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to

Application to Food Standards Australia New Zealand
for the inclusion of
Lepidopteran-protected maize MON 89034
in Standard 1.5.2 - Food Derived from Gene
Technology

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Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
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Study Title

Bioinformatics Analysis of the Cry2Ab2 Protein Utilizing the AD6, TOXIN5, and
ALLPEPTIDES Databases

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Study Completed On

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Laboratory Project ID

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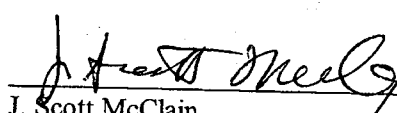
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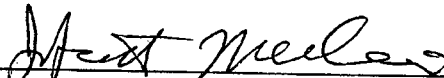
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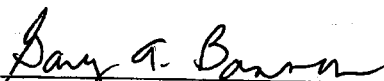
Study Certification

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

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Study Information

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Abbreviations and Definitions

aa	Amino acid
AD6	Allergen, gliadin, and glutenin protein sequence database
ALLPEPTIDES	Protein sequence database comprised of GenBank and SwissProt
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
Cry1A.105	Protein that confers <i>lepidopteran</i> insect resistance and is comprised of portions of naturally occurring <i>Bacillus thuringiensis</i> proteins Cry1Ab (domains I & II), Cry1F (domain III), and Cry1Ac (protoxin domain)
DATASET	Command used to create a GCG data library from a set of sequences in GCG format
EMBL	A public genetic database maintained by the European Molecular Biology Laboratory at the European Bioinformatics Institute, Hinxton, England
FASTA	Algorithm used to find local high scoring alignments between a pair of protein or nucleotide sequences
GCG	Genetics Computer Group, part of Accelrys and called the Wisconsin Package
GenBank	A public genetic database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
GI	Gene Sequence identification number
IUIS	International Union of Immunological Societies
NCBI	National Center of Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
NRL3D	National Research Laboratory's three-dimensional protein database founded at Brookhaven National Laboratory and maintained by the RCSB
NRAA	Non-redundant amino acid databased sourced from Genbank
PubMed	A public MEDLINE citation database maintained by the National Center for Biotechnology Information at the National Institutes of Health, Bethesda, MD, USA
RCSB	Research Collaboratory for Structural Bioinformatics
STRINGSEARCH	Algorithm used to identify sequence entries by searching for character patterns, such as "toxin", in the annotation section of database flatfiles

SeqLab	The graphical X Windows-based interface for the GCG Wisconsin Package
SwissProt	A public protein database maintained by the Swiss Institute of Bioinformatics, Geneva, Switzerland, and the European Molecular Biology Laboratory at the European Bioinformatics Institute, Hinxton, England
TOXINS	Toxin protein sequence database, version 5
UNIX	A computer operating system originally termed "UNiplexed Information and Computing Service"

1.0 Summary

Monsanto has developed corn, MON 89034, which produces the Cry1A.105 and Cry2Ab2 insecticidal proteins and is protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* (Bt) Cry1A protein with 93.6% overall amino acid sequence identity to the Cry1Ac protein. Cry2Ab2 is a Bt (subsp. *kurstaki*) protein. The combination of the Cry1A.105 and Cry2Ab2 insecticidal proteins in a single plant allows better insect control and offers an additional insect-resistance management tool.

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 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 bio-activity of the Cry2Ab2 protein sequence. The comparison was performed with the allergen (AD6), toxin (TOXIN5), and public domain (ALLPEPTIDES) database sequences using bioinformatic tools.

The FASTA sequence alignment tool was used to assess structural relatedness between the query protein, Cry2Ab2 and other 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 relatedness (i.e., secondary and tertiary protein structures). Proteins that share a high degree of congruence 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. Structural congruence between the Cry2Ab2 protein sequence and the aligned allergen (AD6), toxin (TOXIN5), and public domain (ALLPEPTIDES) database sequences were examined. The extent of each sequence alignment was evaluated by visual inspection, the calculated percent identity, and the *E* score value for that alignment.

The Cry2Ab2 protein sequence was also screened against the AD6 sequence database using a pair-wise comparison algorithm. In these analyses, any sequences of eight contiguous amino acids that were found to be identical between the Cry2Ab2 protein and proteins in the AD6 database were defined as immunologically relevant, in that they may indicate the presence of potentially cross-reactive allergenic epitopes.

No biologically relevant structural congruence with allergens, human and animal toxins, or other proteins that may adversely affect animal or human health was observed for the

Cry2Ab2 protein sequence. Furthermore, no short (eight amino acid) polypeptide matches were shared between the Cry2Ab2 protein sequence and proteins in the allergen database.

These data indicate the lack of both structural and immunological congruence between the Cry2Ab2 protein sequence and allergens. These data also demonstrate the lack of biologically relevant correlates with toxins or other bioactive proteins that adversely impact human or animal health for the Cry2Ab2 protein sequence.

2.0 Introduction

Monsanto has developed corn, MON 89034, which produces the Cry1A.105 and Cry2Ab2 insecticidal proteins and is protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* (*Bt*) Cry1A protein with 93.6% overall amino acid sequence identity to the Cry1Ac protein. Cry2Ab2 is a *Bt* (subsp. *kurstaki*) protein. The combination of the Cry1A.105 and Cry2Ab2 insecticidal proteins in a single plant allows better insect control and offers an additional insect-resistance management tool.

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 the protein is not similar to allergenic, toxic, or potentially bioactive proteins that are known to cause adverse health effects. Bioinformatic analyses were performed to assess the potential for toxicity, allergenicity, or bio-activity of the Cry2Ab2 protein sequence. The comparison was performed with the allergen (AD6), toxin (TOXIN5), and public domain (ALLPEPTIDES) database sequences using bioinformatic tools.

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 alignment between a query protein sequence and a database sequence. 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, homologous proteins share secondary structure and common three-dimensional folds (Pearson, 2000). Because the degree of relatedness 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). Such 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, an eight amino acid sliding window search, is 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 an exact sequence identity of at least eight linear and 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 Cry2Ab2 protein. Inspection of the bioinformatic analysis data can be used to indicate whether the Cry2Ab2 protein sequence is structurally congruent with known allergens, toxins, or other bioactive proteins.

3.0 Purpose

The purpose of this study was to evaluate, using bioinformatics techniques, the amino acid sequence structural relatedness of the Cry2Ab2 protein coding sequence to known allergens, toxins, or other bioactive proteins. Sequence identity and amino acid similarity to allergens, toxins, and other proteins was assessed using the sequence alignment tool FASTA.

4.0 Methods

4.1 Sequence Database Preparation. The allergen, gliadin, and glutenin sequence database (AD6) was assembled from sequences found on the FARRP allergen database dated January 2006 located at www.allergenonline.com. Gene identification (GI) numbers for each of the 1537 sequences found on the FARRP database (FARRP, 2006) were used to assemble a list, and this list was used to batch query the NCBI protein sequence database located at <http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi>. 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 collation of short peptide sequences into a single protein sequence, a total of 1,511 GI numbers were found to be valid as of February 13, 2006. These 1511 GI numbers were used to assemble a searchable database AD6 that was released March 6, 2006 (Appendix 1).

The toxin sequence database (TOXIN5) was assembled from public sequence databases, including GenBank and EMBL release 124 and SwissProt release 1. Protein sequences were retrieved using the STRINGSEARCH function (keyword = toxin) of the Wisconsin Package (version 10). This search was used to identify and retrieve 12,771 separate entries containing the word toxin within the flatfile annotation section. The list data file was loaded into the editor window of SeqLab, selected, and compiled into a sub-database using the DATASET database utility. The actual number of unique toxin sequences is fewer than 12,771 because of the redundancy of these public databases and because some entries may contain the word toxin, but are not confirmed protein toxins.

The ALLPEPTIDES sequence database was used to represent all currently known publicly available protein sequences and consisted of SwissProt release 40.0 (May 4, 2005) and NRAA release 65.0 (October 24, 2005).

4.2 Sequence Database Searches. All search analyses were performed using the UNIX-based Wisconsin Package software, Genetics Computer Group (GCG, version 10.3, Madison, WI) on a personal computer supported with Reflection X Client Manager network software (version 7.20, WRQ, Inc. Seattle, WA). The DNA sequence was supplied in MSL 20072 (Rice *et al.*, 2005) and translated to the amino acid sequence with DNASTar, SeqBuilder software version 7.00 (Fig. 1). The structural similarity of the translated protein sequences to sequences in each database (AD6, TOXIN5, and ALLPEPTIDES) was assessed using the FASTA algorithm (Lipman and Pearson, 1985; Pearson and Lipman, 1988). FASTA comparisons are initiated by aligning the first match of a specific wordsize. The alignment is then extended based on the chosen scoring matrix. Specific FASTA comparison parameters used in this study included a wordsize (*k*-tuple) of two, a gap creation penalty of 12, a gap extension penalty of two, and an expectation threshold (*E* score) of ten. The *E* score (expectation 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 1×10^{-5} or smaller 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; Baxevis 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 a biologically relevant correlation.

In addition to the FASTA comparisons of the Cry2Ab2 protein sequence to allergens (to assess overall structural congruence), an eight amino acid sliding-window search was performed. An algorithm (ALLERGENSEARCH) 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 (AD6). 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.* An *E* score of 1×10^{-5} ($1 \text{ e-}5$) was set as an initial high cut-off value for alignment significance. Although all alignments were inspected visually, any aligned sequence that yielded an *E* score less than $1 \text{ e-}5$ was

analyzed further to determine if such an alignment represented *bona fide* sequence homology.

