158 initl: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 258; 22.789% identity (52.891% similar) in 588 aa overlap
(45-595:57-601)

```

```

          20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDI IWGIF
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|155  FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLK---VGLVKGKRI LSELRLGLI
30      40      50      60      70      80

```

```

          80      90      100     110     120
Cry1Ac  GPSQWDAFLVQI---EQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|155  FPGSTNLMQDILRETEKFLNQLRLDITLARVNAELTGL---QANVEEFNRQVDNFLNP
90      100     110     120     130

```

```

          130     140     150     160     170     180
Cry1Ac  ---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS VFGQR
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|155  NRNAVPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADE
140     150     160     170     180     190

```

```

          190     200     210     220     230     240
Cry1Ac  WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLT
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|155  WGVSAATLRTYRDYLNKNTDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFLN
200     210     220     230     240     250

```

```

          250     260     270     280     290     300
Cry1Ac  VLDIVLSFPNYSRSTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSI RSPHLMDI
...:..: : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VFEYVSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYV

```

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```

260      270      280      290      300
Cry1Ac 310      320      330      340      350
LNSIT-----IYTDahrGEYYWSGHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQ
gi|155 310      320      330      340      350      360
LNFGSGARLSNTFPNIGLPGSTTTThALLAARVNYSGGISS---GDIGASPFNQFNCS

```

```

360      370      380      390      400      410
Cry1Ac LGQGVYRtLSStLYRRPFNIGINNqQL-SVLDGTEfAYGTSSNLPSAVYRkSGTVDSLDE
gi|155 370      380      390      400      410      420
T---FLPpLLtPFVRSWLDsGSDREGVATVtNWQTEsFETTLGLRSGaFTARGNSNYFPD

```

```

420      430      440      450      460      470
Cry1Ac IPPQn-NNVP--PRQGFShRLSHVSMFRSGfSNSSV-SIIRAPmFSWIHRSAEFNNIIAS
gi|155 430      440      450      460      470
YfIRNIsgVPLVVRNEDLRRpLHYNEIRNIASpSGTpgGARAYMVS-VHNRK--NNIHAV

```

```

480      490      500      510      520
Cry1Ac DSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNnIQNRgyIEVP-----IH
gi|155 480      490      500      510      520
HE-----NGSMIHlAPNDYtGFTIspVhATQvNNQTRtFIseKfGNQGDsLR

```

```

530      540      550      560      570
Cry1Ac FP--STSTRYrVRVRYASVtPIHLNVN-WGNSSIFs--NTVPATATsLDNLQSSDFGYfE
gi|155 530      540      550      560      570      580
FEQNNTtARYtLRGNsYN-LyLRVSSIGnStIRVtInGRVYtATNvTTTnND-GVND

```

```

580      590      600      610      620      630
Cry1Ac SANaFTS-SLGNIVGVRNfSGTAGVIdRFEFIPVtATLEAEYnLERAQkAVNALFTSTN
gi|155 590      600      610      620      630
NGARfSDINIGNVVASSnSDVPLdINvTLNSGTQfDLmNIMLVPTNISPIY

```

>>gi|155097714|gb|ABT00645.1| Sequence 258 from patent U (634 aa)  
 initn: 169 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 264; 23.400% identity (53.016% similar) in 547 aa overlap  
 (81-595:95-601)

```

60      70      80      90      100      110
Cry1Ac LSEfVPGAGfVLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNL
gi|155 70      80      90      100      110      120
KVGSLVgKRILSElRSLIFpSGSTnLMQDILREtEKfLNQRlNTDTLARVNAELGL---

```

```

120      130      140      150      160
Cry1Ac YQIYAESfREWEADPTNPALREEMRIQf---NDMNSALtTAIPLfAVQNYQVPLLSVYV
gi|155 130      140      150      160      170
-QANVEEFNRQVDNfLNpP-RDIVPLsITSSvNTMQQLfLNRLpQfMQYQLLLPLfA

```

```

170      180      190      200      210      220
Cry1Ac QAAHLHsLVLRdVSVfGQRWGFDAATINsRYNDLrLIGNYtDHAVRWYntGLERVWGPd
gi|155 170      180      190      200      210      220
QAAHLHsLFIrDVIlnADEWGIsaATLrTYRDYLkNYTRDYsNYCINTYtQTAfK---GLN

```

```

180      190      200      210      220      230
Cry1Ac 230      240      250      260      270      280
SR--DWIRYnQFRRELtLVLDIVSLfFPNYDSRtYPIrTVSQtLREIYtNPVLEnFDGSf
gi|155 240      250      260      270      280
TRLHDtL---EFrTYMfLNVfEYVSIWSLfkYQsLLVSSGANL---YASGSGPQQtQsF

```

```

290      300      310      320      330
Cry1Ac RGSaQGIeGSIRSPHLMdILNSIT-----IYTDahrGEYYWSGHQIMASpVGFSGPEFT
gi|155 290      300      310      320      330      340
TQQDWfFLYSLfQVNSNYVLNGfSGARLSNTFPNIVGLPGSTTTThALLAARVNYSGGISS

```

```

340      350      360      370      380      390
Cry1Ac FPLYGTMGNAAPQQRIVaQLGQGVYRtLSStLYRRPFNIGINNqQL-SVLDGTEfAYGTs
gi|155 350      360      370      380      390      400
---GDIGASPFNQFNCS---FLPpLLtPFVRSWLDsGSDREGVATVtNWQTEsFETTL

```

```

400      410      420      430      440      450
Cry1Ac SNLPSAVYRkSGTVDSLDEIPPQn-NNVP--PRQGFShRLSHVSMFRSGfSNSSV-SIIR
gi|155 410      420      430      440      450      460
LGLRSGaFTARGNSNYFPDYfIRNIsgVPLVVRNEDLRRpLHYNEIRNIASpSGTpgGAR

```

```

460      470      480      490      500      510
Cry1Ac APmFSWIHRSAEFNNIIASDSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNn
gi|155 470      480      490      500      510
AYMVS-VHNRK--NNIHAVHE-----NGSMIHlAPNDYtGFTIspIHATQvN

```

```

520      530      540      550
Cry1Ac IQNRgyIEVP-----IHFP--STSTRYrVRVRYASVtPIHLNVN-WGNSSIFs--NTV
gi|155 520      530      540      550      560
NQTRtFVSEKfGNQGDsLRFEQNNTtARYtLRGNsYN-LyLRVSSIGnStIRVtInGR

```

```

560      570      580      590      600      610
Cry1Ac PATATsLDNLQSSDFGYfESANaFTS-SLGNIVGVRNfSGTAGVIdRFEFIPVtATLEA
gi|155 570      580      590      600      610      620
VYtATNvNTTnND-GVNDNGARfSDINIGNVVASSnSDVPLdINvTLNSGTQfDLmNIM

```

```

620      630      640      650      660      670
Cry1Ac EYNLERAQkAVNALFTSTnQLGkTnVtDYHIdQVSNLVtYLSDEfCLDEKRELSEKVKH
gi|155 630
LVPTNISPLY

```

>>gi|155097619|gb|ABT00550.1| Sequence 68 from patent US (634 aa)  
 initn: 128 init1: 128 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06  
 Smith-Waterman score: 261; 22.881% identity (52.373% similar) in 590 aa overlap  
 (81-637:95-629)

```

60      70      80      90      100      110
Cry1Ac LSEfVPGAGfVLGLVDIIWGIgFpSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNL
gi|155 60      70      80      90      100      110
KVGSLVgKRILSElRSLIFpSGSTnLMQDILCEtEKfLNQRlNTDTLARVNAELTGL---

```



gi|273 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490 500 510 520

Cry1Ac STSTRYRVRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|273 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|273 FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097664|gb|ABT00595.1| Sequence 158 from patent U (634 aa)
initn: 128 init1: 128 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 257; 22.452% identity (52.866% similar) in 628 aa overlap
(45-637:57-629)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
20 30 40 50 60 70

gi|155 FQHKSLDTVQEEWMEWKDHNHSLYVDPIVGTVASFLLKKGSLVVKRILSELRSILFPFSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQGLRETEKFLNQRLDITLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGFQ
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFQLNRRQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFNLVFEY
210 220 230 240 250

Cry1Ac VSLFPNYSRTPYPIRVSQQLTREIYTNPVLNFDGSRGSAQIEGSIRSPHLMIDILNSI
250 260 270 280 290 300

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLQVNSVYVNLG-
260 270 280 290 300 310

Cry1Ac TIYTDahrgeyy-----WSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQL
310 320 330 340 350

gi|155 --FSGARLSQTFPNIVGLPGTTHALLAARVNYSGGVSS---GDIGASPFNQFSCST
320 330 340 350 360

Cry1Ac QQGVYRTLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSNLPsAVYKSGTVDLSLDEI
360 370 380 390 400 410

gi|155 ---FLPPLLTPFVRSWLDSGSGRGGVNTVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
370 380 390 400 410 420

Cry1Ac PPQN-NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASD
420 430 440 450 460 470

gi|155 FIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGARAYMVS-VHNRK--NNIYAVH
430 440 450 460 470

Cry1Ac SITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNINQNRGYIEVP-----IHF
480 490 500 510 520

gi|155 E-----NGTMIHLAPEDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRF
480 490 500 510 520

Cry1Ac PSTSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESA
530 540 550 560 570 580

gi|155 EQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNG
530 540 550 560 570 580

Cry1Ac NAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQL
590 600 610 620 630

gi|155 ARFSDINIGNVVA---SDNSNVPLD---INVTLNSGTQFDL-----MNIMFVPTNLP
590 600 610 620 630

Cry1Ac GLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRSLDERNLLQDSNFKDINR
640 650 660 670 680 690

gi|155 PLY

>>gi|155097696|gb|ABT00627.1| Sequence 222 from patent U (634 aa)
initn: 158 init1: 133 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 258; 22.789% identity (52.891% similar) in 588 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLG--LVDDIIGWIF
20 30 40 50 60 70

gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLK---VGSILVVKRILSELRLGI
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQI---EQLINQRIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP
80 90 100 110 120

gi|155 FPSGSTNLMQDILRETEKFLNQRLDITLARVNAELTGL---QANVEEFNRQVDNFLNP
90 100 110 120 130

Cry1Ac ---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQR
130 140 150 160 170 180

gi|155 NRNAVPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADE
140 150 160 170 180 190

Cry1Ac WGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTL
190 200 210 220 230 240



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Smith-Waterman score: 257; 22.452% identity (52.866% similar) in 628 aa overlap (45-637:57-629)

Sequence alignment for Cry1Ac vs gi|155. Includes residue numbers (20-70, 80-140, 130-180, 190-240, 250-300, 310-360, 360-420, 420-470, 480-520, 530-580) and amino acid sequences.

Sequence alignment for Cry1Ac vs gi|155097677|gb|ABT00608.1. Includes residue numbers (530-580, 590-630, 640-690, 20-70, 80-140, 130-180, 190-240, 250-300, 310-360, 370-420) and amino acid sequences. Includes a patent reference: >>gi|155097677|gb|ABT00608.1| Sequence 184 from patent U (634 aa).

gi|155 TFTPPLLTPFVRSWLDSDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFI
370 380 390 400 410 420

Cry1Ac QN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSI
420 430 440 450 460 470

gi|155 RNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE-
430 440 450 460 470 480

Cry1Ac TQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP-
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
490 500 510 520

Cry1Ac -STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESAN
530 540 550 560 570 580

gi|155 NNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVTATNVNTTTNND-GVNDNGA
530 540 550 560 570 580

Cry1Ac AFTS-SLGNIVGRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
590 600 610 620 630 640

gi|155 RFSIDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097635|gb|ABT00566.1| Sequence 100 from patent U (634 aa)
initn: 138 initl: 138 opt: 237 Z-score: 272.3 bits: 61.5 E(): 3e-06
Smith-Waterman score: 257; 22.774% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
20 30 40 50 60 70

gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGVKRIKSELNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEKFLNQRNLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNV
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
130 140 150 160 170 180

gi|155 VPLSISMSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYRNYLKNYTRDYSNYCINTYQTAFAK---GLNTRLHDTL--EFRTYMFILNVPEY
210 220 230 240 250

Cry1Ac VSLFPNYSRTPYIRTVSQTREIYTNPVLENFDGSRGSAQIEGSIKIRSPHLMIDLNSI
250 260 270 280 290 300

gi|155 VSIWSLFKQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260 270 280 290 300 310

Cry1Ac T-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTMGNAAPQQRIVaQLGQG
310 320 330 340 350 360

gi|155 SGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGSISS---GDIGASPFPNQFNFCST---
320 330 340 350 360

Cry1Ac VYRTLSTLYRRFPFNIGINNQL-SVLdGTEfAYGTSSNLPSAVYRKSgTVdSLDEIPpQ
370 380 390 400 410 420

gi|155 FLPPLLTPFVRSWLDSDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
490 500 510 520

Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|155 NNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVTATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|155 FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|120431606|gb|ABM21766.1| cry2Ab-type insecticidal c (633 aa)
initn: 133 initl: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 255; 22.603% identity (52.740% similar) in 584 aa overlap
(45-595:56-600)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
20 30 40 50 60 70

gi|120 FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGVKRIKSELNLIFFPSG
30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
80 90 100 110 120

gi|120 STNLMQDILRETERFLNQRNLNTDTVARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
130 140 150 160 170 180

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gi|120 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLDI

gi|120 AATLRTYRDYLKKNYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFRTYMFNLNVFEY
210 220 230 240 250

Cry1Ac 250 260 270 280 290 300
VSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSIIRSPHLMIDLNSI

gi|120 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260 270 280 290 300 310

Cry1Ac 310 320 330 340 350 360
T-----IYTDahrgeyywshghqimaspvgfsgpeftfplygtmgnaapqqrivavqlgqg

gi|120 SGARLSNTFFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac 370 380 390 400 410 420
VYRTLSSTLYRRPFNIGINNQQQL--SVLDGTEFAYGTSNLPASAVYRKSQVDSLDEIPPQ

gi|120 FLPPLLTFFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGISNYFPDYFIR
370 380 390 400 410 420

Cry1Ac 430 440 450 460 470
N--NNVP--PRQGFshrlshvsmfrsgfnsSV--SIIRAPMFSWIHRSAEFNIIASDSIT

gi|120 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS--VHNrk--NNIHAVHE--
430 440 450 460 470

Cry1Ac 480 490 500 510 520
QIPAVKGNFLFNGSVIS--GPG--FTGGDLVRLNSSGNNIQRNGYIEVP-----IHFP--

gi|120 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQEN
480 490 500 510 520

Cry1Ac 530 540 550 560 570 580
STSTRYRVRVRYASVTPIHNLVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

gi|120 NTTARYTLRGNGNSYN--LYLRVSSIGNSTIRVTINGRVYATNVNTTNNND--GVNDNGAR
530 540 550 560 570 580

Cry1Ac 590 600 610 620 630 640
FTS--SLGNIVGVRNFGSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|120 FSDINIGNVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|155097641|gb|ABT00572.1| Sequence 112 from patent U (634 aa)
initn: 133 init1: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 258; 23.443% identity (52.381% similar) in 546 aa overlap
(81-595:95-601)

Cry1Ac 60 70 80 90 100 110
LSEFVPGAGFVLGLVDIIWGFQWDAFLVQIEQLINQRIEEFARNQAIISRLBGLSNL

gi|155 KVGSLVgkRILSELRSIFPsgSTNLMQDILRETEKFLNQRlNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac 120 130 140 150 160
YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ

gi|155 -QANVEEFNRQVDNPLNPNRrNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLLPLFAQ
130 140 150 160 170 180

Cry1Ac 170 180 190 200 210 220
AANLHLSVLRDVSVFQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS

gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRDYLKKNYTRDYSNYCINTYQTAFK---GLNT
190 200 210 220 230

Cry1Ac 230 240 250 260 270 280
R--DWIRYNQFRELTLTVLDIVSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDGSR

gi|155 RLHDTL---EFRTYMFNLNVFEYVSIWLSFKYQSLLVSSGANL----YACGSGPQQTQSFT
240 250 260 270 280 290

Cry1Ac 290 300 310 320 330
GSAQIEGSIIRSPHLMIDLNSIT-----IYTDahrgeyywshghqimaspvgfsgpeftf

gi|155 SQDWPFLYSLFQVNSNYVLNGFSGARLSNTFFPNIVGLPGSTTHALLAARVNYSGGISS-
300 310 320 330 340

Cry1Ac 340 350 360 370 380 390
PLYGTMGNAAPQQRIVAVQLGQGVYRTLSSTLYRRPFNIGINNQQQL--SVLDGTEFAYGTSS

gi|155 ---GDIGASPFNQNFNCST---FLPPLLTFFVRSWLDGSDREGVATVTNWQTESFETTL
350 360 370 380 390 400

Cry1Ac 400 410 420 430 440 450
NLPASAVYRKSQVDSLDEIPPQN--NNVP--PRQGFshrlshvsmfrsgfnsSV--SIIRA

gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPSGARA
410 420 430 440 450 460

Cry1Ac 460 470 480 490 500 510
PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS--GPG--FTGGDLVRLNSSGNNI

gi|155 YMVVS--VHNrk--NNIHAVHE-----NGSMIHLAPNDYTGFTISPIHATQVNN
470 480 490 500

Cry1Ac 520 530 540 550 560
QNRNGYIEVP-----IHFP--STSTRYRVRVRYASVTPIHNLVN--WGNSSIFS--NTVP

gi|155 QTRTFISEKFGNQGDSLRFQENNTTARYTLRGNGNSYN--LYLRVSSIGNSTIRVTINGRV
510 520 530 540 550 560

Cry1Ac 570 580 590 600 610
ATATSLDNLQSSDFGYFESANAFTS--SLGNIVGVRNFGSGTAGVIIDRFEFIPVTATLEAE

gi|155 YTATNVNTTNNND--GVNDNGARFSDINIGNVASSNSDVPLDINVTLNSGTQFDLMNIML
570 580 590 600 610 620

620 630 640 650 660 670

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Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

gi|155 VPTNISPLY
630

>>gi|155097712|gb|ABT00643.1| Sequence 254 from patent U (634 aa)
initn: 165 initl: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 250; 23.218% identity (53.016% similar) in 547 aa overlap
(81-595:95-601)

Cry1Ac LSEFVPGAGFVGLVDIIWGIIFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISREGLSNL
gi|155 KVGSLVGRKILSELRLIFPSGSTNMQDILRETEKFLNQLRNTDTLARVNAELTGL---

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQ

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYQDYLNKYNTRDYSNYCINTYQTAFAK---GLNT

Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFR
gi|155 RLHDTL---EFRTYMLNVEFYVSIWLSFKYQSLVSSGANL----YASGSGPQQTQSFT

Cry1Ac GSAQGIIEGSIRSPHLMILNSIT-----IYTAHRGEYYWSGHQIMASPVGFSGPEFTF
gi|155 SQDWPFLYSLFQVNSNYVLNPFSGARLSNTFFNIVGLPGSTTTTHALLAARVNYSGGISS-

Cry1Ac PLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSS
gi|155 ---GDIGASPFNQFNFCST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTL

Cry1Ac NLPNAVYRKSQVDSLDEIPPNQ--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRA
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIAASPGTGGARA

Cry1Ac PMFSWIHRSAEFNIIASDSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNNI
gi|155 YMVS-VHNRK--NNIHAVE-----NGSMIHLAPNDYTGFTIGPIHATQVNN

Cry1Ac 520 530 540 550

Cry1Ac QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPHILNVN-WGNSSI---FSNTV
gi|155 QTRTFISEKFGNQDGLRFEQNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRV

Cry1Ac PATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFGTAGVIIDRFEFIPVTATLEA
gi|155 YA-ATNVNVTNTNND-GVNDNGARFSDINIGNVVASSNSDVPLDINVTLSGTFDLNMIM

Cry1Ac EYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKH
gi|155 LVPTNISPLY
630

>>gi|155097699|gb|ABT00630.1| Sequence 228 from patent U (634 aa)
initn: 132 initl: 132 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 263; 22.470% identity (53.345% similar) in 583 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTLQFLLSEF--VPGAGFVGLVDIIWGI
gi|155 FQHKSLDSVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGVSGLVKRILSELRLIFPSG

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAIISREGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFRMQGYQLLLLPLFAQAANMHLSFIRDVVLNADEWGIS

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYN-QFRRELTLTVLDIV
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTR--LRDTLEFRTYMLNVEFYV

Cry1Ac SLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGFSFRGSAQGIIEGS---IRSPHLMILN
gi|155 SIWLSFKYQSLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNHVNLNPF

Cry1Ac SITI---YTAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGV
gi|155 GARLSNTFFNIGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQFNFCST---F

Cry1Ac 370 380 390 400 410 420

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Cry1Ac YRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGTSSNLP...
gi|155 LPPLLPFVRSWLD...
370 380 390 400 410 420

Cry1Ac -NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRS...
gi|155 ISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE---

Cry1Ac IPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--S
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNN

Cry1Ac TSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NIVPATATSLDNLQSSDFGYFESANAF
gi|155 TTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTNN-D-GVNDNGARF

Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLK
gi|155 SDINMGNVAVSSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPIY

>>gi|155097636|gb|ABT00567.1| Sequence 102 from patent U (634 aa)
initn: 133 initl: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 251; 22.810% identity (52.555% similar) in 548 aa overlap
(81-595:95-601)

Cry1Ac LSEFVPGAGFVGLVDIIWGFIPGPSQWDAFLVQIEQLINQRIIEEFARNQAI...
gi|155 KVGSLVQKRIKSELRLIFPSGSTNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---

Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALT...
gi|155 -QANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQ

Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYQDYLNKYNTRDYSNYCINTYQATAFK---GLNT

Cry1Ac R--DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNF...
gi|155 RLHDTL---EFRTYMLNVFEYVSIWLSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDW

290 300 310 320 330

Cry1Ac -----FRGSAQIEGSIRSPHLMIDLNSITIYTD...
gi|155 PFLYLSLFQVNSNYVHLHGFSGARLSNTFPNIVGLPGST-----TTHALLAARVNSYSGGIS

Cry1Ac TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQL-SVLDGTEFAYGT
gi|155 S----GDIGASPFNQNFNCST---FLPPLLTPFVRSWLD...
350 360 370 380 390 400

Cry1Ac SSNLP...
gi|155 TLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGA

Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGN
gi|155 RAYMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTISPIHATQV

Cry1Ac NIQNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NT
gi|155 NNQTRTFISEKFGNQGDSLRFEQNNTTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTING

Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEPFIPVTATLE
gi|155 RVYTATNVNTTNN-D-GVNDNGARFSDINIGNVAVSSNSDVPLDINVTLSNGTQFDLMNI

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
gi|155 MLVPTNISPLY

>>gi|155097649|gb|ABT00580.1| Sequence 128 from patent U (634 aa)
initn: 132 initl: 132 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06
Smith-Waterman score: 263; 22.470% identity (53.345% similar) in 583 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVGLVDIIWGFIP
gi|155 FQHKSLDSVQREWEWKNNHSLYLDPIVGTVASFLLKKGSLVQKRIKSELRLIFPSG

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAI...
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA

130 140 150 160 170 180

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Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFRMQGYQLLLLPLFAQAANMHLFSIRDVVLNADEWGIS
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYN-QFRRELTLTVLDIV
gi|155 AATLRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNTR--LRDTLEFRTYMFNLNVFEYV
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac SLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGS---IRSPHMLDILN
gi|155 SIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFDWPFYLSLQVNSNHVNLGFS
260 270 280 290 300 310

310 320 330 340 350 360
Cry1Ac SITI---YTDahrgeyywsgHQIMASpVGFSGPEFTFPLyGTMGNAAPQRIVAQLGQGV
gi|155 GARLSNTFPNIGGLPGSTTTHALLAARVNYSGGISS---GDIGASPFNFQNCST---F
320 330 340 350 360

370 380 390 400 410 420
Cry1Ac YRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPO
gi|155 LPPLLTTPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
370 380 390 400 410 420

430 440 450 460 470
Cry1Ac -NNVP--PRQGFshrlshvsmfrsGfSnsSV-SIIRAPMFSWIHRSAEFNIIASDSITQ
gi|155 ISGVLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE---
430 440 450 460 470 480

480 490 500 510 520
Cry1Ac IPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP--S
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNN
490 500 510 520 530

530 540 550 560 570 580
Cry1Ac TSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAF
gi|155 TTARVTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGARF
540 550 560 570 580

590 600 610 620 630 640
Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQAVNALFTSTNQLGLK
gi|155 SDINMGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPIY
590 600 610 620 630

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>>gi|155097679|gb|ABT00610.1| Sequence 188 from patent U (634 aa)  
 initn: 133 init1: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06  
 Smith-Waterman score: 254; 22.774% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

20 30 40 50 60 70

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Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF--VPGAGFVLGLVDIIWGF
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVLGKRILSELNLIFFPSG
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL----QANVEEFNRQVDNFLNPRNA
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFRMQGYQLLLLPLFAQAANMHLFSIRDVVLNADEWGIS
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
gi|155 AATLRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLNVFEY
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRFGSAQIEGSIRSPHMLDILNSI
gi|155 VSIWSLFKYQSLLVSSGANL---YASGSGVTNTQSFTSODWPFYLSLQVNSNYVNLGFI
260 270 280 290 300 310

310 320 330 340 350 360
Cry1Ac T-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPLyGTMGNAAPQRIVAQLGQGV
gi|155 SGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGISS---GDIGASPFNFQNCST---
320 330 340 350 360

370 380 390 400 410 420
Cry1Ac VYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPO
gi|155 FLPPLLTTPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
370 380 390 400 410 420

430 440 450 460 470
Cry1Ac N-NNVP--PRQGFshrlshvsmfrsGfSnsSV-SIIRAPMFSWIHRSAEFNIIASDSIT
gi|155 NISGVLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

480 490 500 510 520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP--
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNN
490 500 510 520

530 540 550 560 570 580
Cry1Ac TSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NTTARVTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

```

```

          590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . .
gi|155 FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
          590      600      610      620      630

```

>>gi|155097629|gb|ABT00560.1| Sequence 88 from patent US (634 aa)  
 initn: 133 init1: 133 opt: 236 Z-score: 271.1 bits: 61.3 E(): 3.5e-06  
 Smith-Waterman score: 256; 23.260% identity (52.564% similar) in 546 aa overlap  
 (81-595:95-601)

```

          60      70      80      90      100     110
Cry1Ac LSEFVPGAGFVGLVDIIWGFGPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNL
      . . . . .
gi|155 KVGSLVGRKILSELRSILFPGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
          70      80      90      100     110     120

```

```

          120     130     140     150     160
Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      . . . . .
gi|155 -QANVEEFNRQVDNFLNPNRRAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQ
          130     140     150     160     170     180

```

```

          170     180     190     200     210     220
Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDS
      . . . . .
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTRYDYLNRNYTRDYSNYCINTYQTAFAK---GLNT
          190     200     210     220     230

```

```

          230     240     250     260     270     280
Cry1Ac R--DWIRYNQFRRELTTLVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNVLENFDGFSR
      . . . . .
gi|155 RLHDTL---EFRTYMFLNVFEYVSIWSLFKYQLLVSSGANL---YASGSGPQQTQSFT
          240     250     260     270     280     290

```

```

          290     300     310     320     330
Cry1Ac GSAQGIIEGSIRSPHLMILNSIT-----IYTDahrgeyywsgHqImAsPvGfSGPeFTF
      . . . . .
gi|155 SQDWPFLYSLFQVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGISS-
          300     310     320     330     340

```

```

          340     350     360     370     380     390
Cry1Ac PLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSS
      . . . . .
gi|155 ---GDIGASPPNFQNCST---FLPPLLTFFVRSNLDGSDREGVATVNWQTESFETTL
          350     360     370     380     390     400

```

```

          400     410     420     430     440     450
Cry1Ac NLPsAVYRKSGTVDSLDEIPPQN-NNVP--PRQGFShRLSHVSMFRSGFSNSSV-SIIra
      . . . . .
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARA
          410     420     430     440     450     460

```

```

          460     470     480     490     500     510
Cry1Ac PMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSvis-GPG-FTGDVLRLNssGNNI
      . . . . .
gi|155 YMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTISPIHATQVNN
          470     480     490     500

```

```

          520      530      540      550      560
Cry1Ac QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPIHNLNVN-WGNSSIFS--NTVP
      . . . . .
gi|155 QTRTFISEKFGNGQDLSLRFEQNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTTINGRV
          510     520     530     540     550     560

```

```

          570     580     590     600     610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAE
      . . . . .
gi|155 YTATNVNTTTNND-GVNDNGARFSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIML
          570     580     590     600     610     620

```

```

          620     630     640     650     660     670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
      . . . . .
gi|155 VPTNISPLY
          630

```

>>gi|116248655|gb|ABJ90464.1| Cry2Ad [Bacillus thuringie (432 aa)  
 initn: 137 init1: 137 opt: 233 Z-score: 270.1 bits: 60.5 E(): 4e-06  
 Smith-Waterman score: 233; 25.217% identity (60.435% similar) in 230 aa overlap  
 (45-267:56-275)

```

          20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVGLVDIIWGF
      . . . . .
gi|116 FQHKSLDTIQKEWMEWKDnHSLYVDPIVGTVASFLKLGSLIGKRILSELRLNLFPSG
          30      40      50      60      70      80

```

```

          80      90      100     110     120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLBGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|116 STNLMEDILRETEKFLNQLNNTDTLSRVNAELTGL---QANVEEFNRQVDNFLNPNRRA
          90      100     110     120     130     140

```

```

          130     140     150     160     170     180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF
      . . . . .
gi|116 VPLSITSSVNTMQQLFLNRLSQFMQGYQLLLPLFAQAANLHLSFIRDVILNAVEWGIS
          150     160     170     180     190     200

```

```

          190     200     210     220     230     240
Cry1Ac AATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      . . . . .
gi|116 AATLRTYQHNLNRNYTRDYSNYCIDTYQTAFR---GLNTRLHML---EFRTYMFLNVFEY
          210     220     230     240     250

```

```

          250     260     270     280     290     300
Cry1Ac VSLFPPNYDSRTYPIRTVSQTLTREIYTNVLENFDGFSRGSQAQGIIEGSIRSPHLMILNSI
      . . . . .
gi|116 VSIWSLFKYQLLVSSGANLYASGSGPQQTQLFTSQDWPFLYSLFQVNSNYVLSGFSGAS
          260     270     280     290     300     310

```

>>gi|155718051|gb|ABU37567.1| Sequence 4 from patent US (632 aa)  
 initn: 140 init1: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:56-599)