5.0 Results and Discussion

Bioinformatics analysis was performed on the Cry2Ab2 protein sequence (Figure 1) to assess the potential for structural correlation with allergens, toxins, or other bioactive proteins. Summaries of the significant alignments 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 Cry2Ab2 protein and proteins in the allergen database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 2). None of these proteins had an *E* score of less than 1×10^{-5} indicating that no homology with protein allergens was observed.

The most significant similarity observed (Table 1) was to the *Coprinus comatus* protein Cop c1 (GI no. 4538529), demonstrating 32.7% identity over a 52 aa window with an *E* score of 0.89. This *E* score of 0.89 is not reflective of homology between Cry2Ab2 and *Coprinus comatus* protein Cop c1, as *E* scores of ~ 1 or greater are expected to occur for alignments between random, non-homologous sequences (Pearson, 2000). Therefore, this low quality alignment is considered not relevant from an allergenic assessment perspective.

The length of the overlap is relatively short (8.2%) when compared to full length (637 amino acids) Cry2Ab2 protein and one gap was required to optimize the alignment. Consequently, no structural and/or functional homology between the Cry2Ab2 protein and the *Coprinus comatus* protein Cop c1 protein can be inferred. This alignment neither met nor exceeded the threshold of 35% identity over 80 amino acids (Codex Alimentarius, 2003). Furthermore, a minimum similarity required for allergenic cross-reactivity is likely $\geq 50\%$ identity across the entire length of the protein (Aalberse, 2000). It is extremely unlikely that cross-reactivity exists between the Cry2Ab2 protein and the *Coprinus comatus* protein Cop c1. Inspection of the remaining 7 alignments did not show any significant similarities between the Cry2Ab2 protein and allergens. Based on the low percent-identity and the small alignment window relative to the length of the Cry2Ab2 protein (637 aa), the aforementioned FASTA alignment does not represent a homologous match (Doolittle, 1990) and the Cry2Ab2 protein is, therefore, not likely to be structurally related to known allergens, gliadins, or glutenins.

No immunologically relevant sequences (eight contiguous amino acid identities) were detected when the Cry2Ab2 protein sequence was compared to the AD6 sequence database (Appendix 3). Together these data demonstrate that the Cry2Ab2 protein is unlikely to share structurally relevant or immunologically relevant sequence correlates with known allergens, gliadins, or glutenins.

- 5.2** *Assessment of Potential Toxicity:* Potential structural identity and similarity shared between the Cry2Ab2 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 2) was to the *Bacillus thuringiensis* pesticidal crystal protein (Accession no. P21254), demonstrating 100.0% identity over 632 aa with an *E* score of zero. The Cry2Ab2 protein did not demonstrate any structural congruence with any proteins that may present toxicity to humans and animals.
- 5.3** *Assessment of Potential Adverse Biological Activity to Humans and Animals:* Potential structural similarities shared between the Cry2Ab2 protein and proteins in the ALLPEPTIDES database were evaluated using the FASTA sequence alignment tool. Identified proteins were ranked according to their degree of similarity (Appendix 5). The best similarity observed (Table 3) was to pesticidal crystal protein Cry2Ab (GI no. 117328), demonstrating 100.0% identity over 632 aa with an *E* score of zero. All remaining alignments with significant *E* scores are to Cry protein homologues derived from *Bacillus thuringiensis*, *Clostridium bifermentans*, *Paenibacillus popilliae* or *Paenibacillus lentimorbus*. Based on these data, the Cry2Ab2 protein does not share any structural congruence with any proteins that may have adverse biological activity to humans and animals.

6.0 Conclusions

Bioinformatics analyses were performed on the Cry2Ab2 protein coding sequence to assess its structural congruence with allergens, toxins, and bioactive proteins. No biologically relevant sequence correlates were observed between the Cry2Ab2 protein coding sequence and any allergens, human and animal toxins, or other proteins that may adversely affect animal or human health.

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Figure 1. Amino acid sequence of the Cry2Ab2 protein ^[1]

1 MQAMDNSVLN SGRTTICDAY NVAAHDPFSF QHKSLDTVQK EWTEWKKNNH
51 SLYLDPIVGT VASFLKKVG SLVGKRILSE LKNLIEPESGS TNLMQDILRE
101 TEKFLNQRLN TDTLARVNAE LTGLQANWEE FNRQVDNFLN PNRNAVPLSI
151 TSSVNTMQQL FLNRLPQFQM QGYQLLLPL FAQAANLHLS FIRDVILNAD
201 EWGISAATLR TYRDYLKNYT RQYSNYCINT IQSAFKGLNT RLHDMLEFRT
251 YMFLNVFEYV SIWSLFKYQS LLVSSGAMLY ASGSGPQQTQ SFTSQDWPFL
301 YSLFQVNSNY VLNGFSGARL SNTFPNIVGL PGSTTTHALL AARVNYSGGI
351 SSGDIGASPF NQNFNCSTEL PPILTPFVRS WLDGSDREG VATVTNWQTE
401 SFETTLGLRS GAFTARGNEN YEPDYFIRNI SGVPLVVRNE DLRRPLHYNE
451 IRNIASPSGT PGGARAYMVS VHNKRKNNIHA VHENGSMIHL APNDYTGFTI
501 SPIHATQVNN QTRTFISEKF GNQGDSLRFE QNNTTARYTL RGNGNSYNLY
551 LRVSSIGNST TRWTINERVY TATNVNTTTN NDGVNDNGAR FSDINIGNVV
601 ASSNSDVPLD INVTLNSTGTQ FDLNMIMLVP TNISPLY

[1] Note: file name; cry2ab2_820.pep Length: 637 April 27, 2006 16:18

Table 1. Top alignment observed for the Cry2Ab2 protein sequence from a FASTA search against the AD6 allergen database.

Database	GI #	Description	E-score	% Identity	aa Overlap
AD6	4538529	Cop c1 allergen	0.89	32.7	52

Table 2. Top alignment observed for the Cry2Ab2 protein sequence from a FASTA search against the TOXIN5 database.

Database	Accession #	Description	E-score	% Identity	aa Overlap
TOXIN5	P21254	P21254 <i>Bacillus thuringiensis</i> (subsp. <i>kurstaki</i>). pesticidal crystal protein	0	100.0	632

Table 3. Top alignment observed for the Cry2Ab2 protein sequence from a FASTA search against the ALLPEPTIDES database.

Database	GI #	Description	E-score	% Identity	aa Overlap
ALLPEPTIDES	117328	Pesticidal Crystal Protein Cry2Ab	0	100.0	632

Appendix 1. Allergen, gliadin, and glutenin protein sequence database (AD6)

Venoms

Species	Comments	GI #	AA
Aedes aegypti	D7 protein precursor (Allergen Aed a 2).	118216	321
Aedes aegypti	putative 30 kDa allergen-like protein [Aedes aegypti].	18568322	215
Aedes aegypti	putative 18.2 kDa secreted protein [Aedes aegypti].	18568332	158
Aedes aegypti	30 kDa salivary gland allergen Aed a 3 [Aedes aegypti].	2114497	253
Aedes aegypti	apyrase.	556272	562
Aedes albopictus	putative 30 kDa allergen-like protein 30k-1 [Aedes albopictus].	56417500	210
Aedes albopictus	30 kDa salivary gland allergen 30k-2 [Aedes albopictus].	56417502	210
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 albopictus	putative salivary secreted 30 kDa allergen-like protein 30k-5	56417508	204
Anopheles gambiae	30 kDa protein [Anopheles gambiae].	18389879	182
Apis dorsata	Melittin.	126955	26
Apis mellifera	venom protease precursor [Apis mellifera].	22724911	405
Apis mellifera	Phospholipase A2 precursor (Phosphatidylcholine 2-acylhydrolase)	24418862	167
Apis cerana	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	24638082	134
Apis mellifera	Allergen Api m 6.	34921475	71
Apis dorsata	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase).	47117012	134
Apis mellifera	prepromelittin [Apis mellifera].	5622	70
Apis mellifera	Hyaluronoglucosaminidase precursor (Hyaluronidase) (Hya) (Allergen	585279	382
Apis mellifera	profilin [Apis mellifera].	58585250	126
Apis mellifera	venom acid phosphatase precursor [Apis mellifera].	61656214	388
Apis mellifera	PREDICTED: similar to allergen Bla g 5, partial [Apis mellifera].	66534655	157
Apis mellifera	melittin, minor - honeybee.	69552	27
Apis cerana	phospholipase A2 (EC 3.1.1.4), venom - Indian honeybee.	7435005	134
Bombus terrestris	Phospholipase A2 (Phosphatidylcholine 2-acylhydrolase) (Allergen	14423832	136
Crotalus durissus	phospholipase A2 inhibitor [Crotalus durissus terrificus].	501050	200
Ctenocephalides felis	FSH precursor.	1575479	98
Ctenocephalides felis	salivary antigen 1 precursor [Ctenocephalides felis].	4336703	176
Ctenocephalides felis	salivary allergen 2 [Ctenocephalides felis].	7638032	264
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	Pilosulin-2 precursor (Allergen Myr p 2) (Myr p II).	2498604	75
Myrmecia pilosula	major allergen [Myrmecia pilosula].	312284	112
Myrmecia pilosula	Pilosulin-1 precursor (Major allergen Myr p 1) (Myr p I) [Contains:	730091	112
Phlebotomus papatasi	28 kDa salivary protein precursor [Phlebotomus papatasi].	15963511	254
Phlebotomus papatasi	30 kDa salivary protein precursor [Phlebotomus papatasi].	15963513	253
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
Polybia scutellaris	venom allergen 5 [Polybia scutellaris].	31747352	206
Polybia scutellaris	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Pol s 5) (Pol s V).	47117356	207
Psoroptes ovis	allergen A precursor [Psoroptes ovis].	14388619	143
Psoroptes ovis	Derp1 antigen [Psoroptes ovis].	27450737	263
Psoroptes ovis	glutathione S-transferase [Psoroptes ovis].	6625558	219
Sarcoptes scabiei	cathepsin L-like protease [Sarcoptes scabiei type hominis].	27462834	245
Sarcoptes scabiei	glutathione S-transferase [Sarcoptes scabiei type hominis].	27462836	219
mitochondrion Sarcoptes	cytochrome oxidase subunit I [Sarcoptes scabiei type hominis].	27462838	275
mitochondrion Sarcoptes	cytochrome oxidase subunit II [Sarcoptes scabiei type hominis].	27462840	157
Sarcoptes scabiei	cytochrome Bcl complex chain B-like protein [Sarcoptes scabiei type	27462842	131
Sarcoptes scabiei	vitellogenin-like protein [Sarcoptes scabiei type hominis].	27462844	174
Sarcoptes scabiei	paramyosin [Sarcoptes scabiei type hominis].	27462846	638
Sarcoptes scabiei	major allergen 1 [Sarcoptes scabiei type hominis].	27462848	330
Sarcoptes scabiei	Sar s 3 allergen Yv7016G03 [Sarcoptes scabiei type hominis].	38202313	260
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4005B08 [Sarcoptes scabiei type	38202315	271
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4005G12 [Sarcoptes scabiei type	38202317	251
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv4031D03 [Sarcoptes scabiei type	38202319	264
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5004E08 [Sarcoptes scabiei type	38202321	256
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5018H10 [Sarcoptes scabiei type	38202323	251
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5026E07 [Sarcoptes scabiei type	38202325	242
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5027C11 [Sarcoptes scabiei type	38202327	259
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6017G11 [Sarcoptes scabiei type	38202329	248
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6018H06 [Sarcoptes scabiei type	38202331	262
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6023A04 [Sarcoptes scabiei type	38202333	257
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv6028G11 [Sarcoptes scabiei type	38202335	250
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv7016C10 [Sarcoptes scabiei type	38202337	259
Sarcoptes scabiei	group 3 allergen SMIPP-S YvT003F10 [Sarcoptes scabiei type	38202339	259
Sarcoptes scabiei	group 3 allergen SMIPP-S YvT004A06 [Sarcoptes scabiei type	38202341	263
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv5001A04 [Sarcoptes scabiei type	38202343	233
Sarcoptes scabiei	group 3 allergen SMIPP-S Yv9017F05 [Sarcoptes scabiei type	38202345	261
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 richteri	phospholipase (EC 3.1.-.-), venom - black imported fire ant	321043	20
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 II precursor (Allergen Sol i 2) (Sol i II).	549179	138
Solenopsis richteri	venom allergen Sol r 2 - black imported fire ant.	7512067	119
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
Solenopsis invicta	Venom allergen IV precursor (Allergen Sol i 4) (Sol i IV).	14424465	137
Solenopsis invicta	Venom allergen 3 precursor (Venom allergen III) (Allergen Sol i 3)	14424466	234
Solenopsis richteri	Venom allergen 3 (Venom allergen III) (Allergen Sol r 3) (Sol r	6136163	211
Tityus serrulatus	Tityustoxin-6 (Tityustoxin VI) (TsTX-VI) (TsTXVI) (Toxin VI) (Ts	1173399	62
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 vulgaris	Hyaluronoglucosaminidase (Hyaluronidase) (Allergen Ves v 2) (Ves v	1346323	331
Vespula vulgaris	allergen 5.	162551	227
Vespula maculifrons	phospholipase A1 (EC 3.1.1.32), allergen Ves m 1 - eastern	482382	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
Vespula squamosa	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves s 5) (Ves s V).	549193	205

Vesputia vidua	Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves vi 5) (Ves vi V).	549194	206
Vesputia vulgaris	hyaluronidase b [Vesputia vulgaris].	62147665	340
Vesputia vulgaris	allergen and phospholipase A1.	897647	336

Aeroallergens animals

Species	Comments	GI #	AA
Canis familiaris	precursor Can f II [Canis familiaris].	29292272	177
Canis familiaris	precursor Can f II [Canis familiaris].	29292274	179
Canis familiaris	Major allergen Can f 1 precursor (Allergen Dog 1).	3121745	174
Canis familiaris	Minor allergen Can f 2 precursor (Allergen Dog 2).	3121746	180
Canis familiaris	albumin [Canis familiaris].	3319897	585
Canis familiaris	epithelial dog allergen - Canis familiaris (fragment).	60729635	13
Canis familiaris	albumin [Canis familiaris].	633938	265
Canis familiaris	albumin [Canis familiaris].	6687188	608
Cavia porcellus	Eosinophil granule major basic protein 1 precursor (MBP-1).	119238	233
Cavia porcellus	Major allergen Cav p 2.	32363133	15
Cavia porcellus	Major urinary protein (MUP) (Allergen Cav p 1).	32469617	15
Cavia porcellus	Eosinophil granule major basic protein 2 precursor (MBP-2).	544241	234
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.	163823	109
Felis catus	major allergen I.	163827	88
Felis catus	prostaglandin FP receptor [Felis catus].	17224444	366
Felis catus	cystatin [Felis catus].	17939981	98
Felis catus	Chain A, Crystal Structure Of Fel D 1 - The Major Cat Allergen.	38492847	170
Felis catus	Fel d 4 allergen [Felis catus].	45775300	186
Felis catus	albumin precursor [Felis catus].	886485	608
Felis catus	Major allergen I polypeptide chain 2 precursor (Allergen Fel d 1-B).	232086	109
Macaca mulatta	encephalitogenic peptide M.	229507	14
Mus musculus	androgen-binding protein eta [Mus musculus].	10181188	93
Mus sp.	DEC-205-205 kDa protein allergen {N-terminal} [mice, outbred CD-1	1174278	25
Mus musculus	Major urinary protein 6 precursor (MUP 6) (Alpha-2U-globulin)	20178291	180
Mus musculus	TPA_exp: allergen dI chain C2A [Mus musculus].	28476845	112
Mus musculus	TPA_exp: allergen dI chain C2C [Mus musculus].	28476849	108
Mus musculus	TPA_exp: allergen dI chain C2D [Mus musculus].	28476851	112
Mus musculus	TPA_exp: allergen dI chain C2Y [Mus musculus].	28476853	46
Mus musculus	androgen binding protein zeta [Mus musculus].	30315676	112
Mus musculus	androgen binding protein gamma [Mus musculus].	30315678	112
Mus musculus	androgen binding protein gamma [Mus musculus].	45331198	112
Mus musculus	androgen binding protein beta [Mus musculus].	45331208	112
Mus musculus	cysteine-rich secretory protein [Mus musculus].	56694673	250
Mus musculus	lacrimal androgen-binding protein delta [Mus musculus].	8926324	112
Rattus norvegicus	Major urinary protein precursor (MUP) (Alpha-2u-globulin)	127533	181
Rattus norvegicus	Niemann Pick type C2 [Rattus norvegicus].	27465565	149
Rattus norvegicus	PREDICTED: similar to Major urinary protein precursor (MUP)	62649086	181
Rattus norvegicus	Alpha-2u globulin.	81890324	181
Thaumatococcus pinnatifidus	Tha p 1.	74798355	18