```

          20      30      40      50      60      70

```

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Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF  
 ..... : : : : :  
 gi|155 FQHKSLDTIQEEWMEWKKDNHSLYVDPVIGTVASFLLKKVGLVKRILSELRNLIFFPSG  
 30 40 50 60 70 80

80 90 100 110 120  
 Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A  
 ..... : : : : :  
 gi|155 STNLMQDILRETEKFLNQLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA  
 90 100 110 120 130 140

130 140 150 160 170 180  
 Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF  
 ..... : : : : :  
 gi|155 VPLSITSSVNTMQQLFLNRLTQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS  
 150 160 170 180 190 200

190 200 210 220 230 240  
 Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI  
 ..... : : : : :  
 gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVPEY  
 210 220 230 240 250

250 260 270 280 290 300  
 Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHMLDILNSI  
 ..... : : : : :  
 gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYSLFQVNSNYVNLNGF  
 260 270 280 290 300 310

310 320 330 340 350 360  
 Cry1Ac TI--YDAHRGEYYWSG---HQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG  
 ..... : : : : :  
 gi|155 SGARLTQTFFPNIVGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLTP  
 320 330 340 350 360 370

370 380 390 400 410 420  
 Cry1Ac VYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQN  
 ..... : : : : :  
 gi|155 FVRSWLDSSGDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN  
 380 390 400 410 420

430 440 450 460 470  
 Cry1Ac -NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQ  
 ..... : : : : :  
 gi|155 ISGVLVVRNEDLRRPLHYNQIRNIESPSGTPGGGLRAYMVS-VHNRR--NNIYAVHE---  
 430 440 450 460 470

480 490 500 510 520  
 Cry1Ac IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHPFSTS  
 ..... : : : : :  
 gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDLSRFEQSN  
 480 490 500 510 520

530 540 550 560 570 580  
 Cry1Ac TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT  
 ..... : : : : :  
 gi|155 TTARYTLRGNNGSNYLYLVRVSSIGNSTIRVTINGRVYASNVNTTTNND-GVNDNGARFS  
 530 540 550 560 570 580

590 600 610 620 630 640  
 Cry1Ac S-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKT  
 ..... :  
 gi|155 DINIGNVVASDNTNVPLDINVTLSNGTQFELMNMIFVPTNISPLY  
 590 600 610 620 630

>>gi|155097586|gb|ABT00517.1| Sequence 2 from patent US (632 aa)  
 initn: 140 initl: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:56-599)

20 30 40 50 60 70  
 Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF  
 ..... : : : : :  
 gi|155 FQHKSLDTIQEEWMEWKKDNHSLYVDPVIGTVASFLLKKVGLVKRILSELRNLIFFPSG  
 30 40 50 60 70 80

80 90 100 110 120  
 Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A  
 ..... : : : : :  
 gi|155 STNLMQDILRETEKFLNQLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA  
 90 100 110 120 130 140

130 140 150 160 170 180  
 Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF  
 ..... : : : : :  
 gi|155 VPLSITSSVNTMQQLFLNRLTQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS  
 150 160 170 180 190 200

190 200 210 220 230 240  
 Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI  
 ..... : : : : :  
 gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMFLNVPEY  
 210 220 230 240 250

250 260 270 280 290 300  
 Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHMLDILNSI  
 ..... : : : : :  
 gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYSLFQVNSNYVNLNGF  
 260 270 280 290 300 310

310 320 330 340 350 360  
 Cry1Ac TI--YDAHRGEYYWSG---HQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG  
 ..... : : : : :  
 gi|155 SGARLTQTFFPNIVGLPGTTTTHALLAARVNYSGGVSSGDIGAVFNQNFSCSTFLPPLLTP  
 320 330 340 350 360 370

370 380 390 400 410 420  
 Cry1Ac VYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQN  
 ..... : : : : :  
 gi|155 FVRSWLDSSGDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN  
 380 390 400 410 420

430 440 450 460 470  
 Cry1Ac -NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQ  
 ..... : : : : :  
 gi|155 ISGVLVVRNEDLRRPLHYNQIRNIESPSGTPGGGLRAYMVS-VHNRR--NNIYAVHE---  
 430 440 450 460 470

480 490 500 510 520  
 Cry1Ac IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHPFSTS  
 ..... : : : : :  
 gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDLSRFEQSN  
 480 490 500 510 520

530 540 550 560 570 580  
 Cry1Ac TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT  
 ..... : : : : :  
 gi|155 TTARYTLRGNNGSNYLYLVRVSSIGNSTIRVTINGRVYASNVNTTTNND-GVNDNGARFS  
 530 540 550 560 570 580

```

480      490      500      510      520
Cry1Ac  IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPPSTS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|155  -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSN
      480      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac  TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|155  TTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTND-GVNDNGARFS
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac  S-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|155  DINIGNVVASDNTNVPLDINVTLNSGTQFELMNIMFVPTNLPPLY
      590      600      610      620      630

```

>>gi|23559626|emb|CAD52948.1| unnamed protein product [B (632 aa)  
 initn: 140 init1: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:56-599)

```

20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  FQHKSLDTIQEEMWKKDNHSLYVDPIVGTVASFLLKKGSLVGVKRISELNLIFFPSG
      30      40      50      60      70      80

```

```

80      90      100     110     120
Cry1Ac  GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|235  STNLMQDILRETEKFLNQRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRRA
      90      100     110     120     130     140

```

```

130     140     150     160     170     180
Cry1Ac  LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  VPLSITSSVNTMQQLFLNRLTQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150     160     170     180     190     200

```

```

190     200     210     220     230     240
Cry1Ac  AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|235  AATLRTYQNHLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMLNVFEY
      210     220     230     240     250

```

```

250     260     270     280     290     300
Cry1Ac  VSLFPNYSRTPYPIRTVSQLTREIYTNVPLENFDGSRGSAQGIIEGSIKRSPLHMDILNSI
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|235  VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLSFQVNSNYVLNGF
      260     270     280     290     300     310

```

```

310     320     330     340     350     360
Cry1Ac  TI--YTDARHGEYWSG---HQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQQLGQG
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  SGARLTQTFFPNIVGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLTP
      320     330     340     350     360     370

```

```

370      380      390      400      410      420
Cry1Ac  VYRTLSSSTLYRRPFNIGINNQQSLVDGTEFAYGTSSNLPASAVYRKSSTVSDSLDEIPPQN
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  FVRSWLDSDGSDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
      380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac  -NNVP--PRQGFHRLSHVSMFPRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSITQ
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|235  ISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVS-VHNRK--NNIYAVHE---
      430      440      450      460      470

```

```

480      490      500      510      520
Cry1Ac  IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPPSTS
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSN
      480      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac  TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|235  TTARYTLRGNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTND-GVNDNGARFS
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac  S-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|235  DINIGNVVASDNTNVPLDINVTLNSGTQFELMNIMFVPTNISPLY
      590      600      610      620      630

```

>>gi|158478174|gb|ABW49931.1| Sequence 4 from patent US (632 aa)  
 initn: 140 init1: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:56-599)

```

20      30      40      50      60      70
Cry1Ac  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|158  FQHKSLDTIQEEMWKKDNHSLYVDPIVGTVASFLLKKGSLVGVKRISELNLIFFPSG
      30      40      50      60      70      80

```

```

80      90      100     110     120
Cry1Ac  GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|158  STNLMQDILRETEKFLNQRLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRRA
      90      100     110     120     130     140

```

```

130     140     150     160     170     180
Cry1Ac  LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRWGF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|158  VPLSITSSVNTMQQLFLNRLTQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150     160     170     180     190     200

```

```

190     200     210     220     230     240
Cry1Ac  AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      : : : : : . . . . . : : : : : . . . . . : : : : : . . . . . :
gi|158  AATLRTYQNHLRNYTRDYSNYCINTYQTAFR---GLNTRLHDML---EFRTYMLNVFEY
      210     220     230     240     250

```

```

250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLHMDILNSI
gi|158 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260      270      280      290      300      310

```

```

310      320      330      340      350      360
Cry1Ac TI--YTDHRGEYYWSG----HQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQLGQG
gi|158 SGARLTQTTFPNIVGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLTP
320      330      340      350      360      370

```

```

370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQN
gi|158 FVRSWLDGSDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac -NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQ
gi|158 ISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVS-VHNKR--NNIYAVHE---
430      440      450      460      470

```

```

480      490      500      510      520
Cry1Ac IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHPFSTS
gi|158 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSN
480      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
gi|158 TTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTND-GVNDNGARFS
530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac S-SLGNIVGVRNFGSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKT
gi|158 DINIGNVVASDNTNVPLDINVTLNSGTQFELMNMIFVPTNISPLY
590      600      610      620      630

```

>>gi|155097604|gb|ABT00535.1| Sequence 38 from patent US (633 aa)  
 initn: 140 initl: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:57-600)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPAGFVLGLVDIIGWIF
gi|155 FQHKSLDTIQEEWMEWKDNDHSLYVDPVIGTVASFLLKVKVSLVSKRILSELNLIFFPSG
30      40      50      60      70      80

```

```

80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFQGRWGFD
gi|155 VPLSITSSVNTMQQLFLNRLTQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYQNHLRNYTRDYSNYCINTYQTAFR---GLNTRLHDM---EFRTYMLNLFVFEY
210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIIEGSIKRSPLHMDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260      270      280      290      300      310

```

```

310      320      330      340      350      360
Cry1Ac TI--YTDHRGEYYWSG----HQIMASPVGFSGPEFTFPFLYGTMGNAAPQQRIVAQLGQG
gi|155 SGARLTQTTFPNIVGLPGTTTTHALLAARVNYSGVSSGDIGAVFNQNFSCSTFLPPLLTP
320      330      340      350      360      370

```

```

370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQQLSVLDGTEFAYGTSSNLPASAVYRKSQGTVDLDEIPPQN
gi|155 FVRSWLDGSDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac -NNVP--PRQGFSHRSLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSITQ
gi|155 ISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVS-VHNKR--NNIYAVHE---
430      440      450      460      470

```

```

480      490      500      510      520
Cry1Ac IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHPFSTS
gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQSN
480      490      500      510      520

```

>>gi|155097601|gb|ABT00532.1| Sequence 32 from patent US (633 aa)  
 initn: 140 initl: 140 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.509% identity (53.265% similar) in 582 aa overlap  
 (45-595:57-600)

```

530      540      550      560      570      580
Cry1Ac TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
gi|155 TTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYTASNVTNTTND-GVNDNGARFS
530      540      550      560      570      580

```

```

590      600      610      620      630
Cry1Ac S-SLGNIVGVRNFGSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKT
gi|155 DINIGNVVASDNTNVPLDINVTLNSGTQFELMNMIFVPTNISPLY
590      600      610      620      630

```

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```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . .
gi|155 FQHKSLDTIQEEWMEWKDNHSLYVDPVIGTVASFLKKGVLGKRIKSELRNLIFFPSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|155 VPLSITSSVNTMQQLFLNRLTQFQMGGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . .
gi|155 AATLRTYQNHRLRNYTRDYSNYCINTYQTAFR---GLNTRLHDM---EFRTYMFLNVFEY
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHMLDILNSI
      . . . . .
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac TI--YTDahrgeyywsg---HQIMASpVgFSGPEFTFPlyGTMGNAAPQRIVAQLGQG
      . . . . .
gi|155 SGARLTQTFPNIVGLPGSTTHALLAARVNYSGGVSSGDIGAVNFQNFSCSTFLPPLLTP
      320      330      340      350      360      370

      370      380      390      400      410      420
Cry1Ac VYRTLSSSTLYRRPFNIGINNQLSVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQN
      . . . . .
gi|155 FVRSWLDGSGDRG---GIN---TVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
      380      390      400      410      420

      430      440      450      460      470
Cry1Ac -NNVP--PRQGFshrlshvsmfRsgfSNSSV-SIIRAPMfSWIHRSAEFNNIASDSITQ
      . . . . .
gi|155 ISGVLVVRNEDLRRPLHYNQIRNIESPSGTPGGLRAYMVS-VHNRK--NNIYAVHE---
      430      440      450      460      470

      480      490      500      510      520
Cry1Ac IPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPST
      . . . . .
gi|155 -----NGTMIHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDLSLRFQNS
      480      490      500      510      520

      530      540      550      560      570      580
Cry1Ac TRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFT
      . . . . .
gi|155 TTARYTLRGNMNSYNLYLRVSSIGNSTIRVTINGRVYTAASNVTNTTND-GVNDNGARFS
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac S-SLGNIVGVRNFGSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKT
      . . . . .
gi|155 DINIGNVVASDNTNVPLDINVTLNSGTQFELMNMIFVPTNLPLLY
      590      600      610      620      630

```

```

>>gi|33316454|gb|AAQ04609.1|AF441855_1 Cry2Ab [Bacillus (633 aa)
  initn: 133 initl: 133 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 255; 22.26% identity (53.596% similar) in 584 aa overlap
(45-595:56-600)

```

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . .
gi|333 FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKGVLGKRIKSELRNLIFFPSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRI--EEFAR-NQAIISRLLEGLSNLYQIYAESFREWEADPTNPA
      . . . . .
gi|333 STNLMQDILRETEKFLNQLRNTDTTLARVNAELTELQANVEEFNRQVDNF----LNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|333 VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . .
gi|333 AATLRTYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLHDM---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIKSPHMLDILNSI
      . . . . .
gi|333 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF
      260      270      280      290      300      310

```

```

      310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTFPlyGTMGNAAPQRIVAQLGQG
      . . . . .
gi|333 SGARLNTFPNIVGLPGSTTHALLAARVNYSGGSISS---GDIGASPNQNFNCST---
      320      330      340      350      360

```

```

      370      380      390      400      410      420
Cry1Ac VYRTLSSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQN
      . . . . .
gi|333 FLPPLLPFVRSWLDGSGDREGVATVTNWNQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

```

```

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFshrlshvsmfRsgfSNSSV-SIIRAPMfSWIHRSAEFNNIASDSIT
      . . . . .
gi|333 NISGVLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470

```

```

      480      490      500      510      520
Cry1Ac QIPAVKGNFLFNQSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
      :::::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::
gi|333 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
      480      490      500      510      520

```

```

      530      540      550      560      570      580
Cry1Ac STSTRYRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      :::::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::  ::  :::
gi|333 NITARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|333 FSDINIGNVWASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

```

>>gi|12822556|gb|AAE48997.1| Sequence 10 from patent US (633 aa)  
 initn: 139 init1: 139 opt: 235 Z-score: 270.0 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 257; 21.886% identity (53.030% similar) in 594 aa overlap  
 (45-595:56-600)

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGF
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 FQHKSLDTIQEKWMEWKKDNHSLYVDPVIGTVASFLKLLKGLSLKRIKSELNRLFPSG
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 STNLMEDILRETEKFLNQKLNLTDLRSVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 VPLSITSSVNTMQQLFLNRLSQFQMGGYQLLLLPLFAQAANIHLISYIRDVILNAEHWGIS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 AATLRTYQNHRLRNYTRDYSNYCIDTYQTAFR---GLNTRIHDMML--EFRTYMFNLNVFEY
      210      220      230      240      250

```

```

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRITYPIRTVSQLTREIYTNVPLENFDGSRFGSAQGIIEGSIKIRPHLMDILNSI
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 VSIWS-----LFKYQSLLVSSGANLYASGSGPQQTQLFTS-
      260      270      280      290

```

```

      310      320      330      340      350      360
Cry1Ac TIYTDARHGEYYWSGHQIMASPV--FSGPEF--TFPLYGTM-GNAAPQQRIVAQLGQ--
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 -----QDWPFYLSLQVNSNYVLVSGFSGASLFTTFPNIGLPGSTTTQALLAARVNYSG
      300      310      320      330      340

```

```

      370      380      390      400      410
Cry1Ac GVYR-TLSSSTLYRRPFNIGINNQQLSV-----LDGTEFAYG--TSSNLPsAVYRKSGTV
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 GITSGSIGGSNPNQNFNCNTISPLSTSFVRSWLDSGSDRQGVVTVTNWQTESFETTSGL
      350      360      370      380      390      400

```

```

      420      430      440      450      460      470
Cry1Ac DSLDEIQQNNVPPRQGFSHRLSHVSMFRSFGFSNNSVSIIRAPMFSWIHRSAEFNNIIA
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 RCGAFTPRGNSNYYPGY-FIRNISGVSLV---LRNED---LKRPLYNEKRNIESPSGTP
      410      420      430      440      450

```

```

      480      490      500      510      520
Cry1Ac SDSITQIPAV--KGNFLF----NGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP--
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 GGARAYMVSVHNKNNIYAVHENGTMHILAPEDNTGFTTISPIHATQVNNQTRTFISEKFG
      460      470      480      490      500      510

```

```

      530      540      550      560      570
Cry1Ac ----IHFPSTSTRYRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSS
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 NQGDSLRFEQSNTTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTINGRVYASNVNTTTNN
      520      530      540      550      560      570

```

```

      580      590      600      610      620      630
Cry1Ac DFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNA
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|128 D-GVNDNGARFSDINIGNVWASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
      580      590      600      610      620      630

```

>>gi|155097609|gb|ABT00540.1| Sequence 48 from patent US (634 aa)  
 initn: 156 init1: 131 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 265; 22.967% identity (53.429% similar) in 627 aa overlap  
 (45-637:57-629)

```

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGF
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|155 FQRKSLDTVQREWEWKKNNHSLYLDPIVGTVASFLKLLKVGSLVGRKRIKSELNRLFPSG
      30      40      50      60      70      80

```

```

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|155 STNLMQDILRETEKFLNQKLNLTDLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100      110      120      130      140

```

```

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANLHLSFIRVILNAEHWGIS
      150      160      170      180      190      200

```

```

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::
gi|155 AATLRTYRDFLNKNTYTRDYSNYCINTYQSAFK---GLNTRLHDMML--EFRTYMFNLNVFEY
      210      220      230      240      250

```





```

370      380      390      400      410      420
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430      440      450      460      470      480

```

```

480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 FSDINIGNVVASNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPLY
590      600      610      620      630

```

>>gi|155097605|gb|ABT00536.1| Sequence 40 from patent US (634 aa)  
 initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 261; 22.774% identity (52.740% similar) in 584 aa overlap  
 (45-595:57-601)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVGVKRIKILSELNLIFFPSG
30      40      50      60      70      80

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80      90      100     110     120
Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90      100     110     120     130     140

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130     140     150     160     170     180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150     160     170     180     190     200

```

```

190     200     210     220     230     240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTLTVLDI
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 AATLRTYRDYLNRYRDSYNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVEFY
210     220     230     240     250

```

```

250     260     270     280     290     300
Cry1Ac VSLFNPYDSRTPYPIRTVSQLTREIYTNVLENFDGSRGSAQIEGSIKIRPHLMDILNSI
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 VSIWLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF

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```

260      270      280      290      300      310
Cry1Ac T-----IYTAHRGEYEWYSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 SGARLNTFPNIVGLPGSTTTHALLAARVNYSGGISS---GDIGASPPFNQNFNCST---
320      330      340      350      360

```

```

370      380      390      400      410      420
Cry1Ac VYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQGTVDLSDEIPPQ
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 FLPPLLTPFVRSWLDSGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFFDYFIR
370      380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430      440      450      460      470      480

```

```

480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 -----NGSMIHLAPNGYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 NTTARYTFRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 FSDINIGNVVASNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPIY
590      600      610      620      630

```

>>gi|155097676|gb|ABT00607.1| Sequence 182 from patent U (634 aa)  
 initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVGVKRIKILSELNLIFFPSG
30      40      50      60      70      80

```

```

80      90      100     110     120
Cry1Ac GPSQWDAFLVQIEQLINQRIEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90      100     110     120     130     140

```

```

130     140     150     160     170     180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
: . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . : . . . :
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

```

```

150      160      170      180      190      200
Cry1Ac 190      200      210      220      230      240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLDI
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHLMIDLNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLFQVNSNYVLNGF
      260      270      280      290      300      310

```

```

310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTFLYGTMGNAAPQQRIVAQLGQG
gi|155 SGARLsntfPnIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
      320      330      340      350      360

```

```

370      380      390      400      410      420
Cry1Ac VYRTLsStLYRRPFNIGINNQL-SVLDGTEfAYGTSSNLPSAVYRKSgTVDSLDEIPPQ
gi|155 FLpLLtPFVRSWLDsGSDREGVATVTNWQTESfETTLGLRSgAFtARGNSNYfPDYfIR
      370      380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac N-NNVP--PRQGFshRlshVsmFRSGfSNSSV-SIIRAPmFswIHRSAEFnNIIASDSIT
gi|155 NISGvPLVVRNEDLRRPLHYNEIRNIASpSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

```

```

480      490      500      510      520
Cry1Ac QIPAVKGNFLFNgsVIS-GPG-FTGGDLVRLNssGnNIQRNGYIEVP-----IHFP--
gi|155 -----NGSMIHlAPNDYtGFTISPIHATQVNNQTRTFISEKfGNQGDsLRFEQN
      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVtPIHLNVN-WGNSSIFs--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NtTARyTLRGNGNSYN-LYLRVSSIGNStIRVtInGRVYtATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac FTS-SLGNlVGRNfSGTAGVIIDRFEPiPVtATLEAEYnLERAQKAVNALFTSTnQLGL
gi|155 FSDINIGNVVASSNSDvPLDINvTLNSGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

```

>>gi|155097611|gb|ABT00542.1| Sequence 52 from patent US (634 aa)  
 initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

```

20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGI
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLKVKVGLVgKRILSELRLNIFPsg

```

```

30      40      50      60      70      80
Cry1Ac 80      90      100      110      120
GPSQWDAFLVQIEQLINQRIEEFARNQAIrSLEGLSNLYQIYAESfREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQRlNTDTLARVNAELTGL----QANVEEFNRQVDNfLNPNRNA
      90      100      110      120      130      140

```

```

130      140      150      160      170      180
Cry1Ac LREEMRIQFNdMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLrDVSVfGQRWGFD
gi|155 VPLSITSSVNTMQQLFLNRLPQfMQYQLLLPLFAQAANLHLSfIRDVILNADEWGIS
      150      160      170      180      190      200

```

```

190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLTVLDI
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
      210      220      230      240      250

```

```

250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIRSPHLMIDLNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLFQVNSNYVLNGF
      260      270      280      290      300      310

```

```

310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTFLYGTMGNAAPQQRIVAQLGQG
gi|155 SGARLsntfPnIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
      320      330      340      350      360

```

```

370      380      390      400      410      420
Cry1Ac VYRTLsStLYRRPFNIGINNQL-SVLDGTEfAYGTSSNLPSAVYRKSgTVDSLDEIPPQ
gi|155 FLpLLtPFVRSWLDsGSDREGVATVTNWQTESfETTLGLRSgAFtARGNSNYfPDYfIR
      370      380      390      400      410      420

```

```

430      440      450      460      470
Cry1Ac N-NNVP--PRQGFshRlshVsmFRSGfSNSSV-SIIRAPmFswIHRSAEFnNIIASDSIT
gi|155 NISGvPLVVRNEDLRRPLHYNEIRNIASpSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

```

```

480      490      500      510      520
Cry1Ac QIPAVKGNFLFNgsVIS-GPG-FTGGDLVRLNssGnNIQRNGYIEVP-----IHFP--
gi|155 -----NGSMIHlAPNDYtGFTISPIHATQVNNQTRTFISEKfGNQGDsLRFEQN
      490      500      510      520

```

```

530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVtPIHLNVN-WGNSSIFs--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NtTARyTLRGNGNSYN-LYLRVSSIGNStIRVtInGRVYtATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

```

```

590      600      610      620      630      640
Cry1Ac FTS-SLGNlVGRNfSGTAGVIIDRFEPiPVtATLEAEYnLERAQKAVNALFTSTnQLGL

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gi|155 FSDINIGNVVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY  
 590 600 610 620 630

>>gi|155097595|gb|ABT00526.1| Sequence 20 from patent US (634 aa)  
 initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

20 30 40 50 60 70  
 Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FQHKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVLGKRLISELRNLIFFPSG  
 30 40 50 60 70 80

80 90 100 110 120  
 Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 STNLMQDILRETEKFLNQLRINTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA  
 90 100 110 120 130 140

130 140 150 160 170 180  
 Cry1Ac LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS  
 150 160 170 180 190 200

190 200 210 220 230 240  
 Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY  
 210 220 230 240 250

250 260 270 280 290 300  
 Cry1Ac VSLFPNYDSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQIEGSIKRSPLHMDILNSI  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF  
 260 270 280 290 300 310

310 320 330 340 350 360  
 Cry1Ac T-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGG  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---  
 320 330 340 350 360

370 380 390 400 410 420  
 Cry1Ac VYRTLSSITLYRRPFNIGINNQQ--SVLDGTEFAYGTSSNLPASVYRKSQTVDLDEIPPQ  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FLPLLLTFFVRSWLDSDREGVATVTNWTESFETTLGLRSGAPTARGNSNYFPDYFIR  
 370 380 390 400 410 420

430 440 450 460 470  
 Cry1Ac N--NNVP--PRQGFSHRLSHVSMFRSGFSNSV--SIIRAPMFSWIHRSAEFNIIASDSIT  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS--VHNK--NNIHAVHE--  
 430 440 450 460 470 480

480 490 500 510 520  
 Cry1Ac QIPAVKGNFLFNGSVIS--GPG--FTGGDLVRLNSSGNNIQRNGYIEVP-----IHFP--  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN  
 490 500 510 520

530 540 550 560 570 580  
 Cry1Ac STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND--GVNDNGAR  
 530 540 550 560 570 580

590 600 610 620 630 640  
 Cry1Ac FTS--SLGNIVGVRNFGTAGVIIDRFEFIPVPTATLEAEYNLERAQKAVNALFTSTNQLGL  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FSDINIGNVVASSNSDVPLDINVTLSNGTQFELMNIMLVPTNISPLY  
 590 600 610 620 630

>>gi|155097607|gb|ABT00538.1| Sequence 44 from patent US (634 aa)  
 initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 256; 22.298% identity (52.830% similar) in 583 aa overlap  
 (45-595:57-601)

20 30 40 50 60 70  
 Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVLGKRLISELRNLIFFPSG  
 30 40 50 60 70 80

80 90 100 110 120  
 Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 STNLMQDILRETEKFLNQLRINTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA  
 90 100 110 120 130 140

130 140 150 160 170 180  
 Cry1Ac LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS  
 150 160 170 180 190 200

190 200 210 220 230 240  
 Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY  
 210 220 230 240 250

250 260 270 280 290 300  
 Cry1Ac VSLFPNYDSRTPYIRTVSQTREIYTNPVLNFDGSRGSAQIEGSIKRSPLHMDILNSI  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF  
 260 270 280 290 300 310

310 320 330 340 350 360  
 Cry1Ac T-----IYTDHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGGG  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---  
 320 330 340 350 360

370 380 390 400 410 420  
 Cry1Ac VYRTLSSITLYRRPFNIGINNQQ--SVLDGTEFAYGTSSNLPASVYRKSQTVDLDEIPPQ  
 . . . . . : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .



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gi|155 TVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGI
150 160 170 180 190 200

Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRRELTTLVLD
190 200 210 220 230 240

gi|155 SAATLRTRYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLRHDTL---EFRTYMFNLVFE
210 220 230 240 250

Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDFGSRGSAQIEGSIKSPHMLDILNS
250 260 270 280 290 300

gi|155 YVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLHSLFQVNSNYVLNG
260 270 280 290 300 310

Cry1Ac IT-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTMGNAAPQRIvAQLGQ
310 320 330 340 350 360

gi|155 FSGARLSNTFPNIVGLPGSTTTHallAARVnySGGISS---GDIGASPFNQNFNCST--
320 330 340 350 360

Cry1Ac GvYrTLsStLYRRPFNIGInnQQL-SVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEIPP
370 380 390 400 410

gi|155 -FLPpLLTPFvRSWLDsGSDREGVATvTNWQTEsFETTLGLRSGAfTARgNSNYFPDYFI
370 380 390 400 410 420

Cry1Ac QN-NNVP--PRQGFshRLshVSMFRSGFSNssV-SIIRAPMFSWIHRSAEFNNIASDSI
420 430 440 450 460 470

gi|155 RNISGVPLVVRNEDLRRLPHyNEIRNIASpSGTPGGARAYMVS-VHNrk--NNIHAVHE-
430 440 450 460 470 480

Cry1Ac TQIPAVKGNFLNGSvis-GPG-FTGGDLVRLNssGNNIQNRgyIEVP-----IHFP-
480 490 500 510 520

gi|155 -----NGSMIHlAPNDyTGFTISPIHATQVNNQTRTFISEKFGNQDslRFEQ
490 500 510 520

Cry1Ac -STSTRyRVRVRYASvTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESAN
530 540 550 560 570 580

gi|155 NNTTARyTLRGNgNSYN-LyLRVSSIGNSTIRVTINGRvYtATNVNTTTNND-GVNDNGA
530 540 550 560 570 580

Cry1Ac AfTS-SLGNIVGRNfSGTAGVIIDRFEFIPVTATLEAEYnLERaQKAVALNFTSTNQLG
590 600 610 620 630 640

gi|155 RfSDINIGNVvASSNSdVPLDINVTLNSGTQFDLMNIMLVPTNISPIY
590 600 610 620 630

>>gi|155097600|gb|ABT00531.1| Sequence 30 from patent US (634 aa)
initn: 162 initl: 128 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 254; 22.603% identity (52.740% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGI
20 30 40 50 60 70

gi|155 FQHKSLDtvQREWTEWkKNHSLyLDPIVGTvASfLLKkVGSVlGKRILsELRNLIffPSG
30 40 50 60 70 80

Cry1Ac GpSQWDAFLVQIEQLINQRIEEFARnQAISRLEGLSNLYQIYAESfREWEADPTNP---A
80 90 100 110 120

gi|155 STNLMQDILRETEQFLNQRlNTDTLARVNAELTGL---QANVEEFNRQVDNfLNPnRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQfNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSfVFGQRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPDSR--DWIRYNQFRRELTTLVLDI
190 200 210 220 230 240

gi|155 AAALRTRYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLRHDTL---EFRTYMFNLVFEY
210 220 230 240 250

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDFGSRGSAQIEGSIKSPHMLDILNSI
250 260 270 280 290 300

gi|155 VSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
260 270 280 290 300 310

Cry1Ac T-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPlyGTMGNAAPQRIvAQLGQ
310 320 330 340 350 360

gi|155 SGARLSNTFPNIVGLPGSTTTHallAARVnySGGISS---GDIGASPFNQNFNCST---
320 330 340 350 360

Cry1Ac vYrTLsStLYRRPFNIGInnQQL-SVLDGTEfAYGTSSNLPSAVYRKSgTVdSLDEIPPQ
370 380 390 400 410 420

gi|155 FLPpLLTPFvRSWLDsGSDREGVATvTNWQTEsFETTLGLRSGAfTARgNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFshRLshVSMFRSGFSNssV-SIIRAPMFSWIHRSAEFNNIASDSIT
430 440 450 460 470

gi|155 NISGVPLVVRNEDLRRLPHyNETRNIASpSGTPGGARAYMVS-VHNrk--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLNGSvis-GPG-FTGGDLVRLNssGNNIQNRgyIEVP-----IHFP--
480 490 500 510 520

gi|155 -----NGSMIHlAPNDyTGFTISPIHATQVNNQTRTFISEKFGNQDslRFEQn
490 500 510 520

Cry1Ac STSTRyRVRVRYASvTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580

gi|155 NNTTARyTLRGNgNSYN-LyLRVSSIGNSTIRVTINGRvYtATNVNTTTNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac fTS-SLGNIVGRNfSGTAGVIIDRFEFIPVTATLEAEYnLERaQKAVALNFTSTNQLGL
590 600 610 620 630 640

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      . . . . .
gi|155 FSDINMGVNVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

>>gi|155097686|gb|ABT00617.1| Sequence 202 from patent U (634 aa)
      initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
      Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap
      (45-595:57-601)

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
      . . . . .
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVLGKRILSELRNLIFFPSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . .
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIRSPLHMDILNSI
      . . . . .
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLNGF
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywSGHQIMASpVgFSGPEFTFPlyGTMGNAAPQRiVAQLGQg
      . . . . .
gi|155 SGARLNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
      320      330      340      350      360

      370      380      390      400      410      420
Cry1Ac VYRTLSSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
      . . . . .
gi|155 FLPPLLTPFVRSWLDGSDREGVATVTINWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFShRLSHVSMFRSGFSNSsv-SIRAPMFswIHRSAEFNIIASDSIT
      . . . . .
gi|155 NISGVPVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

      480      490      500      510      520
Cry1Ac QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNniQRgyIEVp-----IHFP--

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      . . . . .
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDLSRFEQN
      490      500      510      520

      530      540      550      560      570      580
Cry1Ac STSTRYRVRVRYASVTPIHLLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      . . . . .
gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
      530      540      550      560      570      580

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLEAQAQAVNALFTSTNQLGL
      . . . . .
gi|155 FSDINIGNVVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

>>gi|155097651|gb|ABT00582.1| Sequence 132 from patent U (634 aa)
      initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
      Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap
      (45-595:57-601)

      20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIGWIF
      . . . . .
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSVLGKRILSELRNLIFFPSG
      30      40      50      60      70      80

      80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRNA
      90      100      110      120      130      140

      130      140      150      160      170      180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150      160      170      180      190      200

      190      200      210      220      230      240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
      . . . . .
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
      210      220      230      240      250

      250      260      270      280      290      300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIRSPLHMDILNSI
      . . . . .
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVNLNGF
      260      270      280      290      300      310

      310      320      330      340      350      360
Cry1Ac T-----IYTDahrgeyywSGHQIMASpVgFSGPEFTFPlyGTMGNAAPQRiVAQLGQg
      . . . . .
gi|155 SGARLNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---
      320      330      340      350      360

      370      380      390      400      410      420
Cry1Ac VYRTLSSSTLYRRPFNIGINNQL-SVLDGTEFAYGTSSNLPsAVYRkSGTVDSLDEIPpQ
      . . . . .
gi|155 FLPPLLTPFVRSWLDGSDREGVATVTINWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370      380      390      400      410      420

      430      440      450      460      470
Cry1Ac N-NNVP--PRQGFShRLSHVSMFRSGFSNSsv-SIRAPMFswIHRSAEFNIIASDSIT
      . . . . .
gi|155 NISGVPVVRNEDLRRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
      430      440      450      460      470      480

      480      490      500      510      520
Cry1Ac QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNssGNniQRgyIEVp-----IHFP--

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Regulatory Product Characterization Team

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL  
 : . . . . . :  
 gi|155 FSDINIGNVVASSNSDVLVDINVTLSNGTQFDLMNIMLVPTNISPLY  
 590 600 610 620 630

>>gi|155097634|gb|ABT00565.1| Sequence 98 from patent US (634 aa)  
 initn: 138 initl: 138 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 252; 22.810% identity (52.737% similar) in 548 aa overlap  
 (81-595:95-601)

60 70 80 90 100 110  
 Cry1Ac LSEFVPGAGFVLGLVDIIWGFPSQWDALVQIEQLINQRIIEEFARNQAISREGLSNL  
 : . . . . . :  
 gi|155 KVGSLVGRKILSELRLIFPSGSTNMQDILRETEKFLNQLRNTDTLARVNAELTGL---  
 70 80 90 100 110 120

120 130 140 150 160  
 Cry1Ac YQIYAESFREWEADPTNP--ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ  
 : . . . . . :  
 gi|155 -QANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFLNRLPQFQMRQYQLLLPLFAQ  
 130 140 150 160 170 180

170 180 190 200 210 220  
 Cry1Ac AANLHLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS  
 : . . . . . :  
 gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNYLKNYTRDYSNYCINTYQSAFK---GLNT  
 190 200 210 220 230

230 240 250 260 270 280  
 Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGS--  
 : . . . . . :  
 gi|155 RLHDTL---EFRTYMFNLVFEYVSIWLSFKYQSLLVSSGANLYASGSGPQQTQSFTSQDW  
 240 250 260 270 280 290

290 300 310 320 330  
 Cry1Ac -----FRGSAQIEGSIKIRSPHMDILNSITTYDAHRGEYWSGHQIMASVPGFSGPEF  
 : . . . . . :  
 gi|155 PFLYSLFQVNSNYVLSGFGARLSNTFPNIVGLPGST-----TTHALLAARVNYSGGIS  
 300 310 320 330 340

340 350 360 370 380 390  
 Cry1Ac TFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQL-SVLDGTEFAYGT  
 : . . . . . :  
 gi|155 S---GDIGASPFNQFNCST---FLPPLLTPFVRSWLDGSGDREGVATVTNWNQTESFET  
 350 360 370 380 390 400

400 410 420 430 440 450  
 Cry1Ac SSNLPSAVYRKSQVSDSLDEIPPN--PRQGFHRLSHVSMFRSGFSNSV-SII  
 : . . . . . :  
 gi|155 TLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRLHYNEIRNIASPSGTPGGA  
 410 420 430 440 450 460

460 470 480 490 500 510  
 Cry1Ac RAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGN  
 : . . . . . :  
 gi|155 RAYMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTTISPIHATQV  
 470 480 490 500

520 530 540 550

Cry1Ac NIQNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPHILNVN-WGNSSIFS--NT  
 : . . . . . :  
 gi|155 NNQTRTFISEKFGNQDLSLRFEQNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTING  
 510 520 530 540 550 560

560 570 580 590 600 610  
 Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE  
 : . . . . . :  
 gi|155 RVYTATNVNTTTNND-GVNDNGARFSDINIGNVVASSNSDVLVDINVTLSNGTQFDLMNI  
 570 580 590 600 610 620

620 630 640 650 660 670  
 Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVK  
 : . . . . . :  
 gi|155 MLVPTNISPLY  
 630

>>gi|155097602|gb|ABT00533.1| Sequence 34 from patent US (634 aa)  
 initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

20 30 40 50 60 70  
 Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTLQFLLSEF--VPGAGFVLGLVDIIWGF  
 : . . . . . :  
 gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKGVSGLVGRKILSELRLIFPSG  
 30 40 50 60 70 80

80 90 100 110 120  
 Cry1Ac GPSQWDALVQIEQLINQRIIEEFARNQAISREGLSNLYQIYAESFREWEADPTNP---A  
 : . . . . . :  
 gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA  
 90 100 110 120 130 140

130 140 150 160 170 180  
 Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF  
 : . . . . . :  
 gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS  
 150 160 170 180 190 200

190 200 210 220 230 240  
 Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI  
 : . . . . . :  
 gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLVFEY  
 210 220 230 240 250

250 260 270 280 290 300  
 Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSFRGSAQIEGSIKIRSPHMDILNSI  
 : . . . . . :  
 gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYSLFQVNSNYVNLGF  
 260 270 280 290 300 310

310 320 330 340 350 360  
 Cry1Ac T-----IYDAHRGEYWSGHQIMASVPGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ  
 : . . . . . :  
 gi|155 SGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNCST---  
 320 330 340 350 360

370 380 390 400 410 420

Cry1Ac VYRTLSSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPO

gi|155 FLPLLLTPFVRSWLDSSDREGVATVTTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP--

gi|155 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQDLSRFEQN
480 490 500 510 520

Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

gi|155 NNTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTNNND-GVNDNGAR
530 540 550 560 570 580

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|155 FSDINIGNVVASNSDVPDLINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630 640

>>gi|155097596|gb|ABT00527.1| Sequence 22 from patent US (634 aa)
initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 257; 22.470% identity (52.659% similar) in 583 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF

gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGLVSKRILSELRNLIFFPSG
20 30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
80 90 100 110 120

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF

gi|155 VPLSITSSVNTMQQLFLNRLPQFQMGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
130 140 150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTLTVLDI

gi|155 AATLRTYRDYLNKTYRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVEFY
190 200 210 220 230 240 250

250 260 270 280 290 300

Cry1Ac VSLFFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQIEGSIRSPHMLDILNSI

gi|155 VSIWLSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWFPLYSLFQVNSNYVNLNGF
260 270 280 290 300 310

Cry1Ac T-----IYTDahrgeyywsgHQIMASpVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG

gi|155 SGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGISS---GDIGASPPFNQNFNCST---
310 320 330 340 350 360

Cry1Ac VYRTLSSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPPO

gi|155 FLPLLLTPFVRSWLDSSDREGVATVTTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370 380 390 400 410 420

Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRGYIEVPI-----HFPST

gi|155 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKLNQDLSRFEQT
480 490 500 510 520

Cry1Ac STRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAF

gi|155 NNTARYTFRGNGNSYNLYLRVSSLGNSTIRVTINGRVYATNVNTTNNND-GVNDNGARF
530 540 550 560 570 580

Cry1Ac TS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLK

gi|155 SDINIGNVVASNSVPLDINVTLNSGTQFDLMNIMLVPTNISPIY
590 600 610 620 630

>>gi|155097710|gb|ABT00641.1| Sequence 250 from patent U (634 aa)
initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF

gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGLVSKRILSELRNLIFFPSG
20 30 40 50 60 70 80

Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
80 90 100 110 120 130 140

130 140 150 160 170 180

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Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI

gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY

Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSGFRGSAQGIIEGSIRSPHLMIDLNSI

gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFQDWPFLYSLFQVNSNYVLNGF

Cry1Ac T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTFPLYGTMGNAAPQQRIVAQLGQG

gi|155 SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST---

Cry1Ac VYRTLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPPQ

gi|155 FLPPLLTPFVRSWLDSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR

Cry1Ac N-NNVP--PRQGFshrlshvsmFRSGFSNssv-SIIRAPMFSWIHRSAEFNNIIASDSIT

gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNssGNNIQNRGYIEVP-----IHFP--

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

Cry1Ac STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR

Cry1Ac FTS-SLGNIVGRNFGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL

gi|155 FSDINIGNVVASNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY

>>gi|155097673|gb|ABT00604.1| Sequence 176 from patent U (634 aa)
initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 258; 22.184% identity (53.413% similar) in 586 aa overlap
(45-595:57-601)

20 30 40 50 60 70

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVGLVLDIIWGF

gi|155 FRHKSldtVQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGSGLIGKRILSELNLIFFPSG

Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A

gi|155 STNLMQDILRETEKFLNQLRLNTDTLARVNAELTGL----QANVEEFNRQVDNFLNPNRRA

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF

gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI

gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY

Cry1Ac VSLFPNYDSRTYPIRTVSQL-----TREIYTNVLENFDGSGFRGSAQGIIEGSIRSPH

gi|155 VSIWLSFKYQSLLVSSGANLYASGSGPQQTQLFTSQDWPFLYSLFQVNSNYVLNGFSGAR

Cry1Ac LMDILNSITIYTDahrgeyywsgHQIMASpVgFSGPEFTFPLYGTMGNAAPQQRIVAQLG

gi|155 LSNTFPNIVGLPGST-----TTHALLAARVNYSGGISS---GDIGASPFNQNFNCST-

Cry1Ac QGVYRTLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIP

gi|155 --FLPPLLTPFVRSWLDSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR

Cry1Ac PQN-NNVP--PRQGFshrlshvsmFRSGFSNssv-SIIRAPMFSWIHRSAEFNNIIASDS

gi|155 IRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE

Cry1Ac ITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNssGNNIQNRGYIEVP-----IHFP

gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

Cry1Ac --STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

gi|155 QNNTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNG

530 540 550 560 570 580

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Cry1Ac 590 600 610 620 630
NAFTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQAVNALFTSTNQL
gi|155 ARFSDINMGVNVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPIY

>>gi|155097698|gb|ABT00629.1| Sequence 226 from patent U (634 aa)
initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGI
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGRKILSELRNLIFFPSG

Cry1Ac 80 90 100 110 120
GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA

Cry1Ac 130 140 150 160 170 180
LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYRDYLNKYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLNVEFY

Cry1Ac 250 260 270 280 290 300
VSLFPNYDSRTYPIRTVSQTLTREIYTNPVLNFDGSRFGSAQIEGSIKSPHMLDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF

Cry1Ac 310 320 330 340 350 360
T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTfPlyGTMGNAAPQQRIVaQLGQg
gi|155 SGARLsntfPNIvGLPGstTThallaarVnYsGGISS---GDIGASpFNQnFNCST---

Cry1Ac 370 380 390 400 410 420
VYRTLSSITLYRRPFNIGINNQQ--SVLDGTEFAyGTSSNlPsaVYrKSGTVDsLDEIPpQ
gi|155 FLpPLLTpFvRSwLdSGsDRGvATvTNwQTESfETTlGLRSGaFTARGNSNYFDyFIR

Cry1Ac 430 440 450 460 470
N-NNVP--PRQGFshRLshVsmFRSGfSnsSV-SIIRaPMfSwIHRsaEFnNIaSDSIT
gi|155 NISGvPLVVRNEDLRrPLHyNEIRNIASpSGTPGgARayMvS-VHnrK--NNIHavHE--

Cry1Ac 480 490 500 510 520
QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNINQRGYIEVP-----IHFP--
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

Cry1Ac 530 540 550 560 570 580
STSTRYRVRVRYASVTPIHNLVN-WGNSSIFS--NTPPATATSLDNLQSSDFGYFESANA
gi|155 NTTARyTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR

Cry1Ac 590 600 610 620 630 640
FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQAVNALFTSTNQLGL
gi|155 FSDINIGNVVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY

>>gi|155097653|gb|ABT00584.1| Sequence 136 from patent U (634 aa)
initn: 133 init1: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06
Smith-Waterman score: 255; 22.603% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac 20 30 40 50 60 70
IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGI
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVGRKILSELRNLIFFPSG

Cry1Ac 80 90 100 110 120
GPSQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA

Cry1Ac 130 140 150 160 170 180
LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
gi|155 AATLRTYRDYLNKYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLNVEFY

Cry1Ac 250 260 270 280 290 300
VSLFPNYDSRTYPIRTVSQTLTREIYTNPVLNFDGSRFGSAQIEGSIKSPHMLDILNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFYLSLQVNSNYVLNGF

Cry1Ac 310 320 330 340 350 360
T-----IYTDahrgeyywsgHQIMASpVgFSGPEFTfPlyGTMGNAAPQQRIVaQLGQg
gi|155 SGARLsntfPNIvGLPGstTThallaarVnYsGGISS---GDIGASpFNQnFNCST---

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          370      380      390      400      410      420
Cry1Ac VVRTLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPQ
      . . . . .
gi|155 FLPLLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
          370      380      390      400      410      420

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          430      440      450      460      470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
      . . . . .
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
          430      440      450      460      470      480

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          480      490      500      510      520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
      . . . . .
gi|155 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
          490      500      510      520

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          530      540      550      560      570      580
Cry1Ac STSTRYRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      . . . . .
gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGAR
          530      540      550      560      570      580

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          590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . .
gi|155 FSDINIGNVVASSNSDVPLDINVTLNLSGTQFDLMNIMLVPTNISPLY
          590      600      610      620      630

```

>>gi|155097639|gb|ABT00570.1| Sequence 108 from patent U (634 aa)  
 initn: 133 initl: 133 opt: 235 Z-score: 269.9 bits: 61.0 E(): 4.1e-06  
 Smith-Waterman score: 250; 21.859% identity (53.701% similar) in 581 aa overlap  
 (45-595:57-601)

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          20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . .
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVSKRILSELRNLIFFPSG
          30      40      50      60      70      80

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          80      90      100      110      120      130
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALRE
      . . . . .
gi|155 STNLMQDILRETEKFLNQRLNTDTLARVNAELTGLQSNVEEFNRQVDNF-LNPNRNAVPL
          90      100      110      120      130      140

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          140      150      160      170      180      190
Cry1Ac EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAANLHLSVLRDVSFVGRWGFGDAAT
      . . . . .
gi|155 SITSSVNTMQQLFLNRLPQFQMGYQLLLLPLFAQAANLHLSFIRDVILNADWEGISAAT
          150      160      170      180      190      200

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          200      210      220      230      240      250
Cry1Ac INSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDIVSL
      . . . . .
gi|155 LRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLNVFEYVSI
          210      220      230      240      250

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          260      270      280      290      300
Cry1Ac FPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSGFRGSAQIEGSIRSPHMLDILNSIT--
      . . . . .
gi|155 WSLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNNQNYLVNLFNGFSGA
          260      270      280      290      300      310

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```

          310      320      330      340      350      360
Cry1Ac ----IYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYR
      . . . . .
gi|155 RLSNTFPNIGLPGSTTTTHALLAARVNYSGGISS----GDIGASPFNQFNFCST---FLP
          320      330      340      350      360

```

```

          370      380      390      400      410      420
Cry1Ac TLSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSLDEIPPQN-N
      . . . . .
gi|155 PLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIRNIS
          370      380      390      400      410      420

```

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          430      440      450      460      470
Cry1Ac NVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSITQIP
      . . . . .
gi|155 GVPLVVRNEDLRRPLVFNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE-----
          430      440      450      460      470      480

```

```

          480      490      500      510      520
Cry1Ac AVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--STS
      . . . . .
gi|155 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNTT
          490      500      510      520      530

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          530      540      550      560      570      580
Cry1Ac TRYRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS
      . . . . .
gi|155 ARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND-GVNDNGARFSD
          540      550      560      570      580      590

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          590      600      610      620      630      640
Cry1Ac -SLGNIVGRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
      . . . . .
gi|155 INIGNVVASSNSDVPLDINVTLNLSGTQFDLMNIMLVPTNISPLY
          600      610      620      630

```

>>gi|155097632|gb|ABT00563.1| Sequence 94 from patent US (634 aa)  
 initn: 133 initl: 133 opt: 234 Z-score: 268.8 bits: 60.8 E(): 4.7e-06  
 Smith-Waterman score: 254; 22.603% identity (52.911% similar) in 584 aa overlap  
 (45-595:57-601)

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          20      30      40      50      60      70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVLGLVDIIWGIF
      . . . . .
gi|155 FQHKSLDTVQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVSKRILSELRSIFPSG
          30      40      50      60      70      80

```

```

          80      90      100      110      120
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQVILRETEKFLNQRLNTDTLARVNAELTGL---QANVEEFNHQVDNLFNPNRNA
          90      100      110      120      130      140

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130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLDI
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYRSFAK---GLNTRLHDTL---EFRTYMFNLNVFEY

250 260 270 280 290 300
Cry1Ac VSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIIRSPHLMIDLNSI
gi|155 VSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF

310 320 330 340 350 360
Cry1Ac T-----IYTDahrgeyywshqimaspvfgsgpeftfplygtmgnaapqqrivaaqlgqg
gi|155 SGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQFNFCST---

370 380 390 400 410 420
Cry1Ac VYRTLSSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQ
gi|155 FLPELLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR

430 440 450 460 470
Cry1Ac N--NNVP--PRQGFshrlshvsmfrsgfsnssv--siirapmfswihrsaefniiadsdit
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--

480 490 500 510 520
Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRNGYIEVP-----IHFP--
gi|155 -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

530 540 550 560 570 580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDNGAR

590 600 610 620 630 640
Cry1Ac FTS-SLGNIVGVRNFGSGTAGVIIDRFEPFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|155 FSDINIGNVVASSNSDVPDLINVTLNSGTQFDLMNIMLVPTNISPLY

>>gi|155097705|gb|ABT00636.1| Sequence 240 from patent U (634 aa)
initn: 133 init1: 133 opt: 234 Z-score: 268.8 bits: 60.8 E(): 4.7e-06
Smith-Waterman score: 254; 23.077% identity (52.381% similar) in 546 aa overlap
(81-595:95-601)

60 70 80 90 100 110
Cry1Ac LSEFVPGAGFVLGLVDIIWGIQFQSDAFVQIEQLINQRIEFAFNQAISRLEGLSNL
gi|155 KVGSLVGRKILSELRSILFPSSGNTLMQDILRETEEFNLQRLNTDILARVNAELTGL---

120 130 140 150 160
Cry1Ac YQIYAESFREWEADPTNPALRE---EMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNLFNPNLDTVPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQ

170 180 190 200 210 220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRDYLNKYNTRDYSNYCINTYRSFAK---GLNT

230 240 250 260 270 280
Cry1Ac R--DWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSR
gi|155 RLHDTL---EFRTYMFNLNVFEYVSIWLSFKYQSLLVSSGANL----YASGSGPQQTQSFT

290 300 310 320 330
Cry1Ac GSAQIEGSIIRSPHLMIDLNSIT-----IYTDahrgeyywshqimaspvfgsgpeftf
gi|155 SQDWPFLYSLFQVNSNYVLNGFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGGISS-

340 350 360 370 380 390
Cry1Ac PLYGTMGNAAPQQRIVAAQLGQGVYRILSSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSS
gi|155 ---GDIGASPFNQFNFCST---FLPELLTPFVRSWLDGSDREGVATVTNWQTESFETTL

400 410 420 430 440 450
Cry1Ac NLPSAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFshrlshvsmfrsgfsnssv--siira
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARA

460 470 480 490 500 510
Cry1Ac PMFSWIHRSAEFNIIADSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNI
gi|155 YMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTISPIHATQVNN

520 530 540 550 560
Cry1Ac QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVP
gi|155 QTRTFISEKFGNQGDSLRFEQNNTTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRV

570 580 590 600 610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFGSGTAGVIIDRFEPFIPVTATLEAE
gi|155 YTATNVNTTTNND-GVNDNGARFSDINIGNVVASSNSDVPDLINVTLNSGTQFDLMNIML

620 630 640 650 660 670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

gi|155 VPTNISPLY
630

>>gi|16240189|gb|AAE79635.1| Sequence 55 from patent US (136 aa)
initn: 215 initl: 109 opt: 225 Z-score: 268.1 bits: 58.5 E(): 5.2e-06
Smith-Waterman score: 225; 35.915% identity (65.493% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|162 PGFIGGALLQRTDHGSLGVLR--VQFPLHL
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
gi|162 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPSMRLGEDLRYGSAFAREFNTSIR
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|162 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRKAXDLXAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|53970036|gb|AAV19129.1| Sequence 55 from patent US (136 aa)
initn: 215 initl: 109 opt: 225 Z-score: 268.1 bits: 58.5 E(): 5.2e-06
Smith-Waterman score: 225; 35.915% identity (65.493% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|539 PGFIGGALLQRTDHGSLGVLR--VQFPLHL
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
gi|539 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPSMRLGEDLRYGSAFAREFNTSIR
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|539 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRKAXDLXAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731253|gb|AAQ37316.1| Sequence 55 from patent US (136 aa)
initn: 215 initl: 109 opt: 225 Z-score: 268.1 bits: 58.5 E(): 5.2e-06
Smith-Waterman score: 225; 35.915% identity (65.493% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|337 PGFIGGALLQRTDHGSLGVLR--VQFPLHL
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
gi|337 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPSMRLGEDLRYGSAFAREFNTSIR
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|337 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRKAXDLXAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504416|gb|AAM57112.1| Sequence 55 from patent US (136 aa)
initn: 215 initl: 109 opt: 225 Z-score: 268.1 bits: 58.5 E(): 5.2e-06
Smith-Waterman score: 225; 35.915% identity (65.493% similar) in 142 aa overlap
(495-633:1-136)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|215 PGFIGGALLQRTDHGSLGVLR--VQFPLHL
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPIHNLVNWGNSSIFSNTPATATSLDNLQSSDFGY--FESANA
gi|215 ---RQQYRIRVRYASTTNIRLSVN-GSFGTISQNLPSMRLGEDLRYGSAFAREFNTSIR
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac FTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|215 PTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRKAXDLXAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|155097631|gb|ABT00562.1| Sequence 92 from patent US (634 aa)
initn: 133 initl: 133 opt: 233 Z-score: 267.6 bits: 60.6 E(): 5.5e-06
Smith-Waterman score: 248; 22.998% identity (53.152% similar) in 587 aa overlap
(45-595:57-601)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESEF--VPGAGFVLGLVDIWIWGF

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gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLKKVGLVSKRILSELNLIFFPSG
      30      40      50      60      70      80
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQDILRGTFRFLNQLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100     110     120     130     140
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150     160     170     180     190     200
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      . . . . .
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQTAFAK---GLNTRLHDTL---EFRTYMLNVFEY
      210     220     230     240     250
Cry1Ac VSLFPNYSRTYPIRTVSQTLREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILNSI
      . . . . .
gi|155 VSIWLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
      260     270     280     290     300     310
Cry1Ac TIYTDAHRGEYYWS--G-----HQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQL
      . . . . .
gi|155 --FSGARLNTFPFIVGLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNCST
      320     330     340     350     360
Cry1Ac GQGVYRTLSTLYRRPFNIGINNQQ-LVLDGTEFAYGTSSNLPSAVYKSGTVDLDEI
      . . . . .
gi|155 ---FLPPLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDY
      370     380     390     400     410     420
Cry1Ac PPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNIIASD
      . . . . .
gi|155 FIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVH
      430     440     450     460     470
Cry1Ac SITQIPAVKGNFLFNNGSVIS-GPG-FTGGDLVRLNSSGNNIQRNGYIEVP-----IHF
      . . . . .
gi|155 E-----NGSMIHLAPNDYTGFTIISPIHATQVNNRTRTFISEKFGNQDGLRFL
      480     490     500     510     520
Cry1Ac P--STSTRYRVRVRYASVTPIHNLVNV-WGNSSIFS--NTVPATATSLDNLQSSDFGYFES
      . . . . .
gi|155 EQNNTTARYTLRGNNGSNYN-LYLRVSSIGNSTIRVTINGRVYATNVNTTTNND-GVNDN
      530     540     550     560     570     580
Cry1Ac P--STSTRYRVRVRYASVTPIHNLVNV-WGNSSIFS--NTVPATATSLDNLQSSDFGYFES
      . . . . .
      580     590     600     610     620     630

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Cry1Ac ANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQ
      . . . . .
gi|155 GARFSDINIGNVVASSNSDVPLDINVTLNSGTQFDLNMIMLVPTNISPLY
      590     600     610     620     630
>>gi|155097597|gb|ABT00528.1| Sequence 24 from patent US (634 aa)
      initn: 131 initl: 131 opt: 233 Z-score: 267.6 bits: 60.6 E(): 5.5e-06
Smith-Waterman score: 255; 22.432% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEF--VPGAGFVGLVLDI IWGIF
      . . . . .
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLKKVGLVSKRILSELNLIFFPSG
      30      40      50      60      70      80
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNP---A
      . . . . .
gi|155 STNLMQDILRETEKFLNQLNTDTLARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
      90      100     110     120     130     140
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      . . . . .
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
      150     160     170     180     190     200
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
      . . . . .
gi|155 AATLRTYRDYLNKYNTRDYSNYCINTYQSAFAK---GLNTRLHDTL---EFRTYMLNVFEY
      210     220     230     240     250
Cry1Ac VSLFPNYSRTYPIRTVSQTLREIYTNPVLENFDGSRGSAQIEGSIKSPHMLDILNSI
      . . . . .
gi|155 VSIWLFKYQSLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF
      260     270     280     290     300     310
Cry1Ac TIYTDAHRGEYYWSHGQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQG
      . . . . .
gi|155 SGARLNTFPNIGLPGSTTTHALLAARVNYSGGISS---GDIGASPFNQFNCST---
      320     330     340     350     360
Cry1Ac VYRTLSTLYRRPFNIGINNQQ-LVLDGTEFAYGTSSNLPSAVYKSGTVDLDEIPPO
      . . . . .
gi|155 FLPPLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR
      370     380     390     400     410     420
Cry1Ac N--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNIIASDSIT
      . . . . .
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE--
      430     440     450     460     470     480
Cry1Ac P--STSTRYRVRVRYASVTPIHNLVNV-WGNSSIFS--NTVPATATSLDNLQSSDFGYFES
      . . . . .
      480     490     500     510     520

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Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
gi|155 -----NGSMIHLAPNDYTGFTIISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NTTARYTLRGNNSYN-LYLRVSSIGNSTIRVTINGRVHTATNVNTTTNND-GVNDNGAR

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|155 FSDINIGNVVASSNSDVPLDINVTFNSGTQFDLMNIMLVPTNISPIY

>>gi|155097644|gb|ABT00575.1| Sequence 118 from patent U (634 aa)
initn: 133 initl: 133 opt: 233 Z-score: 267.6 bits: 60.6 E(): 5.5e-06
Smith-Waterman score: 254; 22.603% identity (52.740% similar) in 584 aa overlap
(45-595:57-601)

Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIWGIF
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVKGKRLSELNLIFFPSG

Cry1Ac GPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A
gi|155 STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QAGIEEFNRQVDNFLNPNRRA

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGF
gi|155 VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
gi|155 AATLRTRYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY

Cry1Ac VSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQIEGSIKIRSPHLMIDLNSI
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVLNGF

Cry1Ac T-----IYTDHAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQG
gi|155 SGARLSNTFFPNIVGLPGSTTHALLAARVNYSGGISS---GDIGASFPNQFNFCST---

Cry1Ac T-----IYTDHAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQG

Cry1Ac VYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPQP
gi|155 FLPLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFIR

Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNNIIASDSIT
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNKR--NNIHAVHE--

Cry1Ac QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFP--
gi|155 -----NGSMIHLAPNDYTGFTIISPIHATQVNNQTRTFISEKFGNQGDSLRFEQN

Cry1Ac STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
gi|155 NTTARYTLRGNNSYN-LYLRVSSIGNSTIRVTINGRVHTATNVNTTTNND-GVNDNGAR

Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|155 FSDVNMGNVVASSNSDVPLDINVTLNSGTQFDLMNIVLVPTNISPIY

>>gi|155097627|gb|ABT00558.1| Sequence 84 from patent US (634 aa)
initn: 133 initl: 133 opt: 233 Z-score: 267.6 bits: 60.6 E(): 5.5e-06
Smith-Waterman score: 253; 22.921% identity (52.680% similar) in 541 aa overlap
(85-595:99-601)

Cry1Ac VPGAGFVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIIEEFARNQAIISRLEGLSNLYQIY
gi|155 LVGKRLSELRSIIFPSGSTNLMQDILRGTEKFLNQLRNTDTLARVNAELTGL---QAN

Cry1Ac AESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
gi|155 VEEFNRQVDNFLNPNRRAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLLPLFAQAANL

Cry1Ac HLSVLRDVSFVQQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
gi|155 HLSFIRDVILNADEWGISAATLRTRYRDLKKNYTRDYSNYCINTYQSAFK---GLNTRLHD

Cry1Ac WIRYNQFRRELTLTVLDIVSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQ
gi|155 TL---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWP

Cry1Ac WIRYNQFRRELTLTVLDIVSLFPNYSRSTYPIRTVSQLTREIYTNPVLENFDFGSRGSAQ





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gi|155 VPLSITSSVNTMQQLFLNRLPQFQMQGYQLLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
190 200 210 220 230 240

gi|155 AATLRTYRDYLNKYNTRYDWNVCINTYQSAFK---GLNTRLHDML---EFRTYMFLNVFEY
210 220 230 240 250

Cry1Ac VS---LFPN-----YDSRTYPIRTVSQLTREIYTNVLENFDGSPFRGSAQGIIEG
250 260 270 280 290

gi|155 VSIWLSFKYQSLLVSSGANLYASGSGPQRTQSFTSQDW---PFLYSL---FRVNSNYVLN
260 270 280 290 300 310

Cry1Ac SIRSPHLMIDILNSITITYDAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQR
300 310 320 330 340 350

gi|155 GFSGARLSNTFPNIVGLPGST-----TTHALLAARVNYSGGISS---GDIG-ASP---
320 330 340 350

Cry1Ac IVAQLGQGVYRT--LSSTLYRRPFNIGINNQQ--SVLDGTEFAYGTSSNLPASVYRKSQTV
360 370 380 390 400 410

gi|155 FSQNFNCSTFTPLLPFVRSWLDGRDREGVATVTNWQTESFETTLGLRSGAFTARGNS
360 370 380 390 400 410

Cry1Ac DSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFN
420 430 440 450 460 470

gi|155 NYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS--VHNRK--N
420 430 440 450 460 470

Cry1Ac NIIASDSITQIPAVKGNFLFNGSVIS--GPG--FTGGDLVRLNSSGNNIQRNGYIEVP----
470 480 490 500 510 520

gi|155 NIHAVHE-----NGSMIHLAPNDHTGFTISP IHATQVNNQTRTFISEKFGNQ
480 490 500 510 520

Cry1Ac ---IHFPS--TSTRYRVRVRYASVTPIHNLVN--WGNSSIFS--NTVPATATSLDNLQSSD
530 540 550 560 570

gi|155 GDSLRFEQNYTTARYTLRGNNGNSYN--LYLRVSSIGNSTIRVTINGRVYTATNVNTTTNND
530 540 550 560 570

Cry1Ac FGYYFESANAFTS--SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNAL
580 590 600 610 620 630

gi|155 -GVNNGGARFSDINIGNVVASNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
580 590 600 610 620 630

>>gi|155097692|gb|ABT00623.1| Sequence 214 from patent U (634 aa)
initn: 128 init1: 128 opt: 231 Z-score: 265.2 bits: 60.2 E(): 7.5e-06
Smith-Waterman score: 255; 22.712% identity (52.542% similar) in 590 aa overlap
(81-637:95-629)

Cry1Ac LSEFVPGAGFVLGLVDIIWIGIFGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLLEGLSNL
60 70 80 90 100 110

gi|155 KVGSLVGRILSELRLIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---
70 80 90 100 110 120

Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
120 130 140 150 160

gi|155 -QASVEEFNRQVDNFLNPNRNNAVPLSVTSSVNTMQQLFLNRLPQFQLRGHQLLLLPLFAQ
130 140 150 160 170 180

Cry1Ac AANLHLSVLRDVSVFGQWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
170 180 190 200 210 220

gi|155 AANLHLSFIRDVILNADEWGISAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
190 200 210 220 230

Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNVLENFDGSR
230 240 250 260 270 280

gi|155 RLHDML---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFT
240 250 260 270 280 290

Cry1Ac GSAQGIIEGSIRSPHLMIDILNSITITYDAHRGEYY-----WSGHQIMASPVGFSGPE
290 300 310 320 330

gi|155 SQDWPFYLSLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGGV
300 310 320 330 340

Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQ--SVLDGTEFAYG
340 350 360 370 380 390

gi|155 SS---GDIGASPFNQFSCST---FLPPLLTPFVRSWLDGSDRGGVNTVTNWQTESFE
350 360 370 380 390 400

Cry1Ac TSSNLPASVYRKSQTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SI
400 410 420 430 440 450

gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
410 420 430 440 450 460

Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS--GP--GFTGGDLVRLNSSG
460 470 480 490 500

gi|155 ARAYMVS--VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISP IHATQ
470 480 490 500

Cry1Ac NNIQRNGYIEVP-----IHFPS--TSTRYRVRVRYASVTPIHNLVN--WGNSSIFS--NT
510 520 530 540 550

gi|155 ANNQTRTFISEKFGNQDLSLRFQSNNTARYTLRGNNGNSYNLYLRVSSIGNSTIRVTING
510 520 530 540 550 560

Cry1Ac VPATATSLDNLQSSDFGFESANAFTS--SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
560 570 580 590 600 610

gi|155 RVYTATNVNTTTNND--GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
570 580 590 600 610

Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVK
620 630 640 650 660 670

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..... : : : :
gi|155 TQFDL-----MNIMFVPTNLPLLY
    620          630

>>gi|155097587|gb|ABT00518.1| Sequence 4 from patent US (634 aa)
  initn: 140 initl: 140 opt: 230 Z-score: 264.0 bits: 60.0 E(): 8.7e-06
Smith-Waterman score: 246; 22.542% identity (52.203% similar) in 590 aa overlap
(81-637:95-629)

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          60          70          80          90          100          110
Cry1Ac LSEFVPGAGFVGLVDIIWGIFGPGSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNL
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 KVGSLVGRKRLSELRLSIFPSGSTNLMQDILRETEKFLNQLRNLDTLARVNAELTGL---
          70          80          90          100          110          120

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          120          130          140          150          160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 -QANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFLNRLTQFQMCGYQLLLPLFAQ
          130          140          150          160          170          180