Aeroallergens fungi

Species	Comments	GI #	AA
Alternaria alternata	proteindisulfidomerase [Alternaria alternata].	1006624	433
Alternaria alternata	Aldehyde dehydrogenase (ALDDH) (Allergen Alt a 10) (Alt a X).	1169290	495
Alternaria alternata	60S acidic ribosomal protein P1 (Allergen Alt a 12) (Alt a XII).	1350779	110
Alternaria alternata	Alt a1 [Alternaria alternata].	1421808	135
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 brassicicola	major allergen-like protein precursor [Alternaria brassicicola].	20279107	158
Alternaria alternata	putative nuclear transport factor 2 [Alternaria alternata].	21748153	124
Alternaria alternata	major allergen alt a1 [Alternaria alternata].	21913174	115
Alternaria alternata	allergen r Alt a 2 [Alternaria alternata].	4097481	190
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 cetera	major allergen alt a1 [Alternaria cetera].	49476471	138
Alternaria mouchaccaae	major allergen alt a1 [Alternaria mouchaccaae].	49476473	138
Alternaria argyranthemii	major allergen alt a1 [Alternaria argyranthemii].	49476475	138
Alternaria conjuncta	major allergen alt a1 [Alternaria conjuncta].	49476477	138
Alternaria photistica	major allergen alt a1 [Alternaria photistica].	49476479	138
Alternaria oregonensis	major allergen alt a1 [Alternaria oregonensis].	49476481	128
Alternaria metachromatica	major allergen alt a1 [Alternaria metachromatica].	49476485	137
Alternaria radicina	major allergen alt a1 [Alternaria radicina].	49476487	137
Alternaria carotiincultae	major allergen alt a1 [Alternaria carotiincultae].	49476489	137
Alternaria petroselini	major allergen alt a1 [Alternaria petroselini].	49476491	137
Alternaria smyrnii	major allergen alt a1 [Alternaria smyrnii].	49476493	137
Alternaria cheiranthi	major allergen alt a1 [Alternaria cheiranthi].	49476495	137
Alternaria blumeae	major allergen alt a1 [Alternaria blumeae].	49476497	137
Alternaria dauci	major allergen alt a1 [Alternaria dauci].	49476499	137
Alternaria crassa	major allergen alt a1 [Alternaria crassa].	49476501	137
Alternaria macrospora	major allergen alt a1 [Alternaria macrospora].	49476503	137
Alternaria pseudorostrata	major allergen alt a1 [Alternaria pseudorostrata].	49476505	137
Alternaria porri	major allergen alt a1 [Alternaria porri].	49476507	137
Alternaria tagetica	major allergen alt a1 [Alternaria tagetica].	49476509	137
Alternaria capsici	major allergen alt a1 [Alternaria capsici].	49476511	137
Alternaria solani	major allergen alt a1 [Alternaria solani].	49476513	137
Alternaria cucumerina	major allergen alt a1 [Alternaria cucumerina].	49476515	137
Alternaria tenuissima	major allergen alt a1 [Alternaria tenuissima].	49476519	137
Alternaria arborescens	major allergen alt a1 [Alternaria arborescens].	49476521	137
Alternaria longipes	major allergen alt a1 [Alternaria longipes].	49476523	137
Alternaria dumosa	major allergen alt a1 [Alternaria dumosa].	49476525	137
Alternaria limoniasperae	major allergen alt a1 [Alternaria limoniasperae].	49476527	137
Alternaria sonchi	major allergen alt a1 [Alternaria sonchi].	49476529	138
Alternaria cinerariae	major allergen alt a1 [Alternaria cinerariae].	49476531	137
Alternaria brassicae	major allergen alt a1 [Alternaria brassicae].	49476533	137
Alternaria mimicula	major allergen alt a1 [Alternaria mimicula].	49476535	137
Alternaria japonica	major allergen alt a1 [Alternaria japonica].	49476539	137
Alternaria eryngii	major allergen alt a1 [Alternaria eryngii].	49476541	137
Alternaria euphorbiicola	major allergen alt a1 [Alternaria euphorbiicola].	49476543	137
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
Arthroderma benhamiae	tri m 2 allergen [Arthroderma benhamiae].	23894248	405
Aspergillus oryzae	Alpha-amylase A precursor (Taka-amylase A) (TAA)	113779	499
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	Possible pathogenesis-related protein precursor [Aspergillus	19309414	164
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	peroxisomal-like protein [Aspergillus fumigatus].	2769700	168
Aspergillus fumigatus	rAsp f 7 [Aspergillus fumigatus].	2879888	112
Aspergillus fumigatus	rAsp f 9 [Aspergillus fumigatus].	2879890	302
Aspergillus niger	serine protease.	289172	533
Aspergillus fumigatus	IgE-binding protein [Aspergillus fumigatus].	2980819	197
Aspergillus fumigatus	rAsp f 4 [Aspergillus fumigatus].	3005839	286

Aspergillus fumigatus	rAsp f 13 [Aspergillus fumigatus].	3005841	152
Aspergillus fumigatus	Aspf1 allergen [Aspergillus fumigatus].	3021374	125
Aspergillus fumigatus	IgE-binding protein [Aspergillus fumigatus].	3219530	185
Aspergillus fumigatus	allergen [Aspergillus fumigatus].	3643813	427
Aspergillus fumigatus	metalloprotease (MEP) [Aspergillus fumigatus].	3776613	634
Aspergillus niger	beta-xylosidase [Aspergillus niger].	4235093	804
Aspergillus fumigatus	suppressor protein spt23-related, with ankyrin repeats [Aspergillus	42820661	1407
Aspergillus flavus	Oryzin precursor (Alkaline proteinase) (ALP) (Elastase)	464318	403
Aspergillus fumigatus	PP1ase [Aspergillus fumigatus].	5019414	178
Aspergillus fumigatus	Asp FII [Aspergillus fumigatus].	664852	250
Aspergillus fumigatus	rAsp f 8 [Aspergillus fumigatus].	6686524	111
Aspergillus flavus	Allergen Asp f1.	74665726	403
Aspergillus fumigatus	Major allergen Asp f 2 precursor (Asp f II)	83300352	310
Aspergillus fumigatus	Heat shock protein 90 (Heat shock protein hsp1) (65 kDa IgE-binding	83303658	706
Aspergillus fumigatus	major allergen I 18kDa antigen [Aspergillus fumigatus].	9280360	150
Aspergillus fumigatus	aspergillopepsin i [Aspergillus fumigatus].	963013	395
Aspergillus fumigatus	Ribonuclease mitogillin precursor (Major allergen Asp f1) (Asp f	54039254	176
Candida albicans	Alcohol dehydrogenase 1 (40 kDa allergen) (Allergen Cand a 1) (Can	1168348	350
Candida boidinii	Putative peroxiredoxin-A (Thioredoxin reductase) (Peroxisomal	130360	167
Candida boidinii	Putative peroxiredoxin-B (Thioredoxin reductase) (Peroxisomal	130361	167
Candida albicans	Fructose-bisphosphate aldolase (37 kDa major allergen) (IgE-binding	18203509	40
Candida albicans	Enolase 1 (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	232054	440
Candida albicans	putative aminoacid permease protein [Candida albicans].	24461764	648
Candida albicans	29 kDa IgE-binding protein [Candida albicans].	37548637	236
Candida albicans	hypothetical protein CaO19.557 [Candida albicans SC5314].	46431500	341
Candida albicans	hypothetical protein CaO19.8192 [Candida albicans SC5314].	46431509	341
Coprinus comatus	Cop c1 allergen [Coprinus comatus].	4538529	81
Coprinus comatus	thioredoxin [Coprinus comatus].	5689669	106
Coprinus comatus	rCop c3 [Coprinus comatus].	5689671	328
Coprinus comatus	rCop c5 [Coprinus comatus].	5689673	141
Coprinus comatus	rCop c7 [Coprinus comatus].	5689675	152
Cryptococcus neoformans	allergen, putative [Cryptococcus neoformans var. neoformans JEC21].	57227639	234
Cryptococcus neoformans	thioredoxin (allergen cop c 2) [Cryptococcus neoformans var.	58265022	104
Davidiella tassiana	ribosomal protein P1 [Davidiella tassiana].	1143425	110
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
Embellisia allii	major allergen alt a1 [Embellisia allii].	49476559	138
Embellisia indefessa	major allergen alt a1 [Embellisia indefessa].	49476561	137
Embellisia novae-zelandiae	major allergen alt a1 [Embellisia novae-zelandiae].	49476563	136
Embellisia telluster	major allergen alt a1 [Embellisia telluster].	49476565	138
Epicoccum nigrum	[Segment 1 of 2] Major allergen Epi p 1 (Epi n I4625*).	24636821	12
Fusarium culmorum	60S acidic ribosomal protein P2 [Fusarium culmorum].	19879657	109
Fusarium culmorum	thioredoxin-like protein [Fusarium culmorum].	19879659	121
Fusarium culmorum	helix-loop-helix protein [Fusarium culmorum].	25361513	450
Fusarium culmorum	hypothetical protein [Fusarium culmorum].	27965571	342
Gibberella zeae	ENO_ALTAL Enolase (2-phosphoglycerate dehydratase)	46108928	438
Gibberella zeae	RLA2_ALTAL 60S acidic ribosomal protein P2 (Minor allergen Alt a 6)	46122455	109
Gibberella zeae	RLA1_CLAHE 60S acidic ribosomal protein p1 (allergen cla h 12) (CLA	46137705	108
Haematocytaria haematococca	Allergen Fus s I3596*.	3122132	8
Lewia ethzedia	major allergen alt a1 [Lewia ethzedia].	49476483	138
Macrospora scirpicola	major allergen alt a1 [Macrospora scirpicola].	49476555	138
Malassezia sympodialis	allergen [Malassezia sympodialis].	1261972	350
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	MF2 [Malassezia furfur].	3445492	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 furfur	allergen Mal f3 - Malassezia furfur.	7514251	166
Malassezia sympodialis	mala s 12 allergen precursor [Malassezia sympodialis].	78038796	618
Neurospora crassa	probable rAsp f 9 allergen [Neurospora crassa].	28949979	301
Neurospora crassa	related to rasp f 7 allergen [Neurospora crassa].	28950043	265
Nimbya caricis	major allergen alt a1 [Nimbya caricis].	49476557	138
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 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
Pleospora tarda	major allergen alt a1 [Pleospora tarda].	49476463	137
Pleospora herbarum	major allergen alt a1 [Pleospora herbarum].	49476469	137
Rhodotorula mucilaginosa	Enolase (2-phosphoglycerate dehydratase) (2-phospho-D-glycerate	37078092	439
Saccharomyces cerevisiae	Chain A, Yeast Profilin, Cubic Crystal Form.	15988101	125
Schizophyllum commune	pSc7 protien [Schizophyllum commune].	169865	204
Schizophyllum commune	pSc14 protein [Schizophyllum commune].	386678	214
Scomber japonicus	parvalbumin [Scomber japonicus].	29420793	109
Stemphylium vesicarium	major allergen alt a1 [Stemphylium vesicarium].	49476465	137
Stemphylium callistephi	major allergen alt a1 [Stemphylium callistephi].	49476467	137
Trichophyton tonsurans	83 kDa hypersensitivity protein (Protein IV).	1708296	26
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
Ulocladium cucurbitae	major allergen alt a1 [Ulocladium cucurbitae].	49476545	137
Ulocladium alternariae	major allergen alt a1 [Ulocladium alternariae].	49476547	138
Ulocladium botrytis	major allergen alt a1 [Ulocladium botrytis].	49476549	137
Ulocladium atrum	major allergen alt a1 [Ulocladium atrum].	49476551	137
Ulocladium chartarum	major allergen alt a1 [Ulocladium chartarum].	49476553	137
Verticillium dahliae	allergen rAsp f9-like protein [Verticillium dahliae].	42742375	403
Verticillium dahliae	allergen Asp f2-like protein [Verticillium dahliae].	42742377	297