```

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          170          180          190          200          210          220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQSAFR---GLNT
          190          200          210          220          230

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          230          240          250          260          270          280
Cry1Ac R--DWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSR
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RLHDM---EFRTYMFNLFVYVSIWLSLFKYQSLLVSSGANL---YASGSGPQQTQSF
          240          250          260          270          280          290

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          290          300          310          320          330
Cry1Ac GSAQGIEGSIRSPHLMILNSITTYDAHRGEYY-----WSGHQIMASPVGFSGPE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SQDWPFLYSLFQVNSNYVLNG---FSGARLSQTFPNIVGLPGTTTTHALLAARVNYSGV
          300          310          320          330          340

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```

          340          350          360          370          380          390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQL--SVLDGTEFAYG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SS---GDIGASPFQNFSCST---FLPPLLTPFVRSWLDGSDRGGVATVTINWQTESFE
          350          360          370          380          390          400

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          400          410          420          430          440          450
Cry1Ac TSSNLPSAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFSHRLSHVSMFRSGFSNSSV--SI
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
          410          420          430          440          450          460

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          460          470          480          490          500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS--GP-GFTGGDLVRLNSSG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 ARAYMVS--VHNRK--NNIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
          470          480          490          500

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          510          520          530          540          550
Cry1Ac NNIQNRGYIEVP-----IHFPSTSTRYRVRVYASVT--PIHLNVN--WGNSSIFS--NT

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: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VNNQTRTFISEKFGNQDGLRFEQSNNTARYTLRGNNGNSYNYLVRVSSIGNSTIRVTING
    510          520          530          540          550          560

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          560          570          580          590          600          610
Cry1Ac VPATATSLDNLQSSDFGFESANAFTS--SLGNIVGVRNFSGTAGVIIDRFEPVVTATLE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 RVYTASNVTNTTND--GVNDNGARFSDINIGNVVA---SDNSNVPLD---INVTLNSG
          570          580          590          600          610

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          620          630          640          650          660          670
Cry1Ac AEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TQFEL-----MNIMFVPTNLPLLY
    620          630

```

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>>gi|155097598|gb|ABT00529.1| Sequence 26 from patent US (634 aa)
  initn: 133 initl: 133 opt: 230 Z-score: 264.0 bits: 60.0 E(): 8.7e-06
Smith-Waterman score: 245; 22.260% identity (52.911% similar) in 584 aa overlap
(45-595:57-601)

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```

          20          30          40          50          60          70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVGLVDIIWGIF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FQHKSLDVTQREWEWKNNHSLYLDPIVGTVASFLKKGVGLVGRKRLSELRLNLFPSG
          30          40          50          60          70          80

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          80          90          100          110          120          130
Cry1Ac GPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEADPTNPALRE
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 STNLMQDILRETEKFLNQLRNLDTLARVNAELTGL---QANVEEFNRQVDNLFNPN--RN
          90          100          110          120          130          140

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          140          150          160          170          180
Cry1Ac EMRIQF---NDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 TVPLSITSSVNTMQQLFLNRLPQFQMCGYQLLLPLFAQAANLHLSFIRDVILNADEWGI
          150          160          170          180          190          200

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```

          190          200          210          220          230          240
Cry1Ac DAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTTLTVLD
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SAATLRTYRDYLNKNYTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFNLFV
          210          220          230          240          250

```

```

          250          260          270          280          290          300
Cry1Ac IVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIEGSIRSPHLMILNS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 YVSIWLSLFKYQSLLVSSGANL---YARGSGPQQTQSFQSDWPFLYSLFQVNSNYVLNG
          260          270          280          290          300          310

```

```

          310          320          330          340          350          360
Cry1Ac IT-----IYDHAHRGEYYWSGHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQ
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FSGARLSNTPNIVGLPGSTTTTHALLAARVNYSGGISS---GDIGASPFNQNFNCST--
          320          330          340          350          360

```

```

          370          380          390          400          410
Cry1Ac GYVRTLSSTLYRRPFNIGINNQL--SVLDGTEFAYGTSSNLPSAVYRKSGTVDSLDEIPP

```

```

      : . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|155 -FLPPLLTPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYPPDYFI
      370      380      390      400      410      420

```

```

      420      430      440      450      460      470
Cry1Ac QN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSI
      . : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|155 RNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVHE-
      430      440      450      460      470      480

```

```

      480      490      500      510      520
Cry1Ac TQIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNNIQNRGYIEVP-----IHFPS
      : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|155 -----NGSMIHLAPNDYTGFITISPIHATQVNNQTRTFISEKFGNQDGLRFEQ
      : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

      530      540      550      560      570      580
Cry1Ac TSTRYRVRVRYASVT-PIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
      . : . : . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|155 TMTTARYTLRGNNGNSYNLYLRVSSLGNSTIRVTINGRVYATNVNNTTND--GVNDNGAR
      530      540      550      560      570      580

```

```

      590      600      610      620      630      640
Cry1Ac FTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : . . . . . :

```

```

gi|155 FSDINIGTVVASSNSDVPDLINVTFNSGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630

```

>>gi|53970013|gb|AAV19106.1| Sequence 9 from patent US 6 (136 aa)  
 initn: 211 initl: 93 opt: 221 Z-score: 263.4 bits: 57.6 E(): 9.5e-06  
 Smith-Waterman score: 221; 34.507% identity (66.197% similar) in 142 aa overlap  
 (495-633:1-136)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|539          PGFTGGDILR-RTDGGXV---GTIRANVNA
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPHILNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|539 PLTQ-QYRIRRLRYASTTSFVVNL-FVNNSAAGFTLPSTMAQNGSLTXESFNTLEVTHXIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|539 FSQSDTTLRLNIFPISIGQXVYVDKXEIVPXNPTREAEEDLEDXKKAVALSLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|16240157|gb|AAE79612.1| Sequence 9 from patent US 6 (136 aa)  
 initn: 211 initl: 93 opt: 221 Z-score: 263.4 bits: 57.6 E(): 9.5e-06  
 Smith-Waterman score: 221; 34.507% identity (66.197% similar) in 142 aa overlap  
 (495-633:1-136)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|162          PGFTGGDILR-RTDGGXV---GTIRANVNA
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPHILNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|162 PLTQ-QYRIRRLRYASTTSFVVNL-FVNNSAAGFTLPSTMAQNGSLTXESFNTLEVTHXIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|162 FSQSDTTLRLNIFPISIGQXVYVDKXEIVPXNPTREAEEDLEDXKKAVALSLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|21504386|gb|AAM57089.1| Sequence 9 from patent US 6 (136 aa)  
 initn: 211 initl: 93 opt: 221 Z-score: 263.4 bits: 57.6 E(): 9.5e-06  
 Smith-Waterman score: 221; 34.507% identity (66.197% similar) in 142 aa overlap  
 (495-633:1-136)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|215          PGFTGGDILR-RTDGGXV---GTIRANVNA
                        10          20

```

```

      530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPHILNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      : . . . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|215 PLTQ-QYRIRRLRYASTTSFVVNL-FVNNSAAGFTLPSTMAQNGSLTXESFNTLEVTHXIR
      30      40      50      60      70      80

```

```

      590      600      610      620      630      640
Cry1Ac SSLGNIVGVRN-FSGTAG--VIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      : . . . : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|215 FSQSDTTLRLNIFPISIGQXVYVDKXEIVPXNPTREAEEDLEDXKKAVALSLF
      90      100      110      120      130

```

```

      650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|33731230|gb|AAQ37293.1| Sequence 9 from patent US 6 (136 aa)  
 initn: 211 initl: 93 opt: 221 Z-score: 263.4 bits: 57.6 E(): 9.5e-06  
 Smith-Waterman score: 221; 34.507% identity (66.197% similar) in 142 aa overlap  
 (495-633:1-136)

```

      470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      : . . . . . : . . . . . : . . . . . : . . . . .

```

```

gi|337          PGFTGGDILR-RTDGGXV---GTIRANVNA
                        10          20

```

```

      530      540      550      560      570      580

```



>>gi|155097711|gb|ABT00642.1| Sequence 252 from patent U (634 aa)
initn: 128 init1: 128 opt: 228 Z-score: 261.7 bits: 59.5 E(): 1.2e-05
Smith-Waterman score: 248; 23.077% identity (52.381% similar) in 546 aa overlap
(81-595:95-601)

60 70 80 90 100 110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIIRLEGLSNL
gi|155 KVGSLVGRKILSELRSIFPSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---

120 130 140 150 160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNLLNPNRNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLLAQ

170 180 190 200 210 220
Cry1Ac AANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDVILNADEWGISAAATLRTYRDYLRNYTRDYSNYCINTYQSFAK---GLNT

230 240 250 260 270 280
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSFR
gi|155 RLHDTL---EFRTYMFLNVFEYVSIWSLFKYQSLLVSSGANL----YASGSGPQQTQSFT

290 300 310 320 330
Cry1Ac GSAQGIIEGSIIRSPHLMIDILNSIT-----IYTDahrgeyywsgHQIMASPVGFSGPEFTF
gi|155 SQDWPFlySLFQVNSNYVINGFSGARLSNTFPNIVGLPGSTTTHALLAARVNYSGGISS-

340 350 360 370 380 390
Cry1Ac PLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSS
gi|155 ---GDIGASPPFNQNFNCST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTL

400 410 420 430 440 450
Cry1Ac NLPsAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFShRLSHVSMFRSGFSNSSV-SIIRA
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARA

460 470 480 490 500 510
Cry1Ac PMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNI
gi|155 YMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTISP IHATQVNN

520 530 540 550 560
Cry1Ac QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPIHLLNVN-WGNSSIFS--NTVP
gi|155 QTRTFISEKFGNQDGLRFEQNNTTARYTLRGNNGSYN-LYLRVSSIGNSTIRVTINGRV

570 580 590 600 610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVNRVNSGTAGVIIDRFEFIPVTATLEAE
gi|155 YTATNVNTTTTND-GVNDNGARFSDINIGNVNVASSNSDVLINVTLSNGTQFDLMNIML
570 580 590 600 610 620
620 630 640 650 660 670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA
gi|155 VPTNISPLY
630

>>gi|155097643|gb|ABT00574.1| Sequence 116 from patent U (634 aa)
initn: 128 init1: 128 opt: 227 Z-score: 260.5 bits: 59.3 E(): 1.4e-05
Smith-Waterman score: 247; 22.894% identity (52.564% similar) in 546 aa overlap
(81-595:95-601)

60 70 80 90 100 110
Cry1Ac LSEFVPGAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAIIRLEGLSNL
gi|155 KVGSLVGRKILSELRSIFPSGSTNLMQDILRETERFLNQLRNTDTLARVNAELTGL---

120 130 140 150 160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
gi|155 -QANVEEFNRQVDNLLNPNRNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQ

170 180 190 200 210 220
Cry1Ac AANLHLSVLRDVSFVGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDS
gi|155 AANLHLSFIRDAILNADEWGISAAATLRTYQDYLNKYNTRDYSNYCISTYQSFAK---GLNT

230 240 250 260 270 280
Cry1Ac R--DWIRYNQFRRELTLTVLDIVSLFPPNYDSRTYPIRTVSQTLTREIYTNPVLENFDGSFR
gi|155 RLHDTL---EFRTYMFLNVFEYVSIWSLFKYQSLLVSSGANL----YASGSGPQQTQSFT

290 300 310 320 330
Cry1Ac GSAQGIIEGSIIRSPHLMIDILNSIT-----IYTDahrgeyywsgHQIMASPVGFSGPEFTF
gi|155 SQDWPFlySLFQVNSNYVINGFSGARLSNTFPNIVGLPGSATTHALLAARVNYSGGISS-

340 350 360 370 380 390
Cry1Ac PLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSS
gi|155 ---GDIGASPPFNQNFNCST---FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTL

400 410 420 430 440 450
Cry1Ac NLPsAVYRKSGTVDSLDEIPPQN--NNVP--PRQGFShRLSHVSMFRSGFSNSSV-SIIRA
gi|155 GLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARA

```

460      470      480      490      500      510
Cry1Ac PMFSWIHRSAEFNNIIASDSITQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNI
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |155 YMVS-VHNRK--NNIHAVHE-----NGSMIHLAPNDYTGFTISPIHATQVNN
      470      480      490      500

```

```

520      530      540      550      560
Cry1Ac QNRGYIEVP-----IHFP--STSTRYRVRVRYASVTPIHNLNVN-WGNSSIFS--NTVP
: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |155 QTRTFISEKFGNQGDSLRFQNNNTARYTLRGNNGNSYN-LYLRVSSIGNSTIRVTINGRV
510      520      530      540      550      560

```

```

570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAE
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |155 YTATNVNNTTTNND-GVNDNGARFSDINIGNVVASSNSDVPLDINVTLNLSGTQFDLNMIML
570      580      590      600      610      620

```

```

620      630      640      650      660      670
Cry1Ac YNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHA

```

```

gi |155 VPTNISPLY
      630

```

```

>>gi|21504410|gb|AAM57107.1| Sequence 45 from patent US (137 aa)
  initn: 170 initl: 126 opt: 218 Z-score: 259.8 bits: 57.0 E(): 1.5e-05
Smith-Waterman score: 218; 35.714% identity (64.286% similar) in 140 aa overlap
(497-633:3-137)

```

```

470      480      490      500      510      520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |215          QXLSGGDVIRRTNTG---GFGAIRVSVTGPL
                        10      20

```

```

530      540      550      560      570      580
Cry1Ac TSTRYRVRVRYASVTPIHNLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |215 TQ-RYRIRFRYASTIDDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNFT
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |215 QSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKAVASLF
90      100      110      120      130

```

```

650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER

```

```

>>gi|53970031|gb|AAV19124.1| Sequence 45 from patent US (137 aa)
  initn: 170 initl: 126 opt: 218 Z-score: 259.8 bits: 57.0 E(): 1.5e-05
Smith-Waterman score: 218; 35.714% identity (64.286% similar) in 140 aa overlap
(497-633:3-137)

```

```

470      480      490      500      510      520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |539          QXLSGGDVIRRTNTG---GFGAIRVSVTGPL
                        10      20

```

```

10      20
Cry1Ac TSTRYRVRVRYASVTPIHNLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |539 TQ-RYRIRFRYASTIDDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNFT
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |539 QSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKAVASLF
90      100      110      120      130

```

```

650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER

```

```

>>gi|33731248|gb|AAQ37311.1| Sequence 45 from patent US (137 aa)
  initn: 170 initl: 126 opt: 218 Z-score: 259.8 bits: 57.0 E(): 1.5e-05
Smith-Waterman score: 218; 35.714% identity (64.286% similar) in 140 aa overlap
(497-633:3-137)

```

```

470      480      490      500      510      520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |337          QXLSGGDVIRRTNTG---GFGAIRVSVTGPL
                        10      20

```

```

530      540      550      560      570      580
Cry1Ac TSTRYRVRVRYASVTPIHNLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |337 TQ-RYRIRFRYASTIDDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNFT
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |337 QSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEEDLEAAKAVASLF
90      100      110      120      130

```

```

650      660      670      680      690      700
Cry1Ac NVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER

```

```

>>gi|16240182|gb|AAE79630.1| Sequence 45 from patent US (137 aa)
  initn: 170 initl: 126 opt: 218 Z-score: 259.8 bits: 57.0 E(): 1.5e-05
Smith-Waterman score: 218; 35.714% identity (64.286% similar) in 140 aa overlap
(497-633:3-137)

```

```

470      480      490      500      510      520
Cry1Ac NNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |162          QXLSGGDVIRRTNTG---GFGAIRVSVTGPL
                        10      20

```

```

530      540      550      560      570      580
Cry1Ac TSTRYRVRVRYASVTPIHNLNVNWNSSSI--FSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi |162 TQ-RYRIRFRYASTIDDFVTRGGTTINNFRFTRTMNRGQESRYESYRTVEFTTTPFNFT
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTSTNQLGLKT
.: : .....: : : .....: : : : : : : : : : : : : : : : : : : : : : : :
gi|162  QSQDIIRTSIQGLSGNGEVYLDRIEIIIPVNPTRAEAEEDLEAAKKAVALSF
90      100      110      120      130

650      660      670      680      690      700
Cry1Ac NVDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPER

```

```

>>gi|155097682|gb|ABT00613.1| Sequence 194 from patent U (634 aa)
  initn: 128 init1: 128 opt: 226 Z-score: 259.3 bits: 59.1 E(): 1.6e-05
Smith-Waterman score: 240; 22.445% identity (52.372% similar) in 548 aa overlap
(81-595:95-601)

```

```

60      70      80      90      100      110
Cry1Ac LSEFVPGAGFVLGLVDIIGWIFGPSQWDAFLVQIEQLINQRIIEFARNQAIISRLEGLSNL
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  KVGSLVGRKRLSELRLIFPSPGSTNMQDILRETEKFLNQRNLADTLARVNAELTGL---
70      80      90      100      110      120

```

```

120      130      140      150      160
Cry1Ac YQIYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQ
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  -QANVEEFNRQVDNPLNPNRNAVPLSITSSVNMQQFLNRLPQQLRDPQLLLPLFAQ
130      140      150      160      170      180

```

```

170      180      190      200      210      220
Cry1Ac AANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERWVGPD
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  AANLHLSPIRDVILNADEWGISAAATLRTYRNHLRNYTRDYSNYCINTYQTAFR---GLNT
190      200      210      220      230

```

```

230      240      250      260      270      280
Cry1Ac R--DWIRYQFRRELTLTVLVDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSR
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RLHDM---EFRTYMFLNVFEYVSIWSLFKYQSLLVSSGANL---YASGSGPQQTQSFT
240      250      260      270      280      290

```

```

290      300      310      320      330
Cry1Ac GSAQGIEGSIRSPHLMILNSITIIYTDahrgeyy-----WSGHQIMASPVGFSGPE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SQDWPFLYSLFQVNSNYVLNG--FSGARLSQTFPNVGLPGTTTTHALLAARVNYSGGV
300      310      320      330      340

```

```

340      350      360      370      380      390
Cry1Ac FTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSTLYRRPFNIGINNOQL-SVLDGTGEFAYG
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  SS---GDIGASPFNQNFSCST---FLPPLLPFVRSWLDGSDRGVNTVNWQTESFE
350      360      370      380      390      400

```

```

400      410      420      430      440      450
Cry1Ac TSSNLPSAVYRKSQIVDSLDEIPPQN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SI
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  TTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRPLHYNQIRNIESPSGTPGG
410      420      430      440      450      460

```

```

460      470      480      490      500
Cry1Ac IRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVIS-GP-GFTGGDLVRLNSSG

```

```

.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  ARAYMVS-VHNRK--NDIYAVHE-----NGTMIHLAPEDYTGFTISPIHATQ
470      480      490      500

```

```

510      520      530      540      550
Cry1Ac NNIQNRYIEVP-----IHFPSTSTRYRVRYASVT-PIHLNVN-WGNSSIFS--NT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  VNNQTRTFISEKFGNQGDSLRFEQSNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTING
510      520      530      540      550      560

```

```

560      570      580      590      600      610
Cry1Ac VPATATSLDNLQSSDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLE
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155  RVYATNVNTTTNND-GVNDNGARFSDINIGNVVASDNSNVPDLINVALNSGTQFDLMNV
570      580      590      600      610      620

```

```

620      630      640      650      660      670
Cry1Ac AEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVK
gi|155  MFVPTNLPPLY
630

```

```

>>gi|16240191|gb|AAE79637.1| Sequence 59 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  PGFXGGGILRRRTTNGT---FGTLRVTVNS
10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRYASVTPIHLNVNNGNSSI---FSNTVP-ATATSLDNLQSSDFGYFES
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFGSTMNRQQLTYESFVTFEFTNQ
30      40      50      60      70      80

```

```

580      590      600      610      620      630
Cry1Ac --ANAFITSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAKAVNALFTST
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|162  DLFFFTQAQENLTLAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKKAVALSF
90      100      110      120      130      140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

```

>>gi|33731255|gb|AAQ37318.1| Sequence 59 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRNGYIEVPIHF
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337  PGFXGGGILRRRTTNGT---FGTLRVTVNS
10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWGNSSI----FSNTVP-ATATSLDNLQSSDFGYFES
: . : : : : : : : : . . . . : : : : : : : : : : : : : : : : : : : :
gi|337 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80

```

```

580      590      600      610      620      630
Cry1Ac --ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|337 DLPFTTQAQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKAVASLF
90      100     110     120     130     140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

```

>>gi|53970038|gb|AAV19131.1| Sequence 59 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|539 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80
          PGFXGGGILRRRTTNGT---FGLTRVTVNS
          10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWGNSSI----FSNTVP-ATATSLDNLQSSDFGYFES
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|539 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80

```

```

580      590      600      610      620      630
Cry1Ac --ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|539 DLPFTTQAQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKAVASLF
90      100     110     120     130     140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

```

>>gi|33731241|gb|AAQ37304.1| Sequence 31 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|337 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80
          PGFXGGGILRRRTTNGT---FGLTRVTVNS
          10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWGNSSI----FSNTVP-ATATSLDNLQSSDFGYFES
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|337 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80

```

```

580      590      600      610      620      630

```

```

Cry1Ac --ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|337 DLPFTTQAQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKAVASLF
90      100     110     120     130     140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

```

>>gi|21504419|gb|AAM57114.1| Sequence 59 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|215 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80
          PGFXGGGILRRRTTNGT---FGLTRVTVNS
          10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWGNSSI----FSNTVP-ATATSLDNLQSSDFGYFES
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|215 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80

```

```

580      590      600      610      620      630
Cry1Ac --ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|215 DLPFTTQAQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKAVASLF
90      100     110     120     130     140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

```

>>gi|16240174|gb|AAE79623.1| Sequence 31 from patent US (142 aa)
  initn: 214 init1: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

```

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|162 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80
          PGFXGGGILRRRTTNGT---FGLTRVTVNS
          10      20

```

```

530      540      550      560      570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWGNSSI----FSNTVP-ATATSLDNLQSSDFGYFES
: . : : : : : : : . . . . : : : : : . . . . : . . . . :
gi|162 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMMNRGQELTYESFVTSEFTTNQS
30      40      50      60      70      80

```

```

580      590      600      610      620      630
Cry1Ac --ANAFTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
: . . . . : . . . . : . . . . : . . . . : . . . . : . . . . :
gi|162 DLPFTTQAQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKAVASLF
90      100     110     120     130     140

```

```

640      650      660      670      680      690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKD

```

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>>gi|53970024|gb|AAV19117.1| Sequence 31 from patent US (142 aa)
initn: 214 initl: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|539 PGFXGGGILRRTTNGT---FGTLRVTVNS
10 20

530 540 550 560 570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI---FSNTVP-ATATSLDNLQSSDFGYFES
gi|539 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMNRRGQELTYESFVTSEFTTNQS
30 40 50 60 70 80

580 590 600 610 620 630
Cry1Ac --ANAFSTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
gi|539 DLPFTTQAEQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKKAVALSLF
90 100 110 120 130 140