Aeroallergens mites

Species	Comments	GI #	AA
Acarus siro	lipid binding protein [Acarus siro].	4049356	64
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	allergen Blo t Mag 1 [Blomia tropicalis].	25989484	338
Blomia tropicalis	major IgE-binding protein Blo t 5 [Blomia tropicalis].	4204917	134
Blomia tropicalis	allergen precursor [Blomia tropicalis].	902012	144

Blomia tropicalis	allergen [Blomia tropicalis].	915347	73
Chironomus thummi	Globin CTT-III precursor (Erythrocrucorin III).	121219	151
Chironomus thummi	Globin CTT-IV precursor.	121227	151
Chironomus thummi	Globin CTT-VIII.	121237	151
Chironomus thummi	Globin CTT-VIIB-3 precursor.	121244	161
Chironomus thummi	Globin CTT-VIIB-6 precursor.	121248	161
Chironomus thummi	Globin CTT-VIIB-7 precursor.	121249	162
Chironomus thummi	Globin CTT-IIIa.	121256	151
Chironomus thummi	Globin CTT-X.	121259	151
Chironomus thummi	Globin CTT-II beta precursor.	1707908	160
Chironomus thummi	Globin CTT-IX precursor.	1707911	161
Chironomus thummi	Globin CTT-I/CTT-IA precursor (Erythrocrucorin).	2506460	158
Chironomus thummi	Globin CTT-VI precursor.	2506461	162
Chironomus thummi	Globin CTT-VIIB-4 precursor (Erythrocrucorin).	56405052	161
Chironomus thummi	Globin CTT-VIIB-5/CTT-VIIB-9 precursor.	56405054	161
Chironomus thummi	Globin CTT-VIIa precursor.	56405306	161
Chironomus kiensis	tropomyosin [Chironomus kiensis].	7321108	285
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	10189811	215
Dermatophagoides pteronyssinus	unnamed protein product [Dermatophagoides pteronyssinus].	10189816	213
Dermatophagoides pteronyssinus	group III allergen - house-dust mite (Dermatophagoides	102832	18
Dermatophagoides pteronyssinus	Der p 7 allergen polypeptide.	1045602	215
Dermatophagoides microceras	Major mite fecal allergen Der m 1, Der m D.	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	allergen Der f II precursor [Dermatophagoides farinae].	13560629	170
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	ferritin heavy chain-like protein [Dermatophagoides pteronyssinus].	15072346	180
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	gelatin-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	trypsin-like protease=Der f III allergen homolog {N-terminal}	259012	20
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	unnamed protein product [Dermatophagoides pteronyssinus].	29786835	302
Dermatophagoides pteronyssinus	trypsin-like serine protease [Dermatophagoides pteronyssinus].	31745576	273
Dermatophagoides pteronyssinus	serine protease LM-1 [Dermatophagoides pteronyssinus].	37654735	261
Dermatophagoides pteronyssinus	HDM allergen [Dermatophagoides pteronyssinus].	37778944	875
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 pteronyssinus	Der p 1 allergen preproenzyme [Dermatophagoides pteronyssinus].	511953	320
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 farinae	98kDa HDM allergen [Dermatophagoides farinae].	5815436	555
Dermatophagoides pteronyssinus	Der p 1 allergen [Dermatophagoides pteronyssinus].	61608445	216
Dermatophagoides farinae	allergen Der f I precursor - house-dust mite (Dermatophagoides	627141	319
Dermatophagoides farinae	Allergen MAG29.	729970	145
Dermatophagoides farinae	Allergen Mag.	729979	341
Dermatophagoides farinae	Major mite fecal allergen Der f 1 precursor (Der f I).	730035	321
Dermatophagoides pteronyssinus	Major mite fecal allergen Der p 1 precursor (Der p I).	730036	320
Dermatophagoides pteronyssinus	Major fecal allergen Der p 1-associated protein.	74798156	23
Dermatophagoides farinae	Major Der f 2 isoform.	74820084	129
Dermatophagoides pteronyssinus	major allergen p Dp 15 [Dermatophagoides pteronyssinus].	807138	219
Dermatophagoides pteronyssinus	IgE-binding protein C-terminal fragment (148 AA) [Dermatophagoides	9072	148
Dermatophagoides pteronyssinus	Der p V allergen [Dermatophagoides pteronyssinus].	913285	132
Euroglyphus maynei	Mite group 2 allergen Eur m 2 precursor.	14423649	145
Euroglyphus maynei	Mite allergen Eur m 3 precursor.	14423685	261
Euroglyphus maynei	group 2 allergen Eur m 2 0102 [Euroglyphus maynei].	3941386	135
Euroglyphus maynei	group 1 allergen Eur m 1 0101 precursor [Euroglyphus maynei].	3941388	321
Euroglyphus maynei	group 1 allergen Eur m 1 0102 [Euroglyphus maynei].	3941390	327
Euroglyphus maynei	alpha-amylase precursor [Euroglyphus maynei].	5059164	521
Euroglyphus maynei	high molecular weight allergen M-177 precursor [Euroglyphus	6492307	1668
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	alpha tubulin [Lepidoglyphus destructor].	19702131	450
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213898	141
Lepidoglyphus destructor	Lep D 2 precursor [Lepidoglyphus destructor].	21213900	141
Lepidoglyphus destructor	allergen Lep d 1.02 precursor - Lepidoglyphus destructor.	2147108	141
Lepidoglyphus destructor	Lep D 2 allergen [Lepidoglyphus destructor].	999462	141
Tyrophagus putrescentiae	group 2 allergen [Tyrophagus putrescentiae].	2182106	141
Tyrophagus putrescentiae	fatty acid-biding protein [Tyrophagus putrescentiae].	51860756	131

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
Ixodes ricinus	allergen like protein [Ixodes ricinus].	28564461	116
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	ribosomal protein S12 [Periplaneta americana].	21217441	139
Periplaneta americana	Rab11 [Periplaneta americana].	21217443	204
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
Pieris rapae	nitrile-specifier protein [Pieris rapae].	40288346	632
Plodia interpunctella	arginine kinase [Plodia interpunctella].	15886861	355
Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335404	285
Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335406	705
Plodia interpunctella	unnamed protein product [Plodia interpunctella].	21335408	254
Polypedilum nubifer	Pol n 1 component MW=allergenic monomeric hemoglobin (N-terminal)	1703681	37
Tenebrio molitor	cockroach allergen-like protein [Tenebrio molitor].	32967475	595

Aeroallergens pollen

Species	Comments	GI #	AA
Agrostis alba	pollen allergen Agr a 1 - bent grass (fragment).	320606	26
Agrostis alba	Group 1 allergen Agr a 1 (Form 2), pollen.	75139987	35
Agrostis alba	Group 1 allergen Agr a 1 (Form 1), pollen.	75139989	35
Alnus glutinosa	Aln g 1 [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 1)	113476	398
Ambrosia artemisiifolia	Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a 1).	113477	397
Ambrosia artemisiifolia	Pollen allergen Amb a 1.4 precursor (Antigen E) (Antigen Amb a 1).	113478	392
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	Nonspecific lipid-transfer protein precursor (LTP) (Pollen allergen	14285595	118
Ambrosia artemisiifolia	antigen E.	166443	397
Ambrosia artemisiifolia	profilin-like protein [Ambrosia artemisiifolia].	34851178	131
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Ambrosia elatior	Pollen allergen Amb a 3 (Amb a III) (Allergen Ra3).	416636	101
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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	allergen Amb a 1.2 precursor - common ragweed.	539048	398
Ambrosia artemisiifolia	allergen Amb a 1.3 precursor - common ragweed.	539049	397
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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
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Betula pendula	Chain A, Birch Pollen Allergen Bet V 1 Mutant N28t, K32q, E45s,	11514622	159
Betula pendula	Calcium-binding allergen Bet v 3 (Bet v III).	1168696	205
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Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542865	160
Betula pendula	pollen allergen Bet v 1 [Betula pendula].	1542867	160
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Chamaecyparis obtusa	Chaol [Chamaecyparis obtusa].	1514943	375
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Chenopodium album	Che a 1 allergen precursor [Chenopodium album].	22074346	168
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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
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Dactylis glomerata	group 5 allergen precursor [Dactylis glomerata].	14423124	290
Dactylis glomerata	unnamed protein product [Dactylis glomerata].	18093971	265
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Dactylis glomerata	pollen allergen (group II) [Dactylis glomerata].	4007040	122
Dicranopteris linearis	2S storage protein-like albumin precursor [Dicranopteris linearis].	6573243	125
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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 1 [Holcus lanatus].	3860384	263
Holcus lanatus	pollen allergen (group II) [Holcus lanatus].	4007084	122
Holcus lanatus	allergen Hol-II [Holcus lanatus].	414703	265
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Humulus scandens	profilin-like protein [Humulus scandens].	34851176	131
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Juniperus ashei	elongation factor [Juniperus ashei].	21632054	172
Juniperus rigida	PR5 allergen Jun r 3.1 precursor [Juniperus rigida].	38456222	225