640 650 660 670 680 690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKD

>>gi|21504400|gb|AAM57100.1| Sequence 31 from patent US (142 aa)
initn: 214 initl: 104 opt: 216 Z-score: 257.2 bits: 56.5 E(): 2.1e-05
Smith-Waterman score: 216; 34.694% identity (65.306% similar) in 147 aa overlap
(495-633:1-142)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|215 PGFXGGGILRRTTNGT---FGTLRVTVNS
10 20

530 540 550 560 570
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSSI---FSNTVP-ATATSLDNLQSSDFGYFES
gi|215 PLTQ-RYRVRVRFASSGNFSIRILRGNTSIAYQRFSTMNRRGQELTYESFVTSEFTTNQS
30 40 50 60 70 80

580 590 600 610 620 630
Cry1Ac --ANAFSTSSLGNI-VGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTST
gi|215 DLPFTTQAEQENLTILAEGVSTGSEYFIDRIEIIIPVNPAREAEEDLEAAKKAVALSLF
90 100 110 120 130 140

640 650 660 670 680 690
Cry1Ac NQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKD

>>gi|112088035|gb|ABI06950.1| Sequence 16 from patent US (132 aa)
initn: 198 initl: 115 opt: 215 Z-score: 256.5 bits: 56.3 E(): 2.3e-05
Smith-Waterman score: 215; 38.017% identity (66.116% similar) in 121 aa overlap
(511-628:14-132)

490 500 510 520 530 540

Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|112 RTRFYRWDILRRITNVGSGFGDMRVNITAP-LSQRYRVRIRYAST
10 20 30 40

550 560 570 580 590
Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANAFSTSSLGNI-VGVRNFS
gi|112 TDLQFFTRINGTSVNGQNFQRTMNRGGNLESGNFRTAGFSTPFSFFKCAKYIHIGYSGFS
50 60 70 80 90 100

600 610 620 630 640 650
Cry1Ac GTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLV
gi|112 NQE-VYIDRIEFVPAEVTFEAESDLERAQKA
110 120 130

660 670 680 690 700 710
Cry1Ac TYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD

>>gi|33765718|gb|AAQ52369.1| Sequence 16 from patent US (132 aa)
initn: 198 initl: 115 opt: 215 Z-score: 256.5 bits: 56.3 E(): 2.3e-05
Smith-Waterman score: 215; 38.017% identity (66.116% similar) in 121 aa overlap
(511-628:14-132)

490 500 510 520 530 540
Cry1Ac VKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASV
gi|337 RTRFYRWDILRRITNVGSGFGDMRVNITAP-LSQRYRVRIRYAST
10 20 30 40

550 560 570 580 590
Cry1Ac TPIHLNVNWNSSIFSNTPATATSLDNLQSSDF--GYFESANAFSTSSLGNI-VGVRNFS
gi|337 TDLQFFTRINGTSVNGQNFQRTMNRGGNLESGNFRTAGFSTPFSFFKCAKYIHIGYSGFS
50 60 70 80 90 100

600 610 620 630 640 650
Cry1Ac GTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLV
gi|337 NQE-VYIDRIEFVPAEVTFEAESDLERAQKA
110 120 130

660 670 680 690 700 710
Cry1Ac TYLSDEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGD

>>gi|155097681|gb|ABT00612.1| Sequence 192 from patent U (634 aa)
initn: 130 initl: 130 opt: 222 Z-score: 254.6 bits: 58.2 E(): 2.9e-05
Smith-Waterman score: 246; 22.564% identity (52.479% similar) in 585 aa overlap
(45-595:57-601)

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VPGAGFVLGLVDIIGWIF
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKVGLVGVKRIKLSLIFPSPG
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLNQRIEEFARNQAI SRLEGLSNLYQIYAESFREWEADPTNP---A

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gi|155 STNLMQGIILRETEKFLNQLRNTDTLARVNAELTGL---QANVEFENRQVDNFLNPNRNA
90 100 110 120 130 140

Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGF
130 140 150 160 170 180

gi|155 VPLSITSSVNTMQQLFLNRLPQFQMRGYQSLLLPLFAQAANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200

Cry1Ac AATINSRYNDLRLIGNYTDHAVRWY-----NTGLERVWGPDSRDWIRYNQFRRELTL
190 200 210 220 230 240

gi|155 AATLRTYQDYLRNYTRDYSNYCINTYQSAFKGLNTGLHDTL--EFRTYMFLNVFEYVSIW
210 220 230 240 250 260

Cry1Ac TVLDIVSLFPNYSRTYPIRTVSQLTREIYTN--PVLENFDGSGFRGSAQGIEGSIRSPHL
250 260 270 280 290 300

gi|155 SLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSL---FQVNSNYVLNGFSGARL
270 280 290 300 310

Cry1Ac MDILNSITIIYTDahrgeyywsgHQIMASPVGFSGPEFTFPLYGTMGNAAPQQRIVAVLQGLQ
310 320 330 340 350 360

gi|155 SNTFPNIWGLPGST-----TTHALLAARVNYSGGISS---GDIGASPFNQNFNCST--
320 330 340 350 360

Cry1Ac GVYRTLSTLYRRPFIININQQL-SVLDGTEFAYGTSSNLPSAVYRKSQVDSLDEIPP
370 380 390 400 410

gi|155 -FLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAFTARGNSNYFPDYFI
370 380 390 400 410 420

Cry1Ac QN-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSI
420 430 440 450 460 470

gi|155 RNISGVPLVVRNEDLRRPLHYNEIRNIIASPSGTPGGARAYMVS--VHNK--NNIHAVHE-
430 440 450 460 470 480

Cry1Ac TQIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP-
480 490 500 510 520

gi|155 -----NGSMIHLAPNDYTGFTTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
490 500 510 520

Cry1Ac -STSTRYRVRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESAN
530 540 550 560 570 580

gi|155 NNTTARYTLRGNNSYN-LYLRVSSIGNSTIRVTINGRAYTATNVNTTTNND-GVNDNGA
530 540 550 560 570 580

Cry1Ac AFTS-SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLG
590 600 610 620 630 640

gi|155 RFSNDINIGNVAVSSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630

>>gi|16240177|gb|AAE79625.1| Sequence 35 from patent US (137 aa)

initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
470 480 490 500 510 520

gi|162 PGFTGGDILRRTGVGT---FGTIRVRTTA
10 20

Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
530 540 550 560 570 580

gi|162 PLTQ-RYRIRFRFASTTNLFIGIRVGDRQVNYFDFGRTMNRGDELRYESFATREFTTDFN
30 40 50 60 70 80

Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|162 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
650 660 670 680 690 700

>>gi|16240179|gb|AAE79627.1| Sequence 39 from patent US (137 aa)
initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
470 480 490 500 510 520

gi|162 PGFTGGDILRRTGVGT---FGTIRVRTTA
10 20

Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
530 540 550 560 570 580

gi|162 PLTQ-RYRIRFRFASTTNLFIGIRVGDRQVNYFDFGRTMNRGDELRYESFATREFTTDFN
30 40 50 60 70 80

Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
590 600 610 620 630 640

gi|162 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP
650 660 670 680 690 700

>>gi|53970034|gb|AAV19127.1| Sequence 51 from patent US (137 aa)
initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQRGYIEVPIHF
470 480 490 500 510 520

gi|539 PGFTGGDILRRRTGVGT---FGTIRVRTTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTP...
gi|539 PLTQ-RYRIRFRFASTTNL...
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac -SSLGNIVGV--RNFSGTAGVI...
gi|539 FRQPQELISVFANAFSAGQ...
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLS...
KTNVTDYHIDQVSNLVTYLSDEFCLDEKRE...

>>gi|33731251|gb|AAQ37314.1| Sequence 51 from patent US (137 aa)
initn: 214 init1: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFL...
gi|337 PGFTGGDILRRRTGVGT---FGTIRVRTTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTP...
gi|337 PLTQ-RYRIRFRFASTTNL...
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac -SSLGNIVGV--RNFSGTAGVI...
gi|337 FRQPQELISVFANAFSAGQ...
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLS...
KTNVTDYHIDQVSNLVTYLSDEFCLDEKRE...

>>gi|21504406|gb|AAM57104.1| Sequence 39 from patent US (137 aa)
initn: 214 init1: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFL...
gi|215 PGFTGGDILRRRTGVGT---FGTIRVRTTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTP...
gi|215 PLTQ-RYRIRFRFASTTNL...
30 40 50 60 70 80

30 40 50 60 70 80
590 600 610 620 630 640
Cry1Ac -SSLGNIVGV--RNFSGTAGVI...
gi|215 FRQPQELISVFANAFSAGQ...
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLS...
KTNVTDYHIDQVSNLVTYLSDEFCLDEKRE...

>>gi|53970028|gb|AAV19121.1| Sequence 39 from patent US (137 aa)
initn: 214 init1: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFL...
gi|539 PGFTGGDILRRRTGVGT---FGTIRVRTTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTP...
gi|539 PLTQ-RYRIRFRFASTTNL...
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac -SSLGNIVGV--RNFSGTAGVI...
gi|539 FRQPQELISVFANAFSAGQ...
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLS...
KTNVTDYHIDQVSNLVTYLSDEFCLDEKRE...

>>gi|53970026|gb|AAV19119.1| Sequence 35 from patent US (137 aa)
initn: 214 init1: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFL...
gi|539 PGFTGGDILRRRTGVGT---FGTIRVRTTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTP...
gi|539 PLTQ-RYRIRFRFASTTNL...
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac -SSLGNIVGV--RNFSGTAGVI...
gi|539 FRQPQELISVFANAFSAGQ...
90 100 110 120 130

```

        650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504414|gb|AAM57110.1| Sequence 51 from patent US (137 aa)
  initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

        470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : : : : : . . . . . : : : : : . . . . . : : : : :
gi|215          PGFTGGDILRRTGVGT---FGTIRVRTTA
                        10                20

```

```

        530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|215 PLTQ-RYRIRFRFASTTNLFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
      30        40        50        60        70        80

```

```

        590      600      610      620      630      640
Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|215 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
      90        100       110       120       130

```

```

        650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|16240186|gb|AAE79633.1| Sequence 51 from patent US (137 aa)
  initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

        470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|162          PGFTGGDILRRTGVGT---FGTIRVRTTA
                        10                20

```

```

        530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 PLTQ-RYRIRFRFASTTNLFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
      30        40        50        60        70        80

```

```

        590      600      610      620      630      640
Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|162 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
      90        100       110       120       130

```

```

        650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731245|gb|AAQ37308.1| Sequence 39 from patent US (137 aa)
  initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05

```

```

Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

        470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|337          PGFTGGDILRRTGVGT---FGTIRVRTTA
                        10                20

```

```

        530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 PLTQ-RYRIRFRFASTTNLFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
      30        40        50        60        70        80

```

```

        590      600      610      620      630      640
Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|337 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
      90        100       110       120       130

```

```

        650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504403|gb|AAM57102.1| Sequence 35 from patent US (137 aa)
  initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

        470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|215          PGFTGGDILRRTGVGT---FGTIRVRTTA
                        10                20

```

```

        530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNNGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|215 PLTQ-RYRIRFRFASTTNLFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
      30        40        50        60        70        80

```

```

        590      600      610      620      630      640
Cry1Ac -SSLGNIVGV--RNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGL
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|215 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
      90        100       110       120       130

```

```

        650      660      670      680      690      700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731243|gb|AAQ37306.1| Sequence 35 from patent US (137 aa)
  initn: 214 initl: 105 opt: 213 Z-score: 253.9 bits: 55.9 E(): 3.2e-05
Smith-Waterman score: 213; 34.507% identity (62.676% similar) in 142 aa overlap
(495-633:1-137)

```

```

        470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
      . . . . . : : . . . . . : . . . . . : . . . . . : . . . . .
gi|337          PGFTGGDILRRTGVGT---FGTIRVRTTA
                        10                20

```

```

                10          20
Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHNLNVNWNSSIFSNTPVATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 PLTQ-RYRIRFRFASTTNLFIGIRVGDROVNYFDGRTMNRGDELRYESFATRETTDFN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac --SSLGNIVGV--RNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDFECLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

```

>>gi|155097661|gb|ABT00592.1| Sequence 152 from patent U (633 aa)  
 initn: 125 initl: 125 opt: 221 Z-score: 253.4 bits: 58.0 E(): 3.4e-05  
 Smith-Waterman score: 237; 21.466% identity (54.276% similar) in 573 aa overlap  
 (45-595:57-600)

```

20 30 40 50 60 70
Cry1Ac IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLESE--VPGAGFVLGLVDIIWGIF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FQHKSLDVTQREWTEWKKNNHSLYLDPIVGTVASFLLKKGSLVKGKRLSELNLIFFPSG
30 40 50 60 70 80

80 90 100 110 120
Cry1Ac GPSQWDAFLVQIEQLINQRIEIEFARNQAIISRLEGLSNLYQIYAESFREWEADPTNP---A
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 STNLMQDILHETEKFLNQRNLNTDTWARVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140

130 140 150 160 170 180
Cry1Ac LREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQGRWGF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VPLSITSSVNTMQQLFLNRSPPQFMQGYQLLLLPLFAQAANMHLFSFIREVILNADEWGIS
150 160 170 180 190 200

190 200 210 220 230 240
Cry1Ac AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYNQFRRELTLTVLDI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 AATLRTRYRDYLNKYNTRDYSNYCINTYQSAFK---GLNTRLHDTL---EFRTYMFLNVFEY
210 220 230 240 250

250 260 270 280 290 300
Cry1Ac VSLFNPYDSRITYPIRTVSQLTREIYTNPVLENFDGSRGSAQIEGSIKIRPHLMDILNSI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 VSIWLSFKYQSLLVSSGANL---YASGSGPQQTQSFTSQDWPFLYSLFQVNSNYVNLG
260 270 280 290 300 310

310 320 330 340 350 360
Cry1Ac T-----IYTDHAHRGEYWSGHQIMASPVGFSGPEFTFLYGTMGNAAPQQRIVAQLGQG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SGARLSNTFFPNIGGLPGSTTHALLAARVNYSGGISS---GDIGASFPNQNFNCST---
320 330 340 350 360

370 380 390 400 410 420

```

```

Cry1Ac VYRTLSTLYRRPFNIGINNQQQL-SVLDGTEFAYGTSSNLPSAVYRKSQVTSVLDLDEIPPO
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 FLPPLLTFFVRSWLDGSDREGVATVTNWQTESFESTIGIRSFARTARGNSNYFFDYFIR
370 380 390 400 410 420

430 440 450 460 470
Cry1Ac N-NNVP--PRQGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWIHRSAEFNIIASDSIT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHAVHENGSMI
430 440 450 460 470 480

480 490 500 510 520 530
Cry1Ac QIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHFSTSTRYRVRV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 HL-APNG---YTGFTISPIHATQVNNTRTFIS-EKFGNQGD-SLRFEQNNTTARYTLRGN
490 500 510 520 530

540 550 560 570 580 590
Cry1Ac YASVTPIHNLVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANAFTS-SLGNIVG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 GNSYN-LYLRVSSIGNSTIRVTINGRVYTATNVNVTNND-GVNDNGARFSDINMGNVVA
540 550 560 570 580 590

600 610 620 630 640 650
Cry1Ac VRNFSGTAGVIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|155 SSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630

>>gi|40286|emb|CAA40536.1| CryIIC delta-endotoxin [Bacil (622 aa)
  initn: 153 initl: 118 opt: 217 Z-score: 248.8 bits: 57.1 E(): 6.1e-05
  Smith-Waterman score: 220; 22.704% identity (55.459% similar) in 577 aa overlap
  (85-637:98-617)

60 70 80 90 100 110
Cry1Ac VPGAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLINQRIEIEFARNQAIISRLEGL-SNLYQI
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 LVGKRLSELQNLIFPSSSIDLMQEIILRATEQFINQRNLADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120

120 130 140 150 160 170
Cry1Ac --YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 NRQVDNFLNPNQNPVPLAIDSV---NTLQQLFLSRLPQFQIQGYQLLLLPLFAQAANF
130 140 150 160 170 180

180 190 200 210 220
Cry1Ac HLSVLRDVSFVQGRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--D
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 NLSFIRGVILNADEWGISAAATVRYRDHLRKFHRDYSNYCINPYQTAFR---GLNHLR
190 200 210 220 230 240

230 240 250 260 270 280
Cry1Ac WIRYNQFRRELTLTVLDIVSLFNPYDSRITYPIRTVSQLTREIYTNPVLENFDGSRGSAQ
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|402 ML---EFRTYMFLNVFEYVSIWLSFKYQSLLVSSGANL---YAS-----GS--GPTQ
250 260 270 280

290 300 310 320 330 340

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Regulatory Product Characterization Team

Cry1Ac GIEGSIRSPHLMIL--NSITIYTDahrgeyywsgHQIMASpVgfsGPeFTFPlyGTmGN
gi|402 SFTAQ-NWFFLYSLFQVNSNYVLNGLSGARTTITFPNIGGLPV-YHNSTLHFARINyRGG
290 300 310 320 330 340

Cry1Ac AAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQLSVLDGTEF-AYGTSSNLPSAVYR
gi|402 VSSSRIGQANLNQNFN---ISTLFN-PLQTPFIRSWLD--SGTDREGVATSTNWQSGAFE
350 360 370 380 390

Cry1Ac KSGTVDSLDEIPPQNNVPPRGFShRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAEF
gi|402 TTLRFsIFsARGNSNFFP----DYFIRNISGVVGTISNADLA--RPLHFNEI-RDI--
400 410 420 430 440

Cry1Ac NNIIASDSITQIPAVKGNFL---FNGSVIS-GPG-FTGGDLVRLNssGNniQnRGYIEVP
gi|402 -GTTAVASLVTVHNrKNNIYDThENgTMHLAPNDYtGFTVSPiHATQVNNQIRTFISEK
450 460 470 480 490 500

Cry1Ac IHFPSTSTRYRVRVRYASVtPIHLNVNWGN-----SSIFsNTVPATa-----TSLDNLQs
gi|402 YGNQGDsLrFELsNPTARyT-LRGNgNSYNLYLrVSSIGsSIRVtINGrVYtANvNTTt
510 520 530 540 550 560

Cry1Ac SDFGYFESANAFTS-SLGNIVGVRNFSGTAGVIIDrFEfIPVtATLEAEYnLERAQKAVn
gi|402 NNDGVLdNGARfSDINIGNVVA---SANTNVPLD---IQVTFNGNPQfEL-----MN
570 580 590 600 610

Cry1Ac ALFTSTNQLGLKTNVTDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQ
gi|402 IMFVPTNLPPly
620

>>gi|53970015|gb|AAV19108.1| Sequence 13 from patent US (135 aa)
initn: 197 init1: 115 opt: 207 Z-score: 246.9 bits: 54.6 E(): 7.8e-05
Smith-Waterman score: 207; 34.752% identity (64.539% similar) in 141 aa overlap
(496-633:1-135)

Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNssGNniQnRGYIEVPiHFP
gi|539 GFIGGALLQRTDHGSLGVLR--VQFPLHL-
10 20

Cry1Ac STSTRYRVRVRYASVtPIHLNVNWGNSSIFsNTVPATATSLDNLQSSDFGY--FESANAF
gi|539 --RQQRiXrYAXtTNIrLsvN-GsFGtISQnLpStMRLGEdLrYGSFAIReFNtSIRP
30 40 50 60 70 80

Cry1Ac TNVTDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPE

Cry1Ac TSSLGNI-VGVRNFSGTAGVIIDrFEfIPVtATLEAEYnLERAQKAVnLFTSTNQLGLK
gi|539 TASPdQIRLTIePsfIRQEVYVDRIEFIPVnPTREAKEdLEAAKkAVASLf
90 100 110 120 130

Cry1Ac TNVTDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPE

>>gi|33731232|gb|AAQ37295.1| Sequence 13 from patent US (135 aa)
initn: 197 init1: 115 opt: 207 Z-score: 246.9 bits: 54.6 E(): 7.8e-05
Smith-Waterman score: 207; 34.752% identity (64.539% similar) in 141 aa overlap
(496-633:1-135)

Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNssGNniQnRGYIEVPiHFP
gi|337 GFIGGALLQRTDHGSLGVLR--VQFPLHL-
10 20

Cry1Ac STSTRYRVRVRYASVtPIHLNVNWGNSSIFsNTVPATATSLDNLQSSDFGY--FESANAF
gi|337 --RQQRiXrYAXtTNIrLsvN-GsFGtISQnLpStMRLGEdLrYGSFAIReFNtSIRP
30 40 50 60 70 80

Cry1Ac TSSLGNI-VGVRNFSGTAGVIIDrFEfIPVtATLEAEYnLERAQKAVnLFTSTNQLGLK
gi|337 TASPdQIRLTIePsfIRQEVYVDRIEFIPVnPTREAKEdLEAAKkAVASLf
90 100 110 120 130

Cry1Ac TNVTDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPE

>>gi|21504389|gb|AAM57091.1| Sequence 13 from patent US (135 aa)
initn: 197 init1: 115 opt: 207 Z-score: 246.9 bits: 54.6 E(): 7.8e-05
Smith-Waterman score: 207; 34.752% identity (64.539% similar) in 141 aa overlap
(496-633:1-135)

Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNssGNniQnRGYIEVPiHFP
gi|215 GFIGGALLQRTDHGSLGVLR--VQFPLHL-
10 20

Cry1Ac STSTRYRVRVRYASVtPIHLNVNWGNSSIFsNTVPATATSLDNLQSSDFGY--FESANAF
gi|215 --RQQRiXrYAXtTNIrLsvN-GsFGtISQnLpStMRLGEdLrYGSFAIReFNtSIRP
30 40 50 60 70 80

Cry1Ac TSSLGNI-VGVRNFSGTAGVIIDrFEfIPVtATLEAEYnLERAQKAVnLFTSTNQLGLK
gi|215 TASPdQIRLTIePsfIRQEVYVDRIEFIPVnPTREAKEdLEAAKkAVASLf
90 100 110 120 130

Cry1Ac TNVTDYHIDQVSNLVtYLSDEfCLDEKRElSEKVKHAKRLSDERNLLQDSNFKDINRQPE

>>gi|16240160|gb|AAE79614.1| Sequence 13 from patent US (135 aa)
initn: 197 init1: 115 opt: 207 Z-score: 246.9 bits: 54.6 E(): 7.8e-05
Smith-Waterman score: 207; 34.752% identity (64.539% similar) in 141 aa overlap
(496-633:1-135)

470 480 490 500 510 520
Cry1Ac FNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|162 GFIGGALLQRTDHGSLGVLRL--VQFPLHL-
10 20

530 540 550 560 570 580
Cry1Ac STSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGY--FESANAF
gi|162 --RQQYRIXRVYAXTTNIRLSVN--GSFGTISQNLPLSTMRLEDLRYGSFAIREFNTSIRP
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac TSSLGNI--VGRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|162 TASPQIRLTIEPSFIRQEVYVDRIEIPVNPTRAEKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac TNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPE

>>gi|53970014|gb|AAV19107.1| Sequence 11 from patent US (137 aa)
initn: 151 init1: 105 opt: 202 Z-score: 240.9 bits: 53.5 E(): 0.00017
Smith-Waterman score: 202; 33.099% identity (61.972% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|539 PGFXGGDILRRRTGVGT---FGTIRVRXTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
gi|539 PLTQ--RYRIRFRFAXTTNLFIFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac --SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|539 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|16240158|gb|AAE79613.1| Sequence 11 from patent US (137 aa)
initn: 151 init1: 105 opt: 202 Z-score: 240.9 bits: 53.5 E(): 0.00017
Smith-Waterman score: 202; 33.099% identity (61.972% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520

Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|162 PGFXGGDILRRRTGVGT---FGTIRVRXTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
gi|162 PLTQ--RYRIRFRFAXTTNLFIFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac --SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|162 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|21504388|gb|AAM57090.1| Sequence 11 from patent US (137 aa)
initn: 151 init1: 105 opt: 202 Z-score: 240.9 bits: 53.5 E(): 0.00017
Smith-Waterman score: 202; 33.099% identity (61.972% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|215 PGFXGGDILRRRTGVGT---FGTIRVRXTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
gi|215 PLTQ--RYRIRFRFAXTTNLFIFIGIRVGDQRVNYFDGRTMNRGDELRYESFATREFTTDFN
30 40 50 60 70 80

590 600 610 620 630 640
Cry1Ac --SSLGNIVGV--RNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
gi|215 FRQPQELISVFANAFSAGQEVYFDRIEIIIPVNPAREAKEDLEAAKAVASLF
90 100 110 120 130

650 660 670 680 690 700
Cry1Ac KTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQP

>>gi|33731231|gb|AAQ37294.1| Sequence 11 from patent US (137 aa)
initn: 151 init1: 105 opt: 202 Z-score: 240.9 bits: 53.5 E(): 0.00017
Smith-Waterman score: 202; 33.099% identity (61.972% similar) in 142 aa overlap
(495-633:1-137)

470 480 490 500 510 520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|337 PGFXGGDILRRRTGVGT---FGTIRVRXTA
10 20

530 540 550 560 570 580
Cry1Ac PSTSTRYRVRVRYASVTPPIHLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT



```

      640      650      660      670      680      690
Cry1Ac TSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSKVKHAKRLSDERNLLQDSN
>>gi|14112762|gb|AAE58177.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|141 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|17920893|gb|AAE86513.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|179      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|179 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|158456689|gb|ABW41362.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|158      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|158 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|23325102|gb|AAN23802.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|233 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|56664657|gb|AAW18082.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : ~ : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|566      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : ~ : : : : : : : : : : : : : : : : : : :
gi|566 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|56642290|gb|AAW12008.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : ~ : : : : : : : : : ~ : : : : : : : : : ~ : : : :
gi|566      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      . . . . . : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : :
gi|566 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|14103757|gb|AAE55191.1| Sequence 42 from patent US (50 aa)
  initn: 176 init1: 176 opt: 182 Z-score: 223.9 bits: 48.9 E(): 0.0015
Smith-Waterman score: 182; 55.102% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPILFAVQN
      : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : : ~ : : : :
gi|141      NNEALQQDVRNRFSTNDNALITAIPILREQG
      10      20      30

```

```

      160      170      180      190      200      210

```



Regulatory Product Characterization Team

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....

gi|158 FEIPLLSVYVQAANLHLSL
40 50

>>gi|14103749|gb|AAE55183.1| Sequence 34 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|141 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|141 FEIPLLSVYVQAANLHLSL
40 50

>>gi|56664648|gb|AAW18073.1| Sequence 33 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|566 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|566 FEIPLLSVYVQAANLHLSL
40 50

>>gi|56664649|gb|AAW18074.1| Sequence 34 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|566 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|566 FEIPLLSVYVQAANLHLSL
40 50

>>gi|17920884|gb|AAE86504.1| Sequence 33 from patent US (50 aa)

initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|179 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|179 FEIPLLSVYVQAANLHLSL
40 50

>>gi|14112754|gb|AAE58169.1| Sequence 34 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|141 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|141 FEIPLLSVYVQAANLHLSL
40 50

>>gi|23325093|gb|AAN23793.1| Sequence 33 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|233 NNAQLREDVRIREFANTDDALITAINNFTLTS
10 20 30

160 170 180 190 200 210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....
gi|233 FEIPLLSVYVQAANLHLSL
40 50

>>gi|14112753|gb|AAE58168.1| Sequence 33 from patent US (50 aa)
initn: 174 initl: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

100 110 120 130 140 150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
: .....
gi|141 NNAQLREDVRIREFANTDDALITAINNFTLTS

```

                10      20      30
Cry1Ac 160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....
gi|141 FEIPLLSVYVQAANLHLSL
      40      50

>>gi|158456681|gb|ABW41354.1| Sequence 34 from patent US (50 aa)
  initn: 174 init1: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|158      NNAQLREDVVRIRFANTDDALITAINNFTLTS
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....
gi|158 FEIPLLSVYVQAANLHLSL
      40      50

>>gi|14103748|gb|AAE55182.1| Sequence 33 from patent US (50 aa)
  initn: 174 init1: 174 opt: 179 Z-score: 220.3 bits: 48.2 E(): 0.0024
Smith-Waterman score: 179; 57.143% identity (83.673% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|141      NNAQLREDVVRIRFANTDDALITAINNFTLTS
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....
gi|141 FEIPLLSVYVQAANLHLSL
      40      50

```

```

>>gi|112088032|gb|ABI06948.1| Sequence 12 from patent US (102 aa)
  initn: 175 init1: 149 opt: 182 Z-score: 219.2 bits: 49.0 E(): 0.0027
Smith-Waterman score: 182; 38.947% identity (68.421% similar) in 95 aa overlap
(539-630:8-102)

```

```

      510      520      530      540      550      560
Cry1Ac GNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNWNWGNSSIFSNTPATATSLDN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|112      VSREIVCSTTDLQFYTNINGTTINIGNFSSTMDSGDD
      10      20      30

```

```

      570      580      590      600      610      620
Cry1Ac LQSSDFGYFESANAFTSSLGN---IVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERA
      : ..... : ..... : ..... : ..... : ..... : .....
gi|112 LQYGRFRVAGFTTTPFTFSDANSTFTIGAFGFSNNVEVYIDRIEFVPAEVTFEAEYDLEKA
      40      50      60      70      80      90

```

```

      630      640      650      660      670      680
Cry1Ac QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDE
      : : : :
gi|112 QKAVN
      100

```

```

>>gi|33765716|gb|AAQ52367.1| Sequence 12 from patent US (102 aa)
  initn: 175 init1: 149 opt: 182 Z-score: 219.2 bits: 49.0 E(): 0.0027
Smith-Waterman score: 182; 38.947% identity (68.421% similar) in 95 aa overlap
(539-630:8-102)

```

```

      510      520      530      540      550      560
Cry1Ac GNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPPIHLNWNWGNSSIFSNTPATATSLDN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|337      VSREIVCSTTDLQFYTNINGTTINIGNFSSTMDSGDD
      10      20      30

```

```

      570      580      590      600      610      620
Cry1Ac LQSSDFGYFESANAFTSSLGN---IVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERA
      : ..... : ..... : ..... : ..... : ..... : .....
gi|337 LQYGRFRVAGFTTTPFTFSDANSTFTIGAFGFSNNVEVYIDRIEFVPAEVTFEAEYDLEKA
      40      50      60      70      80      90

```

```

      630      640      650      660      670      680
Cry1Ac QKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDE
      : : : :
gi|337 QKAVN
      100

```