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Juniperus ashei	pollen major allergen 1-1 [Juniperus ashei].	4138877	367
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Juniperus oxycedrus	pollen allergen Jun o 4 [Juniperus oxycedrus].	5391446	165
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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
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Lolium perenne	Major pollen allergen Lol p 5a precursor (Lol p Va) (Lol p Ib).	2498581	308
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Lolium perenne	Allergen Lol p II.	75220940	88
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Lolium perenne	allergen Lol p II [Lolium perenne].	939932	88
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Olea europaea	Calcium-binding allergen Ole e 8 (PCA18/PCA23).	14423648	171
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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 nonspecific lipid-transfer protein 1 precursor (LTP)	2497749	138
Parietaria judaica	Probable nonspecific lipid-transfer protein 2 precursor (LTP 2)	2497750	133
Parietaria judaica	Probable nonspecific lipid-transfer protein (LTP) (Major pollen	3915783	139
Parietaria judaica	major allergen Par j 1.	741844	143
Parietaria officinalis	Pollen major allergen Par o 1.	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	Polcalcine 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].	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].	2415780	131
Phleum pratense	profilin 4 [Phleum pratense].	2415702	131
Phleum pratense	Chain A, Crystal Structure Of Phl P 1, A Major Timothy Grass Pollen	28777838	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 p1 [Phleum pratense].	3901094	263
Phleum pratense	Phl p 3 allergen [Phleum pratense].	39841264	97
Phleum pratense	Phlp5 [Phleum pratense].	398830	312
Phleum pratense	PHL P11, 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 1 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 4 [Phleum pratense].	54144334	508
Phleum pratense	Pollen allergen Phl p V.	75139900	24
Phleum pratense	Pollen allergen Phl p1 precursor.	75221090	263
Phoenix dactylifera	profilin [Phoenix dactylifera].	21322677	131
Pinus radiata	Pollen allergen	75099285	293
Platanus x	putative invertase inhibitor precursor [Platanus x acerifolia].	26190140	179
Platanus x	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 Poa p 5 [Poa pratensis].	11991227	303
Poa pratensis	pollen allergen Poa-p1 - Kentucky bluegrass (fragment).	280414	20
Poa pratensis	pollen allergen Poa p 1 - 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
Poa pratensis	Pollen allergen KBG 60 precursor (Pollen allergen Poa p 9) (Poa p	113562	307
Quercus alba	major pollen allergen Que a 1 - white oak (fragment).	543675	24
Salsola kali	major antigen-like protein [Salsola kali].	22726221	320
Salsola kali	[Segment 1 of 4] Pollen allergen Sal k 1.	25090948	11
Salsola kali	[Segment 2 of 4] Pollen allergen Sal k 1.	25090949	8
Salsola kali	[Segment 3 of 4] Pollen allergen Sal k 1.	25090950	9
Salsola kali	[Segment 4 of 4] Pollen allergen Sal k 1.	25090951	14
Sambucus nigra	allergen-like protein BRN20 [Sambucus nigra].	6561156	159
Syringa vulgaris	Polcalcin Syr v 3 (Calcium-binding pollen allergen Syr v 3).	14423847	81
Syringa vulgaris	allergen-like protein Syr v 1 isoform 1 - Syringa vulgaris.	631911	145
Syringa vulgaris	allergen-like protein Syr v 1 isoform 2 - Syringa vulgaris.	631912	145
Syringa vulgaris	allergen-like protein Syr v 1 isoform 3 - Syringa vulgaris.	631913	145
Taraxacum officinale	root allergen protein [Taraxacum officinale].	2707295	157

Food allergens animals

Species	Comments	GI #	AA
Batillus cornutus	major allergen Tur c1 - Turbo cornutus.	7441399	146
Bos taurus	allergen Bos d 2.0103 [imported] - bovine.	11277082	156
Bos taurus	allergen Bos d 2.0102 [imported] - bovine.	11277083	156
Bos taurus	kappa-casein [Bos taurus].	1228078	190
Bos taurus	Myelin basic protein (MBP) (Myelin A1 protein) (20 kDa	126796	169
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	S100 calcium-binding protein A7 (Allergen Bos d 3) (Dander minor	2493414	101
Bos taurus	MD-2 protein [Bos taurus].	27806539	160
Bos taurus	Niemann-Pick disease, type C2 [Bos taurus].	27806881	149
Bos taurus	alpha-lactalbumin [Bos taurus].	295774	142
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	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	61819907	171
Bos taurus	beta-lactoglobulin variant B precursor [Bos taurus].	669061	178
Bos taurus	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	76677407	152
Bos taurus	PREDICTED: similar to Odorant-binding protein precursor (OBP) [Bos	76686423	215
Bos taurus	major allergen BDA20 [Bos taurus].	886215	172
Charybdis feriatus	heat stable allergen tropomyosin [Charybdis feriatus].	7024506	264
Crassostrea gigas	tropomyosin [Crassostrea gigas].	15419048	233
Crassostrea virginica	tropomyosin [Crassostrea virginica].	3668408	160
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977825	109
Cyprinus carpio	parvalbumin [Cyprinus carpio].	17977827	109
Farfantepenaeus aztecus	muscle tropomyosin, Pen a I=36 kda major allergen	632782	21
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	Ovomucoid precursor (Allergen Gal d 1) (Gal d I).	124757	210
Gallus gallus	Lysozyme C precursor (1,4-beta-N-acetylmuramidase C) (Allergen Gal	126608	147
Gallus gallus	Ovalbumin (Plakalbumin) (Allergen Gal d 2) (Gal d II).	129293	386
Gallus gallus	Ovotransferrin precursor (Conalbumin) (Allergen Gal d 3) (Gal d	1351295	705
Gallus gallus	Chain A, Loop-Inserted Structure Of P1-P1' Cleaved Ovalbumin Mutant	15826578	385
Gallus gallus	very low density lipoprotein II precursor.	211156	106
Gallus gallus	lysozyme protein.	212279	24
Gallus gallus	vitellogenin.	212881	1852
Gallus gallus	ovalbumin [Gallus gallus].	212900	388
Gallus gallus	Chain D, Crystal Structure Of S-Ovalbumin At 1.9 Angstrom	34811333	385
Gallus gallus	PREDICTED: similar to MD-2 [Gallus gallus].	50731634	155
Gallus gallus	unnamed protein product [Gallus gallus].	63052	155
Gallus gallus	preproalbumin (serum albumin) [Gallus gallus].	63748	615
Gallus gallus	vitellogenin [Gallus gallus].	63885	81
Gallus gallus	vitellogenin [Gallus gallus].	63887	1850
Gallus gallus	ovotransferrin [Gallus gallus].	757851	705
Gallus gallus	unnamed protein product [Gallus gallus].	808969	386
Haliotis diversicolor	tropomyosin [Haliotis diversicolor].	9954249	284

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
Kryptolebias marmoratus	parvalbumin 1 [Rivulus marmoratus].	50953781	109
Kryptolebias marmoratus	parvalbumin 2 [Rivulus marmoratus].	50953783	109
Metapenaeus ensis	tropomyosin.	607633	274
Mimachlamys nobilis	tropomyosin [Chlamys nobilis].	9954253	284
Panulirus stimpsoni	Tropomyosin (Allergen Pan s 1) (Pan s 1).	14285797	274
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.	parvalbumin alpha [Rana sp. CH-2001].	20796733	110
Rana esculenta	parvalbumin beta protein [Rana esculenta].	20797081	109
Rana sp.	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
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531018	109
Theragra chalcogramma	parvalbumin [Theragra chalcogramma].	14531020	109

Food allergens plants

Species

Species	Comments	GI #	AA
Actinidia chinensis	Actinidain precursor (Actinidin) (Allergen Act c 1).	113285	380
Actinidia deliciosa	unnamed protein product [Actinidia deliciosa].	15984	380
Actinidia deliciosa	actinidin.	166317	380
Actinidia deliciosa	phytoecystatin [Actinidia deliciosa].	40807635	116
Actinidia deliciosa	pKIWI501.	450239	184
Actinidia deliciosa	thaumatin-like protein [Actinidia deliciosa].	71057064	225
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
Apium graveolens	Major allergen Api g 1 (Api g 1.0101) (Api g 1).	1346568	154
Apium graveolens	Chlorophyll a-b binding protein, chloroplast precursor (Allergen	14423661	264
Apium graveolens	Api g 1.0201 allergen [Apium graveolens].	1769847	159
Apium graveolens	[Segment 2 of 4] Allergen Api g 5.	32363124	30
Apium graveolens	[Segment 3 of 4] Allergen Api g 5.	32363125	24
Apium graveolens	[Segment 4 of 4] Allergen Api g 5.	32363126	10
Apium graveolens	[Segment 1 of 4] Allergen Api g 5.	33300921	22
Apium graveolens	profilin [Apium graveolens].	4761578	134
Apium graveolens	cofactor-independent phosphoglyceromutase [Apium graveolens].	6706331	559
Apium graveolens	NADP-dependent malate dehydrogenase (decarboxylating) [Apium	6706333	570
Arachis hypogaea	Allergen Ara h 1, clone P17 precursor (Ara h 1).	1168390	614
Arachis hypogaea	Allergen Ara h 1, clone P41B precursor (Ara h 1).	1168391	626
Arachis hypogaea	oleosin variant A [Arachis hypogaea].	13161005	176
Arachis hypogaea	oleosin variant B [Arachis hypogaea].	13161008	176
Arachis hypogaea	unnamed protein product [Arachis hypogaea].	14347293	207
Arachis hypogaea	conglutin [Arachis hypogaea].	17225991	144
Arachis hypogaea	allergen Arah3/Arah4 [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	oleosin isoform [Arachis hypogaea].	47156059	176
Arachis hypogaea	glycinin [Arachis hypogaea].	47933675	510

Arachis hypogaea	Ara h 6 allergen [Arachis hypogaea].	57118278	124
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
Arachis hypogaea	mannose/glucose-binding lectin precursor.	9511118	254
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
Beta vulgaris	RS2 protein [Beta vulgaris subsp. vulgaris].	11691639	158
Brassica rapa	Thioredoxin H-type (TRX-H).	11135129	123
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	Lipid transfer protein [Brassica rapa].	3062791	86
Brassica rapa	[Segment 1 of 5] Chitin-binding allergen Bra r 2.	32363457	33
Brassica rapa	[Segment 2 of 5] Chitin-binding allergen Bra r 2.	32363458	34
Brassica rapa	[Segment 3 of 5] Chitin-binding allergen Bra r 2.	32363459	13
Brassica rapa	[Segment 5 of 5] Chitin-binding allergen Bra r 2.	32363461	8
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 napus	Polcalcic Bra n 1 (Calcium-binding pollen allergen Bra n 1).	59800143	79
Brassica rapa	Polcalcic Bra r 1 (Calcium-binding pollen allergen Bra r 1).	59800144	79
Brassica napus	Polcalcic Bra n 2 (Calcium-binding pollen allergen Bra n 2).	59800145	83
Brassica rapa	Polcalcic Bra r 2 (Calcium-binding pollen allergen Bra r 2).	59800146	83
Brassica rapa	PCP-1 family.	75099036	83
Capsicum annuum	profilin [Capsicum annuum].	16555785	131
Capsicum annuum	osmotin-like protein [Capsicum annuum].	16609959	246
Capsicum annuum	profilin [Capsicum annuum].	40287498	18
Carica papaya	papain precursor.	167391	345
Carya illinoensis	putative allergen I1 [Carya illinoensis].	28207731	143
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	Nonspecific lipid-transfer protein (LTP) (Allergen Cit 13).	52783176	20
Citrus sinensis	Nonspecific 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	putative LEA III protein isoform 1 [Corylus avellana].	14148979	109
Corylus avellana	putative LEA III protein isoform 2 [Corylus avellana].	14148981	87
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].	22688	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 (Cor a 1).	584968	160
Cucumis melo	profilin [Cucumis melo].	31559774	131
Cucumis melo	[Segment 1 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396596	21
Cucumis melo	[Segment 2 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396597	10
Cucumis melo	[Segment 3 of 3] Pathogenesis-related protein (PR-1) (Allergen Cuc	46396598	10
Cucumis melo	profilin [Cucumis melo].	58263793	131
Cucumis melo	pre-pro-cucumisin [Cucumis melo].	807698	731
Cucumis melo	profilin [Cucumis melo var. reticulatus].	57021110	131
Daucus carota	pathogenesis-related protein.	1335877	168
Daucus carota	cr16 [Daucus carota].	1663522	154
Daucus carota	major allergen isoform Dau c 1.0201 [Daucus carota].	18652047	154
Daucus carota	minor allergen Dau c 4 profilin [Daucus carota].	18652049	134
Daucus carota	pathogenesis-related protein-like protein 1 [Daucus carota].	19912791	154
Daucus carota	major allergen [Daucus carota].	2154732	154
Daucus carota	major allergen [Daucus carota].	2154734	154
Daucus carota	major allergen Dau c 1/1 [Daucus carota].	2154736	154
Fagopyrum esculentum	BW8KD allergen protein [Fagopyrum esculentum].	17907758	133
Fagopyrum tataricum	allergenic protein [Fagopyrum tataricum].	22353013	195
Fagopyrum esculentum	legumin-like protein [Fagopyrum esculentum].	2317670	565
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
Fragaria x	major allergen Mal d 1 [Fragaria x ananassa].	54306612	80
Fragaria x	[Segment 1 of 3] Allergen Fra a 1.	60389903	12
Fragaria x	[Segment 2 of 3] Allergen Fra a 1.	60389904	14
Fragaria x	[Segment 3 of 3] Allergen Fra a 1.	60389905	74
Glycine max	34 kDa maturing seed vacuolar thiol protease precursor [Glycine	1199563	379
Glycine max	Hydrophobic seed protein (HPS) (Allergen Gly m 1).	123506	80
Glycine max	allergen Gly m Bd 28K [Glycine max].	12697782	473
Glycine max	P34 probable thiol protease precursor.	129353	379
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	lectin prepeptide.	170006	285
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
Glycine max	trypsin inhibitor subtype A [Glycine max].	18770	217
Glycine max	trypsin inhibitor subtype B [Glycine max].	18772	217
Glycine max	CG4 beta-conglycinin [Glycine max].	256427	439
Glycine max	Kunitz trypsin inhibitor; KTi [Glycine max].	256429	216
Glycine max	Kunitz trypsin inhibitor KTi1 [Glycine max].	256635	203
Glycine max	Kunitz trypsin inhibitor KTi2 [Glycine max].	256636	204
Glycine max	profilin [Glycine max].	3021373	131
Glycine max	Bd 30K [Glycine max].	3097321	379
Glycine max	Profilin-1 (GmPRO1) (Allergen Gly m 3.0101).	3914435	131
Glycine max	Kunitz trypsin inhibitor [Glycine max].	510515	208
Glycine max	unnamed protein product [Glycine max].	732706	562
Glycine soja	Gy5 [Glycine soja].	736002	517
Glycine max	Cytokinin induced message.	75102126	277
Glycine soja	A5A4B3 subunit [Glycine soja].	806556	563
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Helianthus annuus	pre-pro-seed albumin [Helianthus annuus].	18821	141
Helianthus annuus	profilin [Helianthus annuus].	3581965	133
Hordeum vulgare	trypsin inhibitor cme precursor [Hordeum vulgare].	1405736	144
Hordeum vulgare	amylase/protease inhibitor.	167077	117
Hordeum vulgare	alpha-amylase/trypsin inhibitor preprotein [Hordeum vulgare subsp.	18869	147
Hordeum vulgare	alpha-amylase inhibitor [Hordeum vulgare subsp. vulgare].	18955	144
Hordeum vulgare	monomeric alpha-amylase [Hordeum vulgare subsp. vulgare].	19003	146
Hordeum vulgare	CMe [Hordeum vulgare subsp. vulgare].	19009	148
Hordeum vulgare	LTP 1 [Hordeum vulgare].	19039	134
Hordeum vulgare	Alpha-amylase inhibitor BMA1-1 precursor (Allergen Hor v 1)	2506771	146
Hordeum vulgare	BDA1-1; Barley dimeric alpha-amylase inhibitor [Hordeum vulgare	3367714	152
Hordeum vulgare	CMa, component of tetrameric alpha-amylase inhibitor [Hordeum	439275	145
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Hordeum vulgare	pollen allergen Hor v 4 [Hordeum vulgare].	55859462	518
Hordeum vulgare	Alpha-amylase/trypsin inhibitor CMb precursor	585290	149
Hordeum vulgare	BAKER'S ASTHMA allergen BDP.	75198868	20
Hordeum vulgare	Pollen allergen precursor.	75219009	313
Juglans regia	albumin seed storage protein precursor [Juglans regia].	1794252	139
Juglans nigra	2S albumin seed storage protein [Juglans nigra].	31321942	161
Juglans nigra	vicilin seed storage protein [Juglans nigra].	31321944	481
Juglans regia	vicilin-like protein precursor [Juglans regia].	6580762	593
Lens culinaris	allergen Len c 1.0101 [Lens culinaris].	29539109	418
Lens culinaris	allergen Len c 1.0102 [Lens culinaris].	29539111	415
Litchi chinensis	profilin [Litchi chinensis].	15809696	131
Lycopersicon esculentum	Anther-specific protein LAT52 precursor.	125887	161
Lycopersicon esculentum	profilin [Lycopersicon esculentum].	16555787	131
Lycopersicon esculentum	profilin [Lycopersicon esculentum].	17224229	131
Lycopersicon esculentum	minor allergen beta-fructofuranosidase precursor [Lycopersicon	18542113	553
Lycopersicon esculentum	minor allergen beta-fructofuranosidase precursor [Lycopersicon	18542115	636
Malus x	thaumatin-like protein [Malus x domestica].	10334651	246
Malus x	major allergen {N-terminal} [apples, Golden Delicious, Peptide	1174276	37
Malus x	major allergen Mal d 1 [Malus x domestica].	1313966	159
Malus x	major allergen Mal d 1 [Malus x domestica].	1313968	160
Malus x	major allergen Mal d1 [Malus x domestica].	1313970	160
Malus x	major allergen Mal d1 [Malus x domestica].	1313972	160
Malus x	Major allergen Mal d 1 (Mal d 1).	1346478	159
Malus x	Profilin-1 (GD4-1) (Pollen allergen Mal d 4.0301).	14423873	131
Malus x	Profilin-2 (GD4-2) (Pollen allergen Mal d 4.0201).	14423874	131
Malus x	Profilin-3 (GD4-5) (Pollen allergen Mal d 4.0101).	14423875	131
Malus x	18 kda major allergen/Bet v 1 homolog {N-terminal} [Malus	1478292	25
Malus x	31 kda major allergen/disease resistance protein homolog	1478293	26
Malus x	ypr10 [Malus x domestica].	16555783	159
Malus x	major allergen d 1 [Malus x domestica].	21685277	158
Malus x	major allergen Mal d 1 [Malus x domestica].	2443824	159
Malus x	major allergen Mal d 1 [Malus x domestica].	27922941	159
Malus x	profilin [Malus x domestica].	28881453	131
Malus x	profilin [Malus x domestica].	28881455	131
Malus x	profilin [Malus x domestica].	28881457	131
Malus x	Mal d 1-associated protein [Malus x domestica].	32709122	190
Malus x	major allergen Mal d 1 [Malus x domestica].	3309647	159
Malus x	allergen Mal d 3 [Malus x domestica].	38492338	115
Malus x	major allergen mal d 1 [Malus x domestica].	4590364	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590366	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590368	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590376	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590378	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590380	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590382	159
Malus x	major allergen mal d 1 [Malus x domestica].	4590388	159