```

>>gi|23325103|gb|AAN23803.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|233      NNESLQQDVRNRFSTNTDNALITAIPIILREQ
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....
gi|233 FEIPLLTVVYVQAANLHLSL
      40      50

```

```

>>gi|56642291|gb|AAW12009.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAI SRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ..... : ..... : ..... : ..... : .....
gi|566      NNESLQQDVRNRFSTNTDNALITAIPIILREQ
      10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN

```

```

.....
gi|566 FEIPLLTVYVQAANLHLSL
      40      50

>>gi|158456690|gb|ABW41363.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ... ..: ..... :.
gi|158          NNESLQQDVRNRFSTNDNALITAIPILREQG
                        10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....: .....: .....: .....: .....: .....:
gi|158 FEIPLLTVYVQAANLHLSL
      40      50

```

```

>>gi|17920894|gb|AAE86514.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ... ..: ..... :.
gi|179          NNESLQQDVRNRFSTNDNALITAIPILREQG
                        10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....: .....: .....: .....: .....: .....:
gi|179 FEIPLLTVYVQAANLHLSL
      40      50

```

```

>>gi|56664658|gb|AAW18083.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ... ..: ..... :.
gi|566          NNESLQQDVRNRFSTNDNALITAIPILREQG
                        10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....: .....: .....: .....: .....: .....:
gi|566 FEIPLLTVYVQAANLHLSL
      40      50

```

```

>>gi|14103758|gb|AAE55192.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ... ..: ..... :.
gi|141          NNESLQQDVRNRFSTNDNALITAIPILREQG
                        10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....: .....: .....: .....: .....: .....:
gi|141 FEIPLLTVYVQAANLHLSL
      40      50

```

```

>>gi|14112763|gb|AAE58178.1| Sequence 43 from patent US (50 aa)
  initn: 139 init1: 139 opt: 175 Z-score: 215.6 bits: 47.3 E(): 0.0043
Smith-Waterman score: 175; 51.020% identity (87.755% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      : ..... : ... ..: ..... :.
gi|141          NNESLQQDVRNRFSTNDNALITAIPILREQG
                        10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
      .....: .....: .....: .....: .....: .....:
gi|141 FEIPLLTVYVQAANLHLSL
      40      50

```

```

>>gi|112088031|gb|ABI06947.1| Sequence 10 from patent US (113 aa)
  initn: 173 init1: 145 opt: 179 Z-score: 215.0 bits: 48.4 E(): 0.0047
Smith-Waterman score: 179; 37.037% identity (62.037% similar) in 108 aa overlap
(531-633:13-113)

```

```

      510      520      530      540      550      560
Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVTP
      : .. : : : : . . . . . : : :
gi|112          LRVTFGTGRLPQSYIRFRYASGANRSGLSYSQQTSVVISFP
                        10      20      30      40

```

```

      570      580      590      600      610
Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVR----NFSGTAGVIIDRFEFIPVTAT
      : . . . : . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 KTMUDGEPLTSRSF-----AFTTTVTPITFTRAQEEFDLYIQQNVYIDRVEFIPVDAT
      50      60      70      80      90

```

```

      620      630      640      650      660      670
Cry1Ac LEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
      : . . . : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 FEAKSGLERAKKAVNALF
      100      110

```

```

>>gi|33765715|gb|AAQ52366.1| Sequence 10 from patent US (113 aa)
  initn: 173 init1: 145 opt: 179 Z-score: 215.0 bits: 48.4 E(): 0.0047
Smith-Waterman score: 179; 37.037% identity (62.037% similar) in 108 aa overlap
(531-633:13-113)

```

```

      510      520      530      540      550      560

```

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Cry1Ac DLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNTVPI
gi|337 LRVFTTGRLLPQSYIRFRYASGANRSGSLYSQQTSYVVISFP
10 20 30 40

Cry1Ac ATATSLDNLQSSDFGYFESANAFTSSLGNIVGVV----NFSGTAGVIIDRFEFIPVTAT
gi|337 KTM DAGEPLTSRSF-----AFTTTVTPITFTRAQEEFDLYIQQNVYIDRVEFIPVDAT
50 60 70 80 90

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|337 FEAKSDLERAKKAVNALF
100 110

>>gi|51998352|emb|CAH33948.1| unnamed protein product [B (735 aa)
initn: 351 initl: 111 opt: 187 Z-score: 212.4 bits: 50.6 E(): 0.0066
Smith-Waterman score: 639; 27.159% identity (57.928% similar) in 637 aa overlap
(64-635:112-730)

Cry1Ac ETGYTPIDISLSLTQFLLSEFVPGAGFVGLVDIIV--GIFGPSQWDAFLVQIEQLINQR
gi|519 SGTLLAGIGGLTISGPIGIIIGAIISFGTLITVFWPAGEQDKTQVFMKGEIFVDTTP
90 100 110 120 130 140

Cry1Ac IEEFARNQAIISRLGLESLNYQIYAESFREWE-----ADPTNPALREE---MRIQFND
gi|519 LTESIKQLKQLQTELEGRFQILQSYNTALDDWRKLRKQAPGLPPSSALQQAALTLKIRFEN
150 160 170 180 190 200

Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVQQRWGFDF-----AA
gi|519 VHNDFFIREIPGFQLETYKTLLELPIYAQAANFHLNLLQQAELADEWNADIHPSQIEPNAG
210 220 230 240 250 260

Cry1Ac TINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLF
gi|519 TSDDYKLLKENIPKYSNYCANTYRTGLKNLRDEPNMKWSIFNDYRRYMTITVLDTISQF
270 280 290 300 310 320

Cry1Ac PNYDSRTY-----PIRTV-SQLTREIYTNVLENFDGSRFGSAQGIIEGSIK-----S
gi|519 SLYDIKRYRDSIGGIEVKGIKNELTREIYTTTEI--NFDRLPQLRVQPPLATMEYNLTRAS
330 340 350 360 370

Cry1Ac PHLMDILNSITTYTDHRGEYYWSGHQIMASVPGFSGPEFTFPPLYGTMGNAAPQQRIVAQ
gi|519 FKLFSFLEQFIFYTENTNFGNRLVGISNRDAPT-YSNT-ITETLYGER-TGSPPTTKTIRP
380 390 400 410 420 430

360 370 380 390 400 410

Cry1Ac LGQGVYRTLSSSTLYRRPFNIGINNOQLSVLDGTEFAYGTSSNLPASVYRKSQVTDVSLD--
gi|519 FES--YKVSIVTDRQSPVSPV--QPHFIINQIIEYLLNGSSN-NLTKYSAGGSLSNYQNT
440 450 460 470 480 490

Cry1Ac ---EIPPQNN-NV-----PPRQGFSHRLSHVSMFRSGFSNS-SVSIIRAPMFSWIHRS
gi|519 TFFQFPRKDCNLVIDPGCSPNFNNYSHILSHFSLFTYSYVIGLQLQILDGTGVLGWTHSS
500 510 520 530 540 550

Cry1Ac AEFNNIIASDSITQIPAVKGNFL-FNGSVISGPGTGGDLVRLNSSGNNIQNRGYIEVPI
gi|519 VDRYNAISDKIITMIPAIGKNNLDTNSKVIIEGPGHTGGNLVYL-----SQQRLEITC
560 570 580 590 600

Cry1Ac HFPSTSTRYRVRVRYAS----VTP-IHLNVNWNSSIFSNTVTPAT--ATSLDNLQSSDF
gi|519 ETPNSTQSYFIRLRYATNGAGNTLPNISLTIP-GVIGIPPQRLNNTFSGTYNNLQYGDG
610 620 630 640 650 660

Cry1Ac GYFESANAFTSSLG-NIVGVRNFSGTAG--VIIDRFEFIPVTATLEA---EYNLERAQKA
gi|519 GYFQFPSTVTLPLNRNIPFIFNRADVSNLSILIDKIEFIPITSSMHQNRKQKLETIQTK
670 680 690 700 710 720

Cry1Ac VNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNL
gi|519 INTFFTNHKTLL
730

>>gi|33765714|gb|AAQ52365.1| Sequence 8 from patent US 6 (109 aa)
initn: 145 initl: 145 opt: 174 Z-score: 209.4 bits: 47.3 E(): 0.0096
Smith-Waterman score: 174; 35.185% identity (63.889% similar) in 108 aa overlap
(528-633:6-109)

Cry1Ac TGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP IHLNVNWNSSIFSNS
gi|337 LYRKITTKLRYFRYASGANRSGLSYSQQTSYVI
10 20 30

Cry1Ac TVPATATSLDNLQSSDFGYFESAN--AFTSSLGNIVGVVRFSGTAGVIIDRFEFIPVTAT
gi|337 SFPKTM DAGEPLTSRSFAFTTTVTPIAFTRAQEEF----DLYIQQNVYIDRVEFIPVDAT
40 50 60 70 80 90

Cry1Ac LEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEK
gi|337 FEAKSDLERAKKAVNALF
100

>>gi|112088030|gb|ABI06946.1| Sequence 8 from patent US (109 aa)

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initn: 145 init1: 145 opt: 174 Z-score: 209.4 bits: 47.3 E(): 0.0096
Smith-Waterman score: 174; 35.185% identity (63.889% similar) in 108 aa overlap
(528-633:6-109)

500 510 520 530 540 550
Cry1Ac TGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPPIHLNVNWNSSIFS
gi|112 LYRKITTKLLYRFYASGANRSGLSYSQOTSIVI
10 20 30

560 570 580 590 600 610
Cry1Ac TVPATATSLDNLQSSDFGYFESAN--AFTSSLGNIVGVNRFSGTAGVIIDRFEFIPVTAT
gi|112 SFPKTM DAGEPLTSRFAFTTIVTPIAFTRAQEEF----DLYIQQNVYIDRVEFIPVDAT
40 50 60 70 80 90

620 630 640 650 660 670
Cry1Ac LEAEYNLERAKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSK
gi|112 FEAKSDLERAKAVNALF
100

>>gi|2302646|emb|CAA03156.1| unnamed protein product [un (312 aa)
initn: 88 init1: 62 opt: 177 Z-score: 206.1 bits: 48.2 E(): 0.015
Smith-Waterman score: 177; 21.545% identity (58.130% similar) in 246 aa overlap
(5-245:1-230)

10 20 30 40 50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
gi|230 MQNN-NFNTTEINNMINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
10 20 30 40 50

60 70 80 90 100 110
Cry1Ac GAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
gi|230 KQGFALKSEIFPGNT-PATMDKVRIEVQTLLDQRLQD-DRVKILEGEYKGIIDVSKVFT
60 70 80 90 100

120 130 140 150 160 170
Cry1Ac ESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV
gi|230 DVVNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYEGVSIISLFTQMCTFHLGL
110 120 130 140 150 160

180 190 200 210 220 230
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQ
gi|230 LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVLYSKEFGRLAKNLNEAL---N
170 180 190 200 210 220

240 250 260 270 280 290
Cry1Ac FRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSI
gi|230 FRNMCSLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNISPNDWKALYKLLMGAP
230 240 250 260 270 280

>>gi|12806992|gb|AAE42889.1| Sequence 2 from patent US 6 (312 aa)
initn: 88 init1: 62 opt: 177 Z-score: 206.1 bits: 48.2 E(): 0.015

Smith-Waterman score: 177; 21.545% identity (58.130% similar) in 246 aa overlap
(5-245:1-230)

10 20 30 40 50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
gi|128 MQNN-NFNTTEINNMINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
10 20 30 40 50

60 70 80 90 100 110
Cry1Ac GAGFVLGLVDIIWGFPGSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
gi|128 KQGFALKSEIFPGNT-PATMDKVRIEVQTLLDQRLQD-DRVKILEGEYKGIIDVSKVFT
60 70 80 90 100

120 130 140 150 160 170
Cry1Ac ESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV
gi|128 DVVNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYEGVSIISLFTQMCTFHLGL
110 120 130 140 150 160

180 190 200 210 220 230
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQ
gi|128 LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVLYSKEFGRLAKNLNEAL---N
170 180 190 200 210 220

240 250 260 270 280 290
Cry1Ac FRRELTTLVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLNFDGSRGSAQGIIEGSI
gi|128 FRNMCSLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNISPNDWKALYKLLMGAP
230 240 250 260 270 280

>>gi|51998356|emb|CAH33950.1| unnamed protein product [B (694 aa)
initn: 361 init1: 105 opt: 181 Z-score: 205.7 bits: 49.3 E(): 0.016
Smith-Waterman score: 671; 27.982% identity (59.021% similar) in 654 aa overlap
(64-651:61-694)

40 50 60 70 80 90
Cry1Ac ETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDIIW--GIFGSPQWDAFLVQIEQLINQR
gi|519 SGTLLAGIGGLTSSISGPIGIIIGAIISFGTLITVFWPAGEQDKTWTQFIKMGEIFVDTP
40 50 60 70 80 90

100 110 120 130 140
Cry1Ac IEEFARNQAISRLEGLSNLYQIYAESFREW-----EAD--PTNPALREE---MRIQFND
gi|519 LTESIKQLKLTLEGRQILQSYNTALDDWRKLRKQAPGLPPSSALQQAALTLKIRFEN
100 110 120 130 140 150

150 160 170 180 190
Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVFGQRWGF-----AA
gi|519 VHNDFIREIPGFQLETYKTLLEPIYAQAANFHLNLLQQAELADEWNADIHSPQIEPNAG
160 170 180 190 200 210

200 210 220 230 240 250
Cry1Ac TINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNQFRRELTTLVLDIVSLF
: . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . . : : : : . . . . .

gi|519 TSDDYYKLLKENIPKYSNYCANTYREGLNKLNRNEPNMRWSIFNDYRRYMTITVLDTIAQF
220 230 240 250 260 270

Cry1Ac PNYDSRTYP--IRTV---SQLTREIYTNPVLENFDGSRGSAQG---IEGSI-RSP-H
260 270 280 290

gi|519 SFYDIKRYKDSIGRIGGIKTELREIYTTTEI--NFDRLTYLEIQPNLAIMEYNLTRSGLR
280 290 300 310 320

Cry1Ac LMDILNSITIYTDahrgeyywsgHQIMA-----SPVGFSGPEFTFPLYGTMGNAAPQQR
300 310 320 330 340 350

gi|519 LFSFLDELIFYT---KNETY--GNRLVGIANRRNRSTYATTGTEI---IYGERTGPPTTKT
330 340 350 360 370 380

Cry1Ac IVAQLGQGV-YRTLSSTLYRRPF-NIGINNQLSV-LDGT---EFAYGTSSNLPSAVYRK
360 370 380 390 400

gi|519 LIPFESYKVSIVTDRQVTPSPFPNIYFTINQIELYLNNSPSNKLTYSAGGNLSND--KK
390 400 410 420 430

Cry1Ac SGTVD---SLDEIPPQNNN-VPPRQGFSHRSLHVMFRSGFSNS-SVSIIRAPMFSWIHR
410 420 430 440 450 460

gi|519 TTDFQFPVKKCKPIINPNCLPSYNSYSHILSQFSLFNYSYKIGLALNILYTGALGWTHS
440 450 460 470 480 490

Cry1Ac SAEFNIIASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP
470 480 490 500 510 520

gi|519 SVNRNNAISDKIITMIPAIGKNSLDTNSKVIIEGPGHTGGNLVYL-----QSQRLEIT
500 510 520 530 540 550

Cry1Ac IHFPSTSTRYRVRVRYAS-----VTP-IHLNVNWNSSIFSNTVPAT--ATSLDNLQSSD
530 540 550 560 570

gi|519 CRTPNSTQSYIIRLRYATNGAGNTLPNISLTIP-GVIGIPPQRLNNTFSGTNYNNLQYGD
560 570 580 590 600 610

Cry1Ac FGYFESANAFTSSLG-NIVGVRNFSGTAG--VIIDRFEPVPTATLEA---EYNLERAQK
580 590 600 610 620

gi|519 FGYFQFPSTVTLPLNRNIPFIFNRADVNSLLIIDKIEFIPITSSVRQNRKQKLETIQT
620 630 640 650 660 670

Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
630 640 650 660 670 680

gi|519 KINTFFTNTKNTLNIEATNYDID
680 690

>>gi|51998354|emb|CAH33949.1| unnamed protein product [B (744 aa)
initn: 361 init1: 105 opt: 181 Z-score: 205.2 bits: 49.3 E(): 0.016
Smith-Waterman score: 671; 27.982% identity (59.021% similar) in 654 aa overlap
(64-651:111-744)

Cry1Ac ETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIV--GIFGPSQWDAFLVQIEQLINQR
40 50 60 70 80 90

gi|519 SGTLLAGIGGLTISGPIGIIIGAIISFGLTITVFWPAGEQDKTIVTQFIKMGEIFVDTP
90 100 110 120 130 140

Cry1Ac IIEFARNQAIISRLLEGLSNLYQIYAESFREW-----EAD--PTNPALREE---MRIQFND
100 110 120 130 140

gi|519 LTESIKQLKLTLEGFRQILQSYNTALDDWRKLRKQAPGLPPSSALQQAALTLKIRFEN
150 160 170 180 190 200

Cry1Ac MNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDF-----AA
150 160 170 180 190

gi|519 VHNDFIREIPGFQLEYTKTLLLPYQAANFHLNLQQGAELADEWNADIHPSQIEPNAG
210 220 230 240 250 260

Cry1Ac TINSRYNDLTRLIGNYTDHavrwyntgLERVWGPDSRDWIRYQFRRELTTLVLDIVSLF
200 210 220 230 240 250

gi|519 TSDDYYKLLKENIPKYSNYCANTYREGLNKLNRNEPNMRWSIFNDYRRYMTITVLDTIAQF
270 280 290 300 310 320

Cry1Ac PNYDSRTYP--IRTV---SQLTREIYTNPVLENFDGSRGSAQG---IEGSI-RSP-H
260 270 280 290

gi|519 SFYDIKRYKDSIGRIGGIKTELREIYTTTEI--NFDRLTYLEIQPNLAIMEYNLTRSGLR
330 340 350 360 370

Cry1Ac LMDILNSITIYTDahrgeyywsgHQIMA-----SPVGFSGPEFTFPLYGTMGNAAPQQR
300 310 320 330 340 350

gi|519 LFSFLDELIFYT---KNETY--GNRLVGIANRRNRSTYATTGTEI---IYGERTGPPTTKT
380 390 400 410 420 430

Cry1Ac IVAQLGQGV-YRTLSSTLYRRPF-NIGINNQLSV-LDGT---EFAYGTSSNLPSAVYRK
360 370 380 390 400

gi|519 LIPFESYKVSIVTDRQVTPSPFPNIYFTINQIELYLNNSPSNKLTYSAGGNLSND--KK
440 450 460 470 480

Cry1Ac SGTVD---SLDEIPPQNNN-VPPRQGFSHRSLHVMFRSGFSNS-SVSIIRAPMFSWIHR
410 420 430 440 450 460

gi|519 TTDFQFPVKKCKPIINPNCLPSYNSYSHILSQFSLFNYSYKIGLALNILYTGALGWTHS
490 500 510 520 530 540

Cry1Ac SAEFNIIASDSITQIPAVKGNFL-FNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVP
470 480 490 500 510 520

gi|519 SVNRNNAISDKIITMIPAIGKNSLDTNSKVIIEGPGHTGGNLVYL-----QSQRLEIT
550 560 570 580 590 600

Cry1Ac IHFPSTSTRYRVRVRYAS-----VTP-IHLNVNWNSSIFSNTVPAT--ATSLDNLQSSD
530 540 550 560 570

gi|519 CRTPNSTQSYIIRLRYATNGAGNTLPNISLTIP-GVIGIPPQRLNNTFSGTNYNNLQYGD
610 620 630 640 650 660

Cry1Ac FGYFESANAFTSSLG-NIVGVRNFSGTAG--VIIDRFEPVPTATLEA---EYNLERAQK
580 590 600 610 620

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gi|519 FGYFQFPSTVTLPLNRNIPFIFNRADVNSILLIIDKIEFIPITSSVRQNRKQKLETIQT
670 680 690 700 710 720

Cry1Ac AVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERN
630 640 650 660 670 680

gi|519 KINTFFTNTHTKNTLNIEATNYDID
730 740

>>gi|33765723|gb|AAQ52374.1| Sequence 26 from patent US (62 aa)
initn: 200 init1: 165 opt: 165 Z-score: 202.4 bits: 45.2 E(): 0.024
Smith-Waterman score: 165; 81.250% identity (96.875% similar) in 32 aa overlap
(600-631:31-62)

Cry1Ac QSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAV
630 640 650 660 670 680
gi|337 PLTSRSFAHTTLFTPIFSAQEEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAQRAV
10 20 30 40 50 60

Cry1Ac NALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLL
630 640 650 660 670 680
gi|337 NA

>>gi|112088043|gb|ABI06955.1| Sequence 26 from patent US (62 aa)
initn: 200 init1: 165 opt: 165 Z-score: 202.4 bits: 45.2 E(): 0.024
Smith-Waterman score: 165; 81.250% identity (96.875% similar) in 32 aa overlap
(600-631:31-62)

Cry1Ac QSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAV
630 640 650 660 670 680
gi|112 PLTSRSFAHTTLFTPIFSAQEEFDLYIQSGVYIDRIEFIPVTATFEAEYDLERAQRAV
10 20 30 40 50 60

Cry1Ac NALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLL
630 640 650 660 670 680
gi|112 NA

>>gi|971347|emb|CAA60504.1| mosquitocidal toxin [Bacillu (724 aa)
initn: 114 init1: 62 opt: 178 Z-score: 201.9 bits: 48.6 E(): 0.025
Smith-Waterman score: 190; 18.053% identity (53.061% similar) in 637 aa overlap
(5-585:1-613)

Cry1Ac CMQAMDNPNINICIPYCNLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
10 20 30 40 50
gi|971 MQNN-NFNTTEINNMNINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
10 20 30 40 50

Cry1Ac GAGFVGLVDIIWGIFGPSQWDAFLVQIEQLINQRIEIEFARNQAI-SRLEGLSNLYQIYA
60 70 80 90 100 110
gi|971 KQGFAPLKEIFPGNT-PATMDKVRIEVQTLDDQRLQD-DRVKILEGEYKGIIDVSKVFT

60 70 80 90 100
120 130 140 150 160 170
Cry1Ac ESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV
gi|971 DYVNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYBGSISLFTQMCTFHLGL
110 120 130 140 150 160

180 190 200 210 220 230
Cry1Ac LRDVSVFGRQWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNO
gi|971 LKDGILLAGSDWGFAPADKDALICQFNRFVNEYNTRLMVLYSKEFGRLAKNLNEAL--N
170 180 190 200 210 220

240 250 260 270 280 290
Cry1Ac FRRELTTLTVL---DIVSLFPNYSRTYPIRTVSQLTREIYTNPVLNFDGSRFGSAQGIE
gi|971 FRNMCSLYVFPFSEAWSLRLRYEGTKLENTLSLWNFVGESINNIISPNDWKALYKLLMGAP
230 240 250 260 270 280

300 310 320 330 340
Cry1Ac GSIRSPHMLDILNSITIIYTD----HRGEYY----WSGHQIMASVPG---FSGPEFTFP
gi|971 NQ---RLNNVKFNYSYFSDTQATIHRENIHGVLPPTYNGGPTITGWIGNRFSG--LSFP
290 300 310 320 330

350 360 370 380
Cry1Ac LYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRR-----PF--NIGINNQQLS-
gi|971 CSNELEITKIKQEITVNDKGGNFNSIVPAATRNEILTATVPTSDPFPTADINWKYFSP
340 350 360 370 380 390

390 400 410 420 430
Cry1Ac -VLDGTEFAYGTSSNLPSAVYRK-SGTVDLDEIPPQNNVPPRQ---GFSH---RLSHV
gi|971 GLYSGWNIKFDVTTLKSRVPSIIPSNILKYDDYYIRAVSACPKGVSLAYNHDFLTLTYN
400 410 420 430 440 450

440 450 460 470 480 490
Cry1Ac SMFRSGFNSSSVSIIRAPMFSWIHRSAEFNIIIASDSITQIPAVKGNFLFNGSVISG-PG
gi|971 KLEYDAPTQNIIVGFPSPDNTKSFYRSNSHYLSTTDDAYIPALQFSTVSDRSFLEDTPD
460 470 480 490 500 510

500 510 520 530 540 550
Cry1Ac FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRYASVTPHILNV----NWGN
gi|971 QATDGSIKFTDVLGNEAKYSIRLNTGF-NTATRYRLIIRFKAPARLAAGIRVRSQNSGN
520 530 540 550 560 570

560 570 580 590 600
Cry1Ac SSIFSNVTPATATS-----LDNLQSSDFGYFESA-NAFTSSLGNIVGVRNFSGTAGVII
gi|971 NKLLGG-IPVEGNSGWIDYITDSFTFDDLGITTSSTNAFFSIDSDGVNASQQWYLSKLLIL
580 590 600 610 620 630

610 620 630 640 650 660
Cry1Ac DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF

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gi|971 VKESSFTTQIPLKPYVIVRCPDTPFFVSNNSSSTYEQGYNNNYNQSSSMYDQGYNNNSYNP
      640      650      660      670      680      690
>>gi|2302648|emb|CAA03157.1| unnamed protein product [un (724 aa)
  initn: 114 init1: 62 opt: 178 Z-score: 201.9 bits: 48.6 E(): 0.025
Smith-Waterman score: 190; 18.053% identity (53.061% similar) in 637 aa overlap
(5-585:1-613)

      10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  MQNN-NFNTTEINNMNINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
      10      20      30      40      50
Cry1Ac GAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  KQGFALKSEIFPGNT-PATMDKVRIEVQTLDDQRLQD-DRVKILEGEYKGIIDVSKVFT
      60      70      80      90      100
Cry1Ac GAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  KQGFALKSEIFPGNT-PATMDKVRIEVQTLDDQRLQD-DRVKILEGEYKGIIDVSKVFT
      60      70      80      90      100
Cry1Ac ESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  DYVNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYEGVISLFTQMCTFHLGL
      110      120      130      140      150      160
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNO
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVMVLSKEFGRLAKNLNEAL---N
      170      180      190      200      210      220
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNO
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVMVLSKEFGRLAKNLNEAL---N
      170      180      190      200      210      220
Cry1Ac FRRELTLTVL---DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIE
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  FRNMCsLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNIISPNDWKALYKLLMGAP
      230      240      250      260      270      280
Cry1Ac FRRELTLTVL---DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIE
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  FRNMCsLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNIISPNDWKALYKLLMGAP
      230      240      250      260      270      280
Cry1Ac GSIRSPHLMIDLNSITTYTDA----HRGEYY----WSGHQIMASVPG---FSGPEFTFP
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  NQ---RLNNVKFNYSYFSDTQATIHRENIHGVLPTYPNGGPTITGWIGNGRFSG--LSFP
      290      300      310      320      330
Cry1Ac LYGTMGNAAPQRIVAQLGQGVYRTLSTLYRR-----PF--NIGINNQQLS-
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  CSNELEITKIKQEIITYNDKGGNFNSIVPAATRNEILTATVPTSADPFKTDINWKYFSP
      340      350      360      370      380      390
Cry1Ac -VLDGTEFAYGTSSNLPSAVYRK-SGTVDLDEIPPQNNVPPRQ---GFSH---RLSHV
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  GLYSGWNKIFDDTVTLKSRVPSIIPSNILKYDDYYIRAVSACPKGVSLAYNHDFLTLTYN
      400      410      420      430      440      450
Cry1Ac SMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PG
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:

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gi|230 KLEYDAPTTQNIIVGFSPDNTKSFYRSNSHYLSTTDDAYVIPALQFSTVSDRSFLEDTPD
      460      470      480      490      500      510
      500      510      520      530      540      550
Cry1Ac FTGGDLVRLNNSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV----NWGN
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  QATDGSIKFTDVLGNEAKYSIRLNTGF-NTATRYRLIIRFKAPARLAAGIRVRSQNSGN
      520      530      540      550      560      570
      560      570      580      590      600
Cry1Ac SSIFSNTVPATATS-----LDNLQSSDFGYFESA-NAFTSSLGNIVGVRNFSGTAGVII
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|230  NKLLGG-IPVEGNSGWIDYITDSFTFDDLGITTSSTNAFFSIDSDGVNASQQWYLSKLLIL
      580      590      600      610      620      630
      610      620      630      640      650      660
Cry1Ac DRFEFIPVTATLAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
      610      620      630      640      650      660
gi|230 VKESSFTTQIPLKPYVIVRCPDTPFFVSNNSSSTYEQGYNNNYNQSSSMYDQGYNNNSYNP
      640      650      660      670      680      690
>>gi|12806993|gb|AAE42890.1| Sequence 4 from patent US 6 (724 aa)
  initn: 114 init1: 62 opt: 178 Z-score: 201.9 bits: 48.6 E(): 0.025
Smith-Waterman score: 190; 18.053% identity (53.061% similar) in 637 aa overlap
(5-585:1-613)

      10      20      30      40      50
Cry1Ac CMQAMDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  MQNN-NFNTTEINNMNINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
      10      20      30      40      50
Cry1Ac GAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  KQGFALKSEIFPGNT-PATMDKVRIEVQTLDDQRLQD-DRVKILEGEYKGIIDVSKVFT
      60      70      80      90      100
Cry1Ac GAGFVLGLVDIIWGFQPSQWDAFLVQIEQLINQRIEEFARNQAI-SRLEGLSNLYQIYA
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  KQGFALKSEIFPGNT-PATMDKVRIEVQTLDDQRLQD-DRVKILEGEYKGIIDVSKVFT
      60      70      80      90      100
Cry1Ac ESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSV
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  DYVNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYEGVISLFTQMCTFHLGL
      110      120      130      140      150      160
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNO
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVMVLSKEFGRLAKNLNEAL---N
      170      180      190      200      210      220
Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRDWIRYNO
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVMVLSKEFGRLAKNLNEAL---N
      170      180      190      200      210      220
Cry1Ac FRRELTLTVL---DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIE
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  FRNMCsLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNIISPNDWKALYKLLMGAP
      230      240      250      260      270      280
Cry1Ac FRRELTLTVL---DIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLENFDGSRGSAQGIE
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  FRNMCsLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNIISPNDWKALYKLLMGAP
      230      240      250      260      270      280
Cry1Ac GSIRSPHLMIDLNSITTYTDA----HRGEYY----WSGHQIMASVPG---FSGPEFTFP
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  NQ---RLNNVKFNYSYFSDTQATIHRENIHGVLPTYPNGGPTITGWIGNGRFSG--LSFP
      290      300      310      320      330
Cry1Ac LYGTMGNAAPQRIVAQLGQGVYRTLSTLYRR-----PF--NIGINNQQLS-
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  CSNELEITKIKQEIITYNDKGGNFNSIVPAATRNEILTATVPTSADPFKTDINWKYFSP
      340      350      360      370      380      390
Cry1Ac -VLDGTEFAYGTSSNLPSAVYRK-SGTVDLDEIPPQNNVPPRQ---GFSH---RLSHV
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:
gi|128  GLYSGWNKIFDDTVTLKSRVPSIIPSNILKYDDYYIRAVSACPKGVSLAYNHDFLTLTYN
      400      410      420      430      440      450
Cry1Ac SMFRSGFSNSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PG
      .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.: .:.:

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gi|128 NQ---RLNNVKFNYSYFSDTQATIHRENIHGVLPTYNGGPTITGWIGNGRFSG--LSFP
290 300 310 320 330

Cry1Ac LYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRR-----PF--NIGINNQQLS-
350 360 370 380

gi|128 CSNELEITKIKQEIITYNDKGGNFNSIVPAATRNEILTATVPTSADPPFKTADINWKYFSP
340 350 360 370 380 390

Cry1Ac -VLDGTEFAYGTSSNLPSAVYRK-SGTVDLSLDEIPPQNNVPPRQ---GFSH---RLSHV
390 400 410 420 430

gi|128 GLYSGWNKIFDDTVTLKSRVPSIIPSNILKYDDYYIRAVSACPKGVSLAYNHDFLTLTYN
400 410 420 430 440 450

Cry1Ac SMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PG
440 450 460 470 480 490

gi|128 KLEYDAPTQNIIVGFSPTDNTKSFYRSNSHYLSTDDAYVIPALQFSTVSDRSFLEDTPD
460 470 480 490 500 510

Cry1Ac FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV----NWGN
500 510 520 530 540 550

gi|128 QATDGSIKFTDTVLGNEAKYSIRLNTGF-NTATRYRLIIRFKAPARLAAGIRVRSQNSGN
520 530 540 550 560 570

Cry1Ac SSIFSNTVPATATS-----LDNLQSSDFGYFESA-NAFTSSLGNIVGVRNFSGTAGVII
560 570 580 590 600

gi|128 NKLLGG-IPVEGNSGWIDYITDSFTFDDLGITTSSTNAFFSIDSDGVNASQQWYLSKLLIL
580 590 600 610 620 630

Cry1Ac DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
610 620 630 640 650 660

gi|128 VKESSFTTQIPLKPYVIVRCPDTFFVSNSSSTYEQGYNNYNNQNSSSMYDQGYNNSYNP
640 650 660 670 680 690

>>gi|12806994|gb|AAE42891.1| Sequence 6 from patent US 6 (725 aa)
initn: 114 initl: 62 opt: 178 Z-score: 201.8 bits: 48.6 E(): 0.025
Smith-Waterman score: 190; 18.053% identity (53.061% similar) in 637 aa overlap
(5-585:2-614)

Cry1Ac CMQAMDNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLS-LTQFL---LSEFVP
10 20 30 40 50

gi|128 MMQNN-NFNTTEINMINFP---MYNG-RLEPSLAPALIAVAPIAKYLATALAKWAV
10 20 30 40 50

Cry1Ac GAGFVLGLVDIIWGIFGSPQWDAFLVQIEQLINQRIIEEFARNQAI-SRLEGLSNLYQIYA
60 70 80 90 100 110

gi|128 KQGFALKKSEIFPGNT-PATMDKVRIEVQTLQDQRLQD-DRVKILEGKYKGIIDVSKVFT
60 70 80 90 100 110

Cry1Ac ESFRWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAANLHLSV
120 130 140 150 160 170

gi|128 DYNQSKFE-TGTANR----LFFDTSNQLISRLPQFEIAGYEGVVISLFTQMCTFHLGL
120 130 140 150 160

Cry1Ac LRDVSVFGQRWGFDAATINSRYNDLRLIGNYTDHAVRWYNTGLERWVGPDSDRDWIRYNQ
180 190 200 210 220 230

gi|128 LKDGILAGSDWGFAPADKDALICQFNRFVNEYNTRMLVLYSKEFGRLAKNLNEAL---N
170 180 190 200 210 220

Cry1Ac FRRELTLTVL---DIVSLFPNYDSRTYPIRTVSQTLREIYTNPVLNFDFGSRFGSAQGIE
240 250 260 270 280 290

gi|128 FRNMCSLYVFPFSEAWSLRYEGTKLENTLSLWNFVGESINNI SPNDWKALYKLLMGAP
230 240 250 260 270 280

Cry1Ac GSIRSPHMLDILNSITITDA---HRGEYY----WSGHQIMASVPG---FSGPEFTFP
300 310 320 330 340

gi|128 NQ---RLNNVKFNYSYFSDTQATIHRENIHGVLPTYNGGPTITGWIGNGRFSG--LSFP
290 300 310 320 330

Cry1Ac LYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRR-----PF--NIGINNQQLS-
350 360 370 380

gi|128 CSNELEITKIKQEIITYNDKGGNFNSIVPAATRNEILTATVPTSADPPFKTADINWKYFSP
340 350 360 370 380 390

Cry1Ac -VLDGTEFAYGTSSNLPSAVYRK-SGTVDLSLDEIPPQNNVPPRQ---GFSH---RLSHV
390 400 410 420 430

gi|128 GLYSGWNKIFDDTVTLKSRVPSIIPSNILKYDDYYIRAVSACPKGVSLAYNHDFLTLTYN
400 410 420 430 440 450

Cry1Ac SMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PG
440 450 460 470 480 490

gi|128 KLEYDAPTQNIIVGFSPTDNTKSFYRSNSHYLSTDDAYVIPALQFSTVSDRSFLEDTPD
460 470 480 490 500 510

Cry1Ac FTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTPIHNLV----NWGN
500 510 520 530 540 550

gi|128 QATDGSIKFTDTVLGNEAKYSIRLNTGF-NTATRYRLIIRFKAPARLAAGIRVRSQNSGN
520 530 540 550 560 570

Cry1Ac SSIFSNTVPATATS-----LDNLQSSDFGYFESA-NAFTSSLGNIVGVRNFSGTAGVII
560 570 580 590 600

gi|128 NKLLGG-IPVEGNSGWIDYITDSFTFDDLGITTSSTNAFFSIDSDGVNASQQWYLSKLLIL
580 590 600 610 620 630

Cry1Ac DRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEF
610 620 630 640 650 660

gi|128 VKESSFTTQIPLKPYVIVRCPDTFFVSNSSSTYEQGYNNYNNQNSSSMYDQGYNNSYNP
640 650 660 670 680 690

>>gi|21685428|emb|CAD30081.1| pesticidal crystal protei (643 aa)
initn: 105 initl: 105 opt: 175 Z-score: 199.1 bits: 48.0 E(): 0.036

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Smith-Waterman score: 203; 19.516% identity (51.452% similar) in 620 aa overlap (34-601:25-618)

Sequence alignment for Cry1Ac vs gi|216. Shows amino acid sequences with positions 10-50, 60-110, 120-170, 180-220, 230-280, 290-340, 350-400, 410-450, 460-510, 520-550. Includes labels like Cry1Ac and gi|216.

Sequence alignment for Cry1Ac vs gi|592. Shows amino acid sequences with positions 520-570, 580-610, 620-670, 680-710, 720-750, 760-810, 820-870, 880-910, 920-950. Includes labels like Cry1Ac and gi|592. Also contains a reference sequence header: >>gi|592275|gb|AAA53882.1| Sequence 2 from Patent WO 890 (643 aa)...

gi|592 FYQNP... 350 360 370 380 390

Cry1Ac GTEFAYGTSSNLP... 390 400 410 420 430 440

gi|592 GWNIK... 400 410 420 430 440 450

Cry1Ac SGF-SNSSVSIIR... 450 460 470 480 490

gi|592 IEYDSP... 460 470 480 490 500 510

Cry1Ac TGGDLVRLN... 500 510 520 530 540 550

gi|592 ATDGSIK... 520 530 540 550 560 570

Cry1Ac SIFSN-TVPAT... 520 530 540 550 560 570

gi|592 RMLGSFT... 580 590 600 610 620

Cry1Ac VTATLEAEYN... 620 630 640 650 660 670

gi|592 VKESAFTTQINPLLK 630 640

>>gi|142763|gb|AAA22352.1| mosquito-toxic crystal protei (643 aa)
initn: 105 initl: 105 opt: 175 Z-score: 199.1 bits: 48.0 E(): 0.036
Smith-Waterman score: 203; 19.516% identity (51.452% similar) in 620 aa overlap
(34-601:25-618)

Cry1Ac AMDNPNINECIPY... 10 20 30 40 50

gi|142 MEDSSLDTLSIVNETDFPLYNNYTEPTIAPALIAVAPIAQYLATAIGKWAAKAA 10 20 30 40 50

Cry1Ac FVLGLVDIIWGF... 60 70 80 90 100 110

gi|142 FS-KVLSL... 60 70 80 90 100 110

Cry1Ac EWEADPTNPALREEMRIQFNDMMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV 120 130 140 150 160 170

gi|142 QPGFTPATA-----KGYFLNLSGAI... 120 130 140 150 160

Cry1Ac SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD----- 180 190 200 210 220

gi|142 ILAGS... 170 180 190 200 210 220

Cry1Ac -----W--IRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQLTREIYTNPVLEN 230 240 250 260 270

gi|142 YVFPFAEAWSLMRYEGLK... 230 240 250 260 270 280

Cry1Ac FDGSFRGSAQGLEG--SIRSPH-LMDILNSITITYDAHRGEYYW---SGHQIMA--SPV 280 290 300 310 320 330

gi|142 FNYSPFTNEPADIPARENIRGVHP... 290 300 310 320 330 340

Cry1Ac GFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSSTLYRRPFNIGINNQQQL--SVLD 340 350 360 370 380

gi|142 FYQNP... 350 360 370 380 390

Cry1Ac GTEFAYGTSSNLP... 390 400 410 420 430 440

gi|142 GWNIK... 400 410 420 430 440 450

Cry1Ac SGF-SNSSVSIIR... 450 460 470 480 490

gi|142 IEYDSP... 460 470 480 490 500 510

Cry1Ac TGGDLVRLN... 500 510 520 530 540 550

gi|142 ATDGSIK... 520 530 540 550 560 570

Cry1Ac SIFSN-TVPAT... 520 530 540 550 560 570

gi|142 RMLGSFT... 580 590 600 610 620

Cry1Ac VTATLEAEYN... 620 630 640 650 660 670

gi|142 VKESAFTTQINPLLK 630 640

>>gi|12806995|gb|AAE42892.1| Sequence 7 from patent US 6 (644 aa)
initn: 105 initl: 105 opt: 175 Z-score: 199.1 bits: 48.0 E(): 0.036
Smith-Waterman score: 203; 19.516% identity (51.452% similar) in 620 aa overlap
(34-601:26-619)

Cry1Ac AMDNPNINECIPY... 10 20 30 40 50

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      :  :  :...  :...  :...  :
gi|128      MMEDSSLDLTLIVNETDFPLYNNYTEPTIAPALIAVAPIAQYLATAIGKWAAKAA
      10      20      30      40      50

      60      70      80      90      100     110
Cry1Ac  FVLGLVDIIWGFIPGSPQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFR
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  FS-KVLSLIFPGSQPATMEKVRTEVETLINQKLSQDRVNILNAEYRGIIEVSDVFDAYIK
      60      70      80      90      100     110

      120     130     140     150     160     170
Cry1Ac  EWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  QPGFTPATA-----KGYFLNLSGAIIQRLPQFEVQTYEGVSIALFTQMCTLHLTLKDKG
      120     130     140     150     160

      180     190     200     210     220
Cry1Ac  SVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSRD-----
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  ILAGSAWGFQTQADVDSFIKLFNQKVLDRYRTRLMRMYTEEFGRCKVSLKDGTLFRMNCNL
      170     180     190     200     210     220

      230     240     250     260     270     280
Cry1Ac  -----W--IRYNQFRRELTLTLVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNPVLEN
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  YVFPFAEAWSLMRYEGLKQLQSSLSLWDYVGVSIIPVNYNEWGGGLVYKLLMGVEVNRQLTTVK
      230     240     250     260     270     280

      280     290     300     310     320     330     340
Cry1Ac  FDGSRGSAQGIIEG--SIRSPH-LMDILNSITIIYTAHRGGEYIW---SGHQIMA--SFV
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  FNYSTNEPADIPARENIRGVHPIYDPSSGLTGWIGNRTNMFNFADNNGNEIMEVRTQT
      290     300     310     320     330     340

      340     350     360     370     380
Cry1Ac  GFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL--SVLD
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  FYQNPN-NEPI-----APRD-IINQI--LTAPAPADLFFKNADINVKFTQWFQSTLY
      350     360     370     380     390

      390     400     410     420     430     440
Cry1Ac  GTEFAYGTSSNLPSAVYRKSGTVD---SLDEIPPQNNVPPRQ---GFSHRLSHVSMFR
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  GWNIKLGTQTVLSS---RTGTIPPNYLAYDGYIIRAIASACPRGVSLAYNHDLTTLTYNR
      400     410     420     430     440     450

      450     460     470     480     490
Cry1Ac  SGF-SNSSVSIIR--APMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG-PGF
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  IEYDPTTENIIVGFAPDNTKDFYSKSHYLSETNDSYVIPALQFAEVSDFLEDPDQ
      460     470     480     490     500     510

      500     510     520     530     540     550
Cry1Ac  TGGDLVRLNSSGNNIQRNGYIEVPIHFPSTSTRYR--VVRVYASVTPIHNLV---NWGNS
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  ATDGSIKFARTFISNEAKYSIRLNTGF-NTATRYKLIIRVRVPYRLPAGIRVQSQNSGNN
      520     530     540     550     560     570

      560     570     580     590     600     610

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```

Cry1Ac  SIFSN-TVPATATSLDNLQSSDFGYFESANAFTSSLGNIVGVRNFGTAVGIIDRFEFIP
      :  :...  :  :...  :  :...  :  :...  :  :...  :
gi|128  RMLGSFTANANPEWVDFV--TDAFTFNDLGIITTSSTNALFSISSDLSLNGSEEWYLSQLFL
      580     590     600     610     620

      620     630     640     650     660     670
Cry1Ac  VTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRE

gi|128  VKESAFTTQINPLLK
      630     640

>>gi|88687362|dbj|BAE79809.1| Cry31-like 82-kDa protein (726 aa)
      initn: 103 init1: 103 opt: 169 Z-score: 191.2 bits: 46.7 E(): 0.099
Smith-Waterman score: 241; 22.576% identity (51.192% similar) in 629 aa overlap
(42-613:149-726)

      20      30      40      50      60      70
Cry1Ac  NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGI
      :  :...  :  :...  :  :...  :  :...  :
gi|886  QTGSFSALTQSNMNOGGTDINPMLISTFFKVASSLLPPLSSLGALASFYI--TDSQTGA
      120     130     140     150     160     170

      80      90      100     110     120
Cry1Ac  FGSPQWDAFLVQIEQLINQRIIEFARNQAISRLEGLSNLYQIYAESFREWEAD-----P
      :  :...  :  :...  :  :...  :  :...  :
gi|886  MA-NLWRQMVYVEKRIKIDYHNFIMGAELALNASLKEYARVVKIFENDMNRMAEP
      180     190     200     210     220     230

      130     140     150     160     170     180
Cry1Ac  TNPALREEMRIQFNDMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDV--S
      :  :...  :  :...  :  :...  :  :...  :
gi|886  PSTGVITQFRI-LDNFVIKIIAKLQFSTNQSDLYQPVLTPLPRAQACVMHMLLKDATT
      240     250     260     270     280     290

      190     200     210     220
Cry1Ac  VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
      :  :...  :  :...  :  :...  :  :...  :
gi|886  VWGQQ--IDSQQLNGYKAEIIRLIKVVYTNVKTQYDQIDALRRLMELYIQLKSAYFWIYEDWKV
      300     310     320     330     340     350

      230     240     250     260     270
Cry1Ac  PDSR-----DWIRYNQFRRELTLTLVLDIVSLFNPYDSRTYPIRTVSQL-TREIYT
      :  :...  :  :...  :  :...  :  :...  :
gi|886  PDISVLRSNFKEVMKWRVAKYKRGMSALSALALFPFPG-NYPKQALKVQVSRQIFA
      360     370     380     390     400     410

      280     290     300     310     320
Cry1Ac  NPVLENFDGSRGSAQGIIEGSIR---SPHLMIDILNSIT-IYTAHRGGEYIW---SGHQI
      :  :...  :  :...  :  :...  :  :...  :
gi|886  -PVIGIPGGITSQDHSQTFGSMRFDVKTYDQIDALRRLMELYIQLKSAYFWIYEDWKV
      420     430     440     450     460     470

      330     340     350     360     370     380
Cry1Ac  MASPVG-FSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQL
      :  :...  :  :...  :  :...  :  :...  :
gi|886  RATYVNDYIGKR-----GSDTGAANH-----MWSSDPSVIYTSA--LGAAGYAP
      480     490     500     510

      390     400     410     420     430     440

```



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Smith-Waterman score: 151; 48.980% identity (81.633% similar) in 49 aa overlap (127-175:2-50)

Sequence alignment for Smith-Waterman score 151, 48.980% identity. Shows alignment between Cry1Ac and gi|179 from positions 100-210.

>>gi|14103750|gb|AAE55184.1| Sequence 35 from patent US (50 aa)
initn: 151 init1: 151 opt: 151 Z-score: 187.3 bits: 42.1 E(): 0.16
Smith-Waterman score: 151; 48.980% identity (81.633% similar) in 49 aa overlap (127-175:2-50)

Sequence alignment for gi|14103750. Shows alignment between Cry1Ac and gi|141 from positions 100-210.

>>gi|14112755|gb|AAE58170.1| Sequence 35 from patent US (50 aa)
initn: 151 init1: 151 opt: 151 Z-score: 187.3 bits: 42.1 E(): 0.16
Smith-Waterman score: 151; 48.980% identity (81.633% similar) in 49 aa overlap (127-175:2-50)

Sequence alignment for gi|14112755. Shows alignment between Cry1Ac and gi|141 from positions 100-210.

>>gi|114842165|dbj|BAF32570.1| hypothetical protein [Bac (726 aa)
initn: 103 init1: 103 opt: 163 Z-score: 184.1 bits: 45.4 E(): 0.25
Smith-Waterman score: 235; 22.576% identity (51.033% similar) in 629 aa overlap (42-613:149-726)

Sequence alignment for gi|114842165. Shows alignment between Cry1Ac and gi|114 from positions 120-170.

Large sequence alignment block showing multiple alignments between Cry1Ac and various gi| sequences (gi|114, gi|179, gi|141) across positions 80-670.

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        680      690      700      710      720
Cry1Ac  TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSE
        620      630      640      650      660      670
gi|403  TLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSE

>>gi|4033727|gb|AAC97162.1| d-endotoxin [Bacillus thurin (750 aa)
  initn: 109 initl: 82 opt: 163 Z-score: 183.9 bits: 45.4 E(): 0.25
Smith-Waterman score: 170; 18.593% identity (50.503% similar) in 796 aa overlap
(17-729:6-749)

        10      20      30      40      50
Cry1Ac  CMQAMDNNPNINECIPYNCLSNPEVEV--LGGERIETGYTPIDISLS-LTQFLLSEFVPG
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  MENNSFNVLANNMSSFPLFNSKIEPSIAPALIAVAPIAKYLATALAKW
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
        60      70      80      90     100     110
Cry1Ac  AGFVLGLVDIIWGIWGFPSQWDAFL---VQIEQLINQRIEEFARNQAIISRLEGLSNLYQI
        : . . . . : : . . . : . . . . . : . . . . . : . . . . .
gi|403  A-LKQGFALKKSEIF-PGNETATMEKVRLEVQTIILNQLTQTDVATLKAIEYEGFIHLGKV
        50      60      70      80      90     100
        120     130     140     150     160     170
Cry1Ac  YAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHL
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  FTDYVSQSTFTPATA-----KTHFLNMSNLLIQRLPQFEIAGYEGVVISLFTQMCTLHL
        110     120     130     140     150     160
        180     190     200
Cry1Ac  SVLRDVSVFGQRWGF---DAATINSRYNDL-----TRLIGNYT-----DHAVRW
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  GLLKDGILAGSDWGFTPEDKDSLICQFNRYVNEYNTRMMGLYSIEFGRLAKLNLEALNF
        170     180     190     200     210     220
        220     230     240     250     260
Cry1Ac  YNTGLERWVGPDSRDW--IRYNQFRRELTLTVLDIVS-----LFPNYDSRTYPIRTVVSQ
        : . . . . : : . . . : . . . . . : . . . . . : . . . . .
gi|403  RNMCSLYVF-PFSEAWYLLRYEGTKLENTLSLWNFVGEDIGGILHNDWKGALYKLLMGA-
        230     240     250     260     270
        270     280     290     300     310     320
Cry1Ac  LTREIYTNVPLEN--FDGSAQIEGSIKIRPHLMDILNSITTYTDAHRGEYYWSGHQ
        : : . . . : : . . . : . . . . . : . . . . . : . . . . .
gi|403  -----TNQRLANVRFNYSYFSDTQG-----TIHRENILGAHPTY-NGEQTPTWIGNG
        280     290     300     310     320
        330     340     350     360     370
Cry1Ac  IMASPVGFSGP-----EFTFPLYGTMGNAAPQQRIVAQLGGVYRTLSSTLYR
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  RLGR---FSAPYSNELEITKVEQEITYNNKGDHSNSIVPANTRNEILTATVPITADPPFFK
        330     340     350     360     370     380
        380     390     400     410     420
Cry1Ac  -----RPFNIGIN-NQQLSVLDGTEFAYGTSSNLPNAVYRSGT-VDSLDEIPPQNNNV
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|403  TADINWRVYFSGQLYGNWIKFDDRVLNSRVPGIIPSNRLEYDGYIRAVSACP---RNV
        390     400     410     420     430     440
        430     440     450     460     470     480

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Cry1Ac  PPRQGFSSH-RLSHVSMFRSGFSNSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPAVKG
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|403  PLSYHNHNYLTLTYNRLEYDAPTTQNIIVGFSPNNTKSFYARNSHYLSATNDAYVIPALQF
        450     460     470     480     490     500
        490     500     510     520     530     540
Cry1Ac  NFLFNQSVISG-PGFTGGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYASVTP
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  ATVSDRSFLEDTPDQATDGSIKFTETVLGNEAKYSIRLNTGF-NTATRYRLVIRFKATAR
        510     520     530     540     550
        550     560     570     580
Cry1Ac  IHLNV----NWGNSSIFSNVTPATATS-----LDNLQSSDFGYFE-SANAFTS-----
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  LAAGIRVRSQNSGNRLLGG-IPVEGNSGWVDYITDSFTFNDLGIITASTNAFFSIDSDG
        560     570     580     590     600     610
        590     600     610     620     630
Cry1Ac  -----SLGNIVGVRNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTN-
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|403  VNASQQWYLSKLLILVKDFVNNSGF---RNQ-VPL-----APYVIARCP---NTFFVSNNT
        620     630     640     650     660
        640     650     660     670     680     690
Cry1Ac  QLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLQDSNFKDI
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|403  SSGYEQGYNDNYNQNTSS-----GYEQGYNDNYNQNTSSGYEQGYNDNYNQNTSSGYEQ-
        670     680     690     700     710     720
        700     710     720     730     740     750
Cry1Ac  NRQPERGWGGSTGITIQGGDDVFKENYVTLSTGTFDECYPTYLYQKIDESKLFKAFTRYQLR
        . . . . . : . . . . . : . . . . . : . . . . . : . . . . .
gi|403  GYNDNYNQNTSSGYE-QGYNDNYNQNT--TSSGV
        730     740     750
        760     770     780     790     800     810
Cry1Ac  GYIEDSQDLEIYSIRYNAKHETVNVVPGTGLWPLSAQSPIGKCGEPNRCAPHEWNPDL
>>gi|136352573|gb|EBN58813.1| hypothetical protein GOS_8 (416 aa)
  initn: 90 initl: 61 opt: 159 Z-score: 183.0 bits: 44.4 E(): 0.28
Smith-Waterman score: 159; 25.212% identity (51.841% similar) in 353 aa overlap
(253-592:79-411)

        230     240     250     260     270     280
Cry1Ac  WGPDSRDWIRYNQFRRELTLTVLDIVSLFNPYDSRTYPIRTVSQLTREIYTNVPLENFDG
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|136  ESVSIGTHFSPPKGGIEERGQNFLEGMRFNTDLNTEFYNHGEWRQFTYISEVQNSPSS
        50      60      70      80      90     100
        290     300     310     320     330     340
Cry1Ac  SFRGSAQIEGSIKIRPHLMDILNSITTYTDAHRGEYYWSGHQIMA-SPVGFSGPEFTFPL
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|136  SGRAVYGGGNNSP-TPPAADVFTSINIHTLGNSSHFGDSQHSNVALAGGCGDRRGIFA-
        110     120     130     140     150     160
        350     360     370     380     390
Cry1Ac  YGTMGNAAPQQRRI---VAQLGGV-YRTLSTLYRRPFGINNNQQLSVLDGTEFAYGT
        : . . . . : . . . . : . . . . : . . . . : . . . . : . . . .
gi|136  -GGLPNASHYNTIEYITVASAGNAINFGLSNSQGRDSSGGAATTSTRMCI---TGLSRYT

```

```

170      180      190      200      210      220
Cry1Ac 400      410      420      430      440      450
SSNLPASV--YRKSQTVDSLDEIPQNNVPPRQGFSHRLSHVSMFRSGFSNSSVSIIRA
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|136 PGNTASNIIDYVETQTLGNALDFGDQIINMCNNGNGFSSPTRGF-FFGTGFNNPSIPIHF
230      240      250      260      270      280

```

```

460      470      480      490      500
Cry1Ac PMFSWIHRSAEFNIIASDSITQIPAVKGNFLFNGSVISG--PGFTGG--DLVRLNSSG
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|136 ITIASKGNSADFGD---STSIRQYPG-GGSSSVRG-VISGGNTPSSTIQTIDYVTMSSSG
290      300      310      320      330

```

```

510      520      530      540      550      560
Cry1Ac NNIQNRGYIEVP IHFPSTSTRYRVRVRYASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|136 NATV-FGDLTLARHSPAGASS-KTRTVFAGG---YTDESSENTDV-NNMDYITIASTGNA
340      350      360      370      380      390

```

```

570      580      590      600      610      620
Cry1Ac QSSDFGYFESANAFTSSLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|136 Q--DFGDLYYKTSFLCSASSCHGGLGGY
400      410

```

>>gi|112088059|gb|ABI06964.1| Sequence 44 from patent US (72 aa)  
 initn: 120 initl: 120 opt: 149 Z-score: 182.6 bits: 41.7 E(): 0.3  
 Smith-Waterman score: 149; 39.706% identity (72.059% similar) in 68 aa overlap  
 (560-624:5-72)

```

530      540      550      560      570      580
Cry1Ac RYRVRVRYASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFTSSL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 VADFPKTIIDRGENLEYGSRFRTAGFTTPFSFVSST
10      20      30

```

```

590      600      610      620      630      640
Cry1Ac GNI-VGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|112 NNFTLVGVQSVSSGNEIFVDRIEFVPADATFEAEYDLER
40      50      60      70

```

```

650      660      670      680      690      700
Cry1Ac DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG

```

>>gi|33765732|gb|AAQ52383.1| Sequence 44 from patent US (72 aa)  
 initn: 120 initl: 120 opt: 149 Z-score: 182.6 bits: 41.7 E(): 0.3  
 Smith-Waterman score: 149; 39.706% identity (72.059% similar) in 68 aa overlap  
 (560-624:5-72)

```

530      540      550      560      570      580
Cry1Ac RYRVRVRYASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNLQSSDF--GYFESANAFTSSL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 VADFPKTIIDRGENLEYGSRFRTAGFTTPFSFVSST
10      20      30

```

```

590      600      610      620      630      640
Cry1Ac GNI-VGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVT

```

```

... : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 NNFTLVGVQSVSSGNEIFVDRIEFVPADATFEAEYDLER
40      50      60      70

```

```

650      660      670      680      690      700
Cry1Ac DYHIDQVSNLVTYLSDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWG

```

>>gi|33731238|gb|AAQ37301.1| Sequence 25 from patent US (108 aa)  
 initn: 121 initl: 80 opt: 150 Z-score: 181.1 bits: 42.1 E(): 0.36  
 Smith-Waterman score: 150; 34.444% identity (61.111% similar) in 90 aa overlap  
 (495-584:1-85)

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 PGFXGGDILRRNTIGEFVS---LQVNINS
10      20

```

```

530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|337 PITQ-RYRLRFRYASSRDARITVAIGGQIRVXMTLEKTMEIGESLTSRTFSYTNFNSPPFS
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN

```

```

gi|337 FRANPDIIRIAEELPIRGGELVY
90      100

```

>>gi|53970021|gb|AAV19114.1| Sequence 25 from patent US (108 aa)  
 initn: 121 initl: 80 opt: 150 Z-score: 181.1 bits: 42.1 E(): 0.36  
 Smith-Waterman score: 150; 34.444% identity (61.111% similar) in 90 aa overlap  
 (495-584:1-85)

```

470      480      490      500      510      520
Cry1Ac EFNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 PGFXGGDILRRNTIGEFVS---LQVNINS
10      20

```

```

530      540      550      560      570      580
Cry1Ac PSTSTRYRVRVRYASVTPIHLLNVNWNWGNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|539 PITQ-RYRLRFRYASSRDARITVAIGGQIRVXMTLEKTMEIGESLTSRTFSYTNFNSPPFS
30      40      50      60      70      80

```

```

590      600      610      620      630      640
Cry1Ac SSLGNIVGVRNFGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTN

```

```

gi|539 FRANPDIIRIAEELPIRGGELVY
90      100

```

>>gi|21504396|gb|AAM57097.1| Sequence 25 from patent US (108 aa)  
 initn: 121 initl: 80 opt: 150 Z-score: 181.1 bits: 42.1 E(): 0.36  
 Smith-Waterman score: 150; 34.444% identity (61.111% similar) in 90 aa overlap  
 (495-584:1-85)

```

470      480      490      500      510      520

```

Regulatory Product Characterization Team

Cry1Ac EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|215 PGFXGGDILRRNTIGEFVS---LQVNNINS
10 20

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
gi|215 PITQ-RYRLRFYASSRDARITVAIGGQIRVXMTLEKTMEIGESLTSRTFSYTNFNSNPF
30 40 50 60 70 80

Cry1Ac 590 600 610 620 630 640
SSLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|215 FRANPDIIRIAEELPIRGGELVY
90 100

>>gi|16240169|gb|AAE79620.1| Sequence 25 from patent US (108 aa)
initn: 121 initl: 80 opt: 150 Z-score: 181.1 bits: 42.1 E(): 0.36
Smith-Waterman score: 150; 34.444% identity (61.111% similar) in 90 aa overlap
(495-584:1-85)

Cry1Ac 470 480 490 500 510 520
EFNNIIASDSITQIPAVKGNFLFNGSVISGPGFTGGDLVRLNSSGNNIQNRGYIEVPIHF
gi|162 PGFXGGDILRRNTIGEFVS---LQVNNINS
10 20

Cry1Ac 530 540 550 560 570 580
PSTSTRYRVRVRYASVTPIHLLNVNWNSSIFSNTVPATATSLDNLQSSDFGYFESANAFT
gi|162 PITQ-RYRLRFYASSRDARITVAIGGQIRVXMTLEKTMEIGESLTSRTFSYTNFNSNPF
30 40 50 60 70 80

Cry1Ac 590 600 610 620 630 640
SSLGNIVGVRNFSGTAGVIIDRFEPVPTATLEAEYNLERAQKAVNALFTSTNQLGLKTN
gi|162 FRANPDIIRIAEELPIRGGELVY
90 100

>>gi|75812162|dbj|BAE44985.1| hypothetical protein [Baci (378 aa)
initn: 103 initl: 103 opt: 155 Z-score: 178.9 bits: 43.5 E(): 0.48
Smith-Waterman score: 178; 24.088% identity (53.650% similar) in 274 aa overlap
(42-277:97-362)

Cry1Ac 20 30 40 50 60 70
NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEFVPGAGFVLGLVDIIWGI
gi|758 QTGSFALTQSNMNGGTDINPMLISTFFKVASSLLPPLSLGALASFYI--TDSQTGA
70 80 90 100 110 120

Cry1Ac 80 90 100 110 120
FGPSQWDAFLVQIEQLINQRIEAFARNQAISRLEGLSNLYQIYAESFREWEAD-----P
gi|758 MA-NLWRQMVYDVEKRIDSKILDYHNFIMGAELAALNASLKEYARVVKIFENDMNRMAEP
130 140 150 160 170 180

Cry1Ac 130 140 150 160 170 180
TNPALREEMRIQFNDMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDVS--S

gi|758 190 200 210 220 230 240
PSTGVITQFRI-LNDNFIKYIAKLQFSTNQSDLQYVPLTLPLRAQACVMHMLLLKDATTS

Cry1Ac 190 200 210 220
VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
gi|758 VWGQQ--IDSQQLNGYKAEILRLIKVYTNVNTTYNQGLELEKAKPLNYSDPPEYLQAGR
250 260 270 280 290 300

Cry1Ac 230 240 250 260 270
PDSR-----DWIRYNQFRRELTTLVLDIVSLFPNYDSRTYPIRTVSQL-TREIYT
gi|758 PDISVLRSNFKEVMKWRVAKYKRGMSALSALALFPPTFGP-NYPKQALKVVQSRQIFA
310 320 330 340 350

Cry1Ac 280 290 300 310 320 330
NPVLENFDGFRGSAQIEGSIKRSPLMDILNSITTYTDAHRGEYYWSGHQIMASVPVGF
gi|758 -PVIGIPGGITSQDHSQTFG
360 370

>>gi|145843786|gb|ABP96900.1| cry4B [Bacillus thuringien (94 aa)
initn: 142 initl: 94 opt: 147 Z-score: 178.5 bits: 41.4 E(): 0.51
Smith-Waterman score: 147; 45.902% identity (77.049% similar) in 61 aa overlap
(595-652:33-93)

Cry1Ac 570 580 590 600 610 620
SLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEPVPTATL--EAE-YN
gi|145 EEFYKDPFDAIVPMLRSSNQLITIAIQPLNMTSNNQVIIDRIEIIIPITQSVLDETENQN
10 20 30 40 50 60

Cry1Ac 630 640 650 660 670 680
LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKR
gi|145 LESEREVVNALFTNDAKDALNIGTTDYDIDQA
70 80 90

Cry1Ac 690 700 710 720 730 740
LSDERNLLQDSNFKDINRQPERGWGGSTGITIQGGDDVFKENYVTLSGTFDECYPTTYLYQ

>>gi|118640569|gb|ABL09855.1| Cry4B [Bacillus thuringien (95 aa)
initn: 142 initl: 94 opt: 147 Z-score: 178.4 bits: 41.4 E(): 0.51
Smith-Waterman score: 147; 45.902% identity (77.049% similar) in 61 aa overlap
(595-652:35-95)

Cry1Ac 570 580 590 600 610 620
SLDNLQSSDFGYFESANAFTSSLGNIVGVRNFSGTAGVIIDRFEPVPTATL--EAE-YN
gi|118 EVFRYKDPFDAIVPMLRSSNQLITIAIQPLNMTSNNQVIIDRIEIIIPITQSVLDETENQN
10 20 30 40 50 60

Cry1Ac 630 640 650 660 670 680
LERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKRESEKVKHAKR
gi|118 LESEREVVNALFTNEAKDALNIGTTDYDIDQ
70 80 90



```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|233          DNPVTRTRVVDRFRILDGLLERDIPSFRIAG
                    10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
gi|233 FEVPLLSVYAQAANLHLAI
                    40      50

```

>>gi|158456684|gb|ABW41357.1| Sequence 37 from patent US (50 aa)  
 initn: 143 init1: 143 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 44.898% identity (73.469% similar) in 49 aa overlap  
 (127-175:2-50)

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|158          DNPVTRTRVVDRFRILDGLLERDIPSFRIAG
                    10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
gi|158 FEVPLLSVYAQAANLHLAI
                    40      50

```

>>gi|14112757|gb|AAE58172.1| Sequence 37 from patent US (50 aa)  
 initn: 143 init1: 143 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 44.898% identity (73.469% similar) in 49 aa overlap  
 (127-175:2-50)

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|141          DNPVTRTRVVDRFRILDGLLERDIPSFRIAG
                    10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
gi|141 FEVPLLSVYAQAANLHLAI
                    40      50

```

>>gi|17920900|gb|AAE86520.1| Sequence 49 from patent US (50 aa)  
 initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap  
 (131-173:6-48)

```

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|179          NDARSRSIIIRERYIALELDITTAIPLFSIRNEEVP
                    10      20      30

```

```

      170      180      190      200      210      220

```

```

Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|179 LLMVYAQAANLHLLL
                    40      50

```

>>gi|14103764|gb|AAE55198.1| Sequence 49 from patent US (50 aa)  
 initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap  
 (131-173:6-48)

```

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|141          NDARSRSIIIRERYIALELDITTAIPLFSIRNEEVP
                    10      20      30

```

```

      170      180      190      200      210      220
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|141 LLMVYAQAANLHLLL
                    40      50

```

>>gi|14112769|gb|AAE58184.1| Sequence 49 from patent US (50 aa)  
 initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap  
 (131-173:6-48)

```

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|141          NDARSRSIIIRERYIALELDITTAIPLFSIRNEEVP
                    10      20      30

```

```

      170      180      190      200      210      220
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|141 LLMVYAQAANLHLLL
                    40      50

```

>>gi|23325109|gb|AAN23809.1| Sequence 49 from patent US (50 aa)  
 initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55  
 Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap  
 (131-173:6-48)

```

      110      120      130      140      150      160
Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|233          NDARSRSIIIRERYIALELDITTAIPLFSIRNEEVP
                    10      20      30

```

```

      170      180      190      200      210      220
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|233 LLMVYAQAANLHLLL
                    40      50

```

>>gi|56664664|gb|AAW18089.1| Sequence 49 from patent US (50 aa)  
 initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55

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Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap (131-173:6-48)

Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|566 NDARSRSIIRERYIALELDITTAIPLFSIRNEEVP
10 20 30
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|566 LLMVYAQAANLHLLL
40 50

>>gi|158456696|gb|ABW41369.1| Sequence 49 from patent US (50 aa)
initn: 138 init1: 138 opt: 143 Z-score: 177.9 bits: 40.3 E(): 0.55
Smith-Waterman score: 143; 53.488% identity (79.070% similar) in 43 aa overlap (131-173:6-48)

Cry1Ac ISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVP
gi|158 NDARSRSIIRERYIALELDITTAIPLFSIRNEEVP
10 20 30
Cry1Ac LLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE
gi|158 LLMVYAQAANLHLLL
40 50

>>gi|75812164|dbj|BAE44986.1| hypothetical protein [Baci (397 aa)
initn: 103 init1: 103 opt: 154 Z-score: 177.4 bits: 43.3 E(): 0.58
Smith-Waterman score: 177; 24.088% identity (53.650% similar) in 274 aa overlap (42-277:116-381)

Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQPLLSEFVPGAGFVLGLVDI IWGI
gi|758 QTGSFSALTQSNMNOGGTDINPMLISTFFKVASLLPFPSSLGALASFYV--TDSQTGA
90 100 110 120 130 140
Cry1Ac FGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEAD-----P
gi|758 MA-NLWRQMVVDYVEKRIDS KILDYHNFIMGAELAAALNASLKEYARVVKIFENDMNRMAEP
150 160 170 180 190 200

Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDVS-S
gi|758 PSTGVITQFRI-LNDNFIKYIAKLFQSTNQSDLQYPVLTPLRAQACVMHMLMLLDKDATTS
210 220 230 240 250 260

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
gi|758 VWGQQ--IDSQQLNGYKABLIRLIKVYTDVNTTNYNQLGLELEKAKPLNYSDPPEEYLQAGR

270 280 290 300 310
Cry1Ac PDSR-----DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQL-TREIYT
gi|758 PDISVLRSNFKEVMKWNRVAKYKRGMMAMSALSALFPFTFGP-NYPKQALKVQSRQIFA
320 330 340 350 360 370
Cry1Ac NPVLENFDFGSRFGSAQIEGSIRSPLMDILNSITTYTDahrGEYYWSGHQIMASPVGFS
gi|758 -PVIGIPGGITSQDHSGETFG
380 390

>>gi|14112756|gb|AAE58171.1| Sequence 36 from patent US (50 aa)
initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap (127-175:2-50)

Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|141 NNPETRTRVIDRFRILDGLLERDIPSPFRISG
10 20 30
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
gi|141 FEVPLLSVYAQAANLHLAI
40 50

>>gi|56642284|gb|AAW12002.1| Sequence 36 from patent US (50 aa)
initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap (127-175:2-50)

Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|566 NNPETRTRVIDRFRILDGLLERDIPSPFRISG
10 20 30
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
gi|566 FEVPLLSVYAQAANLHLAI
40 50

>>gi|23325096|gb|AAN23796.1| Sequence 36 from patent US (50 aa)
initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap (127-175:2-50)

Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
gi|233 NNPETRTRVIDRFRILDGLLERDIPSPFRISG
10 20 30

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```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....:.....
gi|233 FEVPLLSVYAQAANLHLAI
      40      50

>>gi|56664651|gb|AAW18076.1| Sequence 36 from patent US (50 aa)
  initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      :: : .. .: ... : :: : ...
gi|566          NNPETRTRVIDRFRILDGLLERDIPSFRISG
                  10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....:.....
gi|566 FEVPLLSVYAQAANLHLAI
      40      50

```

```

>>gi|14103751|gb|AAE55185.1| Sequence 36 from patent US (50 aa)
  initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      :: : .. .: ... : :: : ...
gi|141          NNPETRTRVIDRFRILDGLLERDIPSFRISG
                  10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....:.....
gi|141 FEVPLLSVYAQAANLHLAI
      40      50

```

```

>>gi|158456683|gb|ABW41356.1| Sequence 36 from patent US (50 aa)
  initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64
Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      :: : .. .: ... : :: : ...
gi|158          NNPETRTRVIDRFRILDGLLERDIPSFRISG
                  10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....:.....
gi|158 FEVPLLSVYAQAANLHLAI
      40      50

```

```

>>gi|17920887|gb|AAE86507.1| Sequence 36 from patent US (50 aa)
  initn: 142 init1: 142 opt: 142 Z-score: 176.7 bits: 40.1 E(): 0.64

```

```

Smith-Waterman score: 142; 44.898% identity (73.469% similar) in 49 aa overlap
(127-175:2-50)

```

```

      100      110      120      130      140      150
Cry1Ac RNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLFAVQN
      :: : .. .: ... : :: : ...
gi|179          NNPETRTRVIDRFRILDGLLERDIPSFRISG
                  10      20      30

```

```

      160      170      180      190      200      210
Cry1Ac YQVPLLSVYVQAANLHLSVLRDVSVFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYN
.....:.....
gi|179 FEVPLLSVYAQAANLHLAI
      40      50

```

```

>>gi|75812158|dbj|BAE44983.1| hypothetical protein [Baci (397 aa)
  initn: 102 init1: 102 opt: 152 Z-score: 175.1 bits: 42.8 E(): 0.79
Smith-Waterman score: 175; 24.088% identity (53.650% similar) in 274 aa overlap
(42-277:116-381)

```

```

      20      30      40      50      60      70
Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGI
      .. :: : :: . : : : . : : : .
gi|758 QTGSFSALTQSNMNGGGTDINPMLISAFFKVGAGSLLPFPPLSSLGALASFYV--TDSQTGA
      90      100      110      120      130      140

```

```

      80      90      100      110      120
Cry1Ac FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD-----P
      .. .: .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|758 MA-NLWRQMVDYVEKRIDSKILDYHNFIMGAEALALNASLKEYARVVKIFENDMNRMAEP
      150      160      170      180      190      200

```

```

      130      140      150      160      170      180
Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDV--S
      .. .: .. : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|758 PSTGVITQFRI-LNDFIKYIAKLQFSTNQSDLQYPVLTPLPLRAQARVMHMLLLKDATTS
      210      220      230      240      250      260

```

```

      190      200      210      220
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|758 VWGQQ--IDSQQLNGYKAEILIRLIKVYTNVDVNTTYNQGLELEKAKPLNYSDPPEEYLQAGR
      270      280      290      300      310

```

```

      230      240      250      260      270
Cry1Ac PDSR-----DWIRYNQFRRELTTLVLDIVSLFPPNYDSRSTYPIRTVSQL-TREIYT
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|758 PDISVLRSNFKEVMKWNRVAKYKRGMSALSALSLAALFPFPG-NYPKQALKVQSRQIFA
      320      330      340      350      360      370

```

```

      280      290      300      310      320      330
Cry1Ac NPVLENFDGSRGSAQIEGSIKRSRPHLMDILNSITIYTDahrgeyYWSGHQIMASVPGFS
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|758 -PVIGIPGGITSDHSGSTFG
      380      390

```

```

>>gi|88687360|dbj|BAE79808.1| Cry31-like 81-kDa protein (723 aa)
  initn: 103 init1: 103 opt: 155 Z-score: 174.7 bits: 43.6 E(): 0.82

```

Regulatory Product Characterization Team

Smith-Waterman score: 213; 22.275% identity (50.237% similar) in 633 aa overlap (42-613:149-723)

Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGI
gi|886 QTGSFSALTQSNMNGGTDINPMLISTFFKVASSLLPFPPLSSLGALASFYV--TDSQTGA

Cry1Ac FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD-----P
gi|886 MA-NLWRQMVDVVEKRIDSKILDYHNFIMGAEALANASLKEYARVVKIFENDMNRMAEP

Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQ--NYQVPLLSV--YVQAANLHLSVLRDV--S
gi|886 PSTGVITQFRI-LNDNFIKYYIAKLFSTNQSDLPVLTLPRAQACVMHMLMLLKDATT

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLE-----RVWG
gi|886 VWGQQ--IDSQQLNGYKAEILIRLIKVYTNVNTTYNQGLELEKAKPLNYSDPPEYLQAGR

Cry1Ac PDSR-----DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQL-TREIYT
gi|886 PDISVLRSNFKEVMKWNRVAKYKRGMSALSALALFPFPG-NYPKQALKVVQSRQIFA

Cry1Ac NPVLENFDGSRFGSAQIEGSIR---SPHLMIDILNSIT-IYTDHRGEYYW---SGHQI
gi|886 -PVIGIPGGITSQDHSQTFGSMRFDVKTYDQIDALRRLMELYIQPLKSAYFYIYESDQKV

Cry1Ac MASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS
gi|886 RATYVN-----DYIGKRSNTG-----LAWGMWSSDPVSIYTS--LGAAGYAPN

Cry1Ac VLDGTEFAYGTSNLPASVYRKSQTVDSLDEIPPQNNVPPRQGFSSH--RLSHVSMFRS
gi|886 VV-GVRYSHGGS-----YTKG-----MAPPNTNAYAPFE-FKYPGYKLSHSVAY--

Cry1Ac GFSNSVSIIRAPMFSW--IHRSAEFNIIASDSITQIPAVKGNFLFNGSVISGPGFT--
gi|886 GLSKAP-DTADSVMPGFRPVLENEANQLL--TDTALQIPAEIG---ITDVPAPFGRTEE

Cry1Ac ---GGDLVRLNSSGNINQNRGYIEVPIHFPSTSTRYRVRVRYAS-VTPIHLNVNWGNSSI

gi|886 PINGQDAIIWESFTS--GFGFTYT-VDSPQ-KQKYKIIYRIANNLSASTVSLTYNNQTF
610 620 630 640 650 660

Cry1Ac FSNTVPATATSLD-NLQSSDFGYF---ESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFI
610 620 630 640 650 660 670

gi|886 FTDIL---NTSLDPNGVRNGYSYTLVEGPIIEFSGQGTNIFKLRQKGE--FAIDSIIIFS
670 680 690 700 710 720

Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
620 630 640 650 660 670

gi|886 PVS

>>gi|9798640|dbj|BAB11757.1| 81-kDa leukemia toxin [Baci (723 aa)
initn: 103 initl: 103 opt: 155 Z-score: 174.7 bits: 43.6 E(): 0.82
Smith-Waterman score: 213; 22.275% identity (50.237% similar) in 633 aa overlap
(42-613:149-723)

Cry1Ac NECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLSEFVPGAGFVLGLVDIIWGI
gi|979 QTGSFSALTQSNMNGGTDINPMLISTFFKVASSLLPFPPLSSLGALASFYV--TDSQTGA

Cry1Ac FGPSQWDAFLVQIEQLINQRIEEFARNQAISRLEGLSNLYQIYAESFREWEAD-----P
gi|979 MA-NLWRQMVDVVEKRIDSKILDYHNFIMGAEALANASLKEYARVVKIFENDMNRMAEP

Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQ--NYQVPLLSV--YVQAANLHLSVLRDV--S
gi|979 PSTGVITQFRI-LNDNFIKYYIAKLFSTNQSDLPVLTLPRAQACVMHMLMLLKDATT

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLE-----RVWG
gi|979 VWGQQ--IDSQQLNGYKAEILIRLIKVYTNVNTTYNQGLELEKAKPLNYSDPPEYLQAGR

Cry1Ac PDSR-----DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQL-TREIYT
gi|979 PDISVLRSNFKEVMKWNRVAKYKRGMSALSALALFPFPG-NYPKQALKVVQSRQIFA

Cry1Ac NPVLENFDGSRFGSAQIEGSIR---SPHLMIDILNSIT-IYTDHRGEYYW---SGHQI
gi|979 -PVIGIPGGITSQDHSQTFGSMRFDVKTYDQIDALRRLMELYIQPLKSAYFYIYESDQKV

Cry1Ac MASPVGFSGPEFTFFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS

```

gi|979 RATYVN-----DYIGKRGSNLTG-----LAWGMWSSDPSVIYNTSA--LGAAGYAPN
          480          490          500          510

```

```

Cry1Ac VLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFsH--RLSHVSMFRS
          390          400          410          420          430          440

```

```

gi|979 VV-GVRYSHGGs-----YTKG-----MAPPNTNAYAPFE--FKYPGYKLHsVSAY--
          520          530          540          550

```

```

Cry1Ac GFSNssVSIIRAPMFsW--IHRSAEFNIIASDSITQIPAVKGNFLFNGSvisGPGFT--
          450          460          470          480          490

```

```

gi|979 GLSKAP-DTADsVMFGRFPVLLENEANQLL--TDTALQIPAEIG---ITDvVPAFGRTEE
          560          570          580          590          600

```

```

Cry1Ac --GGDLVRLNssGNNIQRGYIEVPIHFPSTSTRYRVRVRYAS-VTPIHLNVNWGNssI
          500          510          520          530          540          550

```

```

gi|979 PINGQDAIIWESFts--GFGFTYT-VDSPQ--KQKYKIIYRIANNLsASTVSLTYNNQTF
          610          620          630          640          650          660

```

```

Cry1Ac FSNTVPATATSLD-NLQSSDFGYF--ESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFI
          560          570          580          590          600          610

```

```

gi|979 FTDIL---NTSLDPNGVRGNYGSYTLVGEPIIEFsqGTNIFKLRsQKGE--FAIDSIIFS
          670          680          690          700          710          720

```

```

Cry1Ac PVTATLEAEYnLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
          620          630          640          650          660          670

```

gi|979 PVS

```

>>gi|114842169|dbj|BAF32572.1| hypothetical protein [Bac (723 aa)
  initn: 103 init1: 103 opt: 154 Z-score: 173.6 bits: 43.4 E(): 0.96
Smith-Waterman score: 213; 22.397% identity (50.473% similar) in 634 aa overlap
(42-613:149-723)

```

```

Cry1Ac NECIPYNCLSNPEVEVLGGERIEtGYTPIDISLSLTQFLLEsFVPGAGFVLGLVDIIWGI
          20          30          40          50          60          70

```

```

gi|114 QTGSFsALTQSNMnQGgTDINPMLISTFFKvASSLLPFPLSSLgALASfYV--TDSQGTGA
          120          130          140          150          160          170

```

```

Cry1Ac FGPSQWDAFLVQIEQLINQRIEFARNQAIrSRLGLEGLSNLYQIYAESfREWEAD-----P
          80          90          100          110          120

```

```

gi|114 MA-NLWRQmVDYVEKRIDSKILDYHNFIMGAELALNASLKKEYARVVKIIFENDMNRMAEP
          180          190          200          210          220          230

```

```

Cry1Ac TNPALREEMRIQFNdMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDv--S
          130          140          150          160          170          180

```

```

gi|114 PSTGVIQFRI-LNDNFIKYIAKLQFSTNQSDLQYPVLTLPLRAQACVMHMLMLLDATTS
          240          250          260          270          280          290

```

```

Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
          190          200          210          220

```

```

gi|114 VWGQQ--IDSQQLNGYKAEILIRLIKVYNTDvNTTYNQGLELEKAKPLNYSDPPEEYLQAGR
          300          310          320          330          340          350

```

```

Cry1Ac PDSR-----DWIRYNQFRRELTTLTVLDIVSLFPNYDSRTYPIRTVSQL-TREIYT
          230          240          250          260          270

```

```

gi|114 PDISILRSNFKEVMKWNRVAKYKRGmAMSALSLAALFPPTFGP-NYPKQALKVVQSRQIFA
          360          370          380          390          400          410

```

```

Cry1Ac NPVLENFDGSFRGSAQIEGSIR---SPHLMdILNSIT-IYDahRGEYYW---SGHQI
          280          290          300          310          320

```

```

gi|114 -PVIGIPGGITsQDHSgTfGSMRFdvKTYDQIDALRRLMELYIQPLKSAYfWIYESDkWV
          420          430          440          450          460          470

```

```

Cry1Ac MASPVG-FSGPEFTFPLYGTMGNAAPQQRIVaQLGQGVYRTLsSTLYRRFPNIGINNQQL
          330          340          350          360          370          380

```

```

gi|114 RATYVNDYIGKR-----GSNTGAAWH-----MWSSDPSVIYNTSA--LGAAGYAP
          480          490          500          510

```

```

Cry1Ac SVLDGTEFAYGTSSNLPsAVYRKSGTVDSLDEIPPQNNVPPRQGFsH--RLSHVSMFRS
          390          400          410          420          430          440

```

```

gi|114 NVV-GVRYSHGGs-----YTKG-----MAPPNTNAYAPFE--FKYPGYKLHsVSAY--
          520          530          540          550

```

```

Cry1Ac SGFSNssVSIIRAPMFsW--IHRSAEFNIIASDSITQIPAVKGNFLFNGSvisGPGFT-
          450          460          470          480          490

```

```

gi|114 -GLSKAP-DAADsVMFGRFPVLLENEANQLL--TDTALQIPAEIG---ITDvVPAFGRTE
          560          570          580          590          600

```

```

Cry1Ac ---GGDLVRLNssGNNIQRGYIEVPIHFPSTSTRYRVRVRYAS-VTPIHLNVNWGNss
          500          510          520          530          540          550

```

```

gi|114 EPINGQDAIIWESFts--GFGFTYT-VDSPQ--KQKYKIIYRIANNLsASTVSLTYNNQTF
          610          620          630          640          650          660

```

```

Cry1Ac IFSNTVPATATSLD-NLQSSDFGYF--ESANAFTSSLGNIVGVRNFSGTAGVIIDRFEF
          560          570          580          590          600

```

```

gi|114 FFTDIL---NTSLDPNGVRGNYGSYTLVGEPIIEFsqGTNIFKLRsQKGE--FAIDSIIF
          670          680          690          700          710

```

```

Cry1Ac IPVATLEAEYnLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEK
          610          620          630          640          650          660

```

gi|114 SPVS  
720

```

>>gi|114842167|dbj|BAF32571.1| hypothetical protein [Bac (723 aa)
  initn: 103 init1: 103 opt: 154 Z-score: 173.6 bits: 43.4 E(): 0.96
Smith-Waterman score: 212; 22.275% identity (50.237% similar) in 633 aa overlap
(42-613:149-723)

```

```

Cry1Ac NECIPYNCLSNPEVEVLGGERIEtGYTPIDISLSLTQFLLEsFVPGAGFVLGLVDIIWGI
          20          30          40          50          60          70

```

Regulatory Product Characterization Team

```

.. :: : :: . :. . : :
gi|114 QTGSFSALTQSNMNQGGTDINPMLISTFFKVASLLPPLSSLGALASFYV--TDSQTA
120 130 140 150 160 170

80 90 100 110 120
Cry1Ac FGPSQWDAFLVQIEQLINQRIEEFARNQAIISRLEGLSNLYQIYAESFREWEAD-----P
.. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 MA-NLWRQMVYVEKRIDSKILDYHNFIMGAEALANASLKEYARVVKIFENDMNRMAEP
180 190 200 210 220 230

130 140 150 160 170 180
Cry1Ac TNPALREEMRIQFNDMNSALTTAIPLFAVQ-NYQVPLLSV--YVQAANLHLSVLRDV--S
.. . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 PSTGVITQFRI-LDNDFIKYIAKLQFSTNQSDLQYPVLTLPRAQACVMHMLLLKDATT
240 250 260 270 280 290

190 200 210 220
Cry1Ac VFGQRWGFDAATINSRYNDLTRLIGNYTDHAVRWYNTGLE-----RVWG
.: : . : . : . : : : : : . : : : : :
gi|114 VWGQQ--IDSQQLNGYKAELIRLIKVYTNVNTTYNQGLELEKAKPLNYSDPPEYLQAGR
300 310 320 330 340 350

230 240 250 260 270
Cry1Ac PDSR-----DWIRYNQFRRELTLTVLDIVSLFPNYDSRTYPIRTVSQI-TREIYT
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 PDISVLRSNFKEVMKWRVAKYKRGMAASLSAALFPFPG-NYPKQALKVVQSRQIFA
360 370 380 390 400 410

280 290 300 310 320
Cry1Ac NPVLENFDGSRGSAQGLEGSIR---SPHLMIDILNSIT-IYTDHRGEYYW---SGHQI
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 -PVIGIPGGITSQDHSQTFGSMRFDVKTYDQIDALRRLMELYIQPLKSAYFYIYESDWKV
420 430 440 450 460 470

330 340 350 360 370 380
Cry1Ac MASPVGFSGPEFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSSTLYRRPFNIGINNQQLS
.: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 RATYVN-----DYIGKRGSNITG-----LAWGMWSSDPSVIYTS--LGAAGYAPN
480 490 500 510

390 400 410 420 430 440
Cry1Ac VLDGTEFAYGTSSNLPASVYRKSGTVDSLDEIPPQNNVPPRQGFH--RLSHVSMFRS
.: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 VV-GVRYSHGGS-----YTKG-----MAPPNTNAYAPFE-FKYPGYKLHVSAY--
520 530 540 550

450 460 470 480 490
Cry1Ac GFSNSSVSIIRAPMFSW--IHRSAEFNNIIASDSITQIPAVKGNFLFNGSVISGPGFT--
.: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 GLSKAP-DTADSVMPGFRPVLLENEANQLL-TDTALQIPAEIG---ITDVPVAFGRTEE
560 570 580 590 600

500 510 520 530 540 550
Cry1Ac ---GGDLVRLNSSGNNIQNRGYIEVPIHFPSTSTRYRVRVRYAS-VTPIHLNVNWNSSII
.: : . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 PINGQDAIIWESFTS--GFGFTYT-VDSPQ-KQYKIIYRIANNLSASTVSLTYNNQTF
610 620 630 640 650 660

560 570 580 590 600 610

```

```

Cry1Ac FSNTVPATATSLD-NLQSSDFGYF---ESANAFTSSLGNIVGVRNFSGTAGVIIDRFEFI
.: . : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
gi|114 FTDIL--NTSLDPNGVRNGYSYTLVEGPIMEFSQGTNIFRLRSQKGE--FAIDSIIFS
670 680 690 700 710 720

620 630 640 650 660 670
Cry1Ac PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTYLSDEFCLDEKR
.: .
gi|114 PVS

```

1182 residues in 1 query sequences  
3227582627 residues in 12963194 library sequences  
Scomplib [34t26]  
start: Mon Oct 6 17:28:54 2008 done: Mon Oct 6 18:02:59 2008  
Total Scan time: 1886.700 Total Display time: 130.640

Function used was FASTA [version 3.4t26 July 7, 2006]