Malus x	lipid transfer protein precursor [Malus x domestica].	50659879	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659879	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659885	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659889	115
Malus x	lipid transfer protein precursor [Malus x domestica].	50659891	115
Malus x	lipid transfer protein precursor [Malus x domestica].	6715522	115
Malus x	Mal d 1 [Malus x domestica].	747852	159
Manihot esculenta	allergenic-related protein Pt2L4 [Manihot esculenta].	21585695	177
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Oryza sativa	beta-expansin [Oryza sativa].	11346546	271
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304216	111
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304217	109
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1304218	113
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398913	166
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398915	160
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398916	157
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	1398918	160
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	15624049	208
Oryza sativa	glyoxalase I [Oryza sativa (japonica cultivar-group)].	16580747	291
Oryza sativa	putative pollen allergen Jun o 4 [Oryza sativa (japonica cultivar-group)].	19386815	185
Oryza sativa	putative allergen Amb a 1.2 precursor [Oryza sativa (japonica cultivar-group)].	20146453	364
Oryza sativa	Putative pollen allergen [Oryza sativa (japonica cultivar-group)].	20502989	289
Oryza sativa	expansin Os-EXPA2 [Oryza sativa (japonica cultivar-group)].	21104587	251
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	218193	165
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	218195	162
Oryza sativa	allergenic protein [Oryza sativa (japonica cultivar-group)].	218197	157
Oryza sativa	beta-expansin [Oryza sativa].	2224915	261
Oryza sativa	putative allergenic protein [Oryza sativa (japonica cultivar-group)].	23616947	160
Oryza sativa	Major pollen allergen Ole s 1 precursor (Ory s 1).	2498586	263
Oryza sativa	allergenic protein [Oryza sativa].	2827316	157
Oryza sativa	Pollen allergen Ory s 2-A.	32363197	15
Oryza sativa	seed allergen RA17 [Oryza sativa (japonica cultivar-group)].	34900094	163
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Oryza sativa	allergen RA16 [Oryza sativa (japonica cultivar-group)].	34900104	157
Oryza sativa	allergen RAB precursor [Oryza sativa (japonica cultivar-group)].	34900132	160
Oryza sativa	putative pollen allergen [Oryza sativa (japonica cultivar-group)].	37536544	275
Oryza sativa	putative Ole s 1 pollen allergen [Oryza sativa (japonica cultivar-group)].	38175617	384
Oryza sativa	glyoxalase I [Oryza sativa (japonica cultivar-group)].	4126809	291
Oryza sativa	putative latex protein allergen [Oryza sativa (japonica cultivar-group)].	42408062	430
Oryza sativa	putative latex protein allergen [Oryza sativa (japonica cultivar-group)].	42408066	431
Oryza sativa	putative policalcin Phl p 7 (Calcium-binding pollen allergen Phl p 7).	45736119	82
Oryza sativa	putative expansin 11 precursor [Oryza sativa (japonica cultivar-group)].	45736177	269
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	49388537	207
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	50251668	180
Oryza sativa	pollen Ole e 1 allergen and extensin family protein-like [Oryza sativa (japonica cultivar-group)].	50251728	155
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	50252014	204
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	51536378	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075909	118
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075910	118
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075913	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075914	113
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075915	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075917	117
Oryza sativa	putative group 3 pollen allergen [Oryza sativa (japonica cultivar-group)].	52075924	117
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	52077086	146
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	52077087	158
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	53791938	206
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	53791944	206
Oryza sativa	Bet v 1 allergen-like [Oryza sativa (japonica cultivar-group)].	53792800	207
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Oryza sativa	pollen allergen-like [Oryza sativa (japonica cultivar-group)].	54291022	313
Oryza sativa	Seed allergenic protein RA5 precursor.	548657	157
Oryza sativa	Seed allergenic protein RA14 precursor.	548658	165
Oryza sativa	Seed allergenic protein RA17 precursor.	548660	162
Oryza sativa	Seed allergenic protein RAG2 precursor.	548671	166
Oryza sativa	allergen-like protein [Oryza sativa (japonica cultivar-group)].	57900264	139
Oryza sativa	putative expansin [Oryza sativa (japonica cultivar-group)].	6069656	284
Oryza sativa	Allergenic protein.	75102358	160
Oryza sativa	Allergenic protein.	75102382	111
Oryza sativa	Allergenic protein.	75102383	109
Oryza sativa	Allergenic protein.	75102384	113
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Oryza sativa	Allergenic protein.	75221023	166
Oryza sativa	Allergenic protein.	75221024	157
Oryza sativa	Allergenic protein.	75221025	160
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Oryza sativa	beta-expansin [Oryza sativa].	8118423	268
Oryza sativa	beta-expansin [Oryza sativa].	8118425	286
Oryza sativa	beta-expansin [Oryza sativa].	8118428	275
Oryza sativa	beta-expansin [Oryza sativa].	8118430	275
Oryza sativa	beta-expansin [Oryza sativa].	8118432	327
Oryza sativa	beta-expansin [Oryza sativa].	8118437	269
Oryza sativa	beta-expansin [Oryza sativa].	8118439	267
Persea americana	endochitinase [Persea americana].	3201547	326
Petroselinum crispum	pathogenesis-related protein 1 [Petroselinum crispum].	1843451	155
Phaseolus vulgaris	pathogenesis-related protein 1 (PvPR1) [Phaseolus vulgaris].	21044	156
Phaseolus vulgaris	pathogenesis-related protein 2 (PvPR2) [Phaseolus vulgaris].	21048	155
Pisum sativum	Vicilin [Pisum sativum].	42414627	415
Pisum sativum	Vicilin [Pisum sativum].	42414629	415
Pisum sativum	Orf protein.	75221106	258
Plantago lanceolata	plantain pollen major allergen, Pla 1 1.0101 [Plantago lanceolata].	14422359	131
Plantago lanceolata	plantain pollen major allergen, Pla 1 1.0102 [Plantago lanceolata].	14422361	131
Plantago lanceolata	plantain pollen major allergen, Pla 1 1.0103 [Plantago lanceolata].	14422363	131
Plantago lanceolata	unnamed protein product [Plantago lanceolata].	29163771	65
Plantago lanceolata	unnamed protein product [Plantago lanceolata].	29163773	65
Prunus avium	thaumatin-like protein precursor.	1144346	245
Prunus avium	Chain A, Solution Structure Of The Major Cherry Allergen Pru Av 1.	13787043	159
Prunus avium	cherry-allergen PRUA1.	1513216	160
Prunus persica	pru p 1 [Prunus persica].	17974195	91
Prunus dulcis	profilin [Prunus dulcis].	24473794	131
Prunus armeniaca	major allergen protein homolog [Prunus armeniaca].	2677826	160
Prunus persica	profilin [Prunus persica].	27528310	131
Prunus persica	profilin [Prunus persica].	27528312	131
Prunus persica	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru p	3287877	91
Prunus avium	Chain A, Solution Structure Of The Major Cherry Allergen Pru Av 1	34809853	159
Prunus avium	major cherry allergen Pru av 1.0201 [Prunus avium].	44409451	160
Prunus avium	major cherry allergen Pru av 1.0202 [Prunus avium].	44409474	160
Prunus avium	major cherry allergen Pru av 1.0203 [Prunus avium].	44409496	160
Prunus avium	profilin [Prunus avium].	4761582	131
Prunus armeniaca	putative allergen protein [Prunus armeniaca].	4887129	168
Prunus avium	lipid transfer protein precursor [Prunus avium].	6715520	117
Prunus armeniaca	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru ar	7404406	91
Prunus domestica	Nonspecific lipid-transfer protein 1 (LTP 1) (Major allergen Pru d	9297015	91
Pyrus communis	Nonspecific lipid-transfer protein precursor (LTP) (Allergen Pyr c	14423813	115
Pyrus communis	major allergen Pyrcl [Pyrus communis].	3044216	159
Pyrus communis	isoflavone reductase related protein [Pyrus communis].	3243234	308
Pyrus communis	profilin [Pyrus communis].	4761580	131
Ricinus communis	2S albumin precursor (Allergen Ric c 1/3) [Contains: Allergen Ric c	112762	258
Secale cereale	pollen allergen Sec c 4 [Secale cereale].	55859454	518
Secale cereale	pollen allergen Sec c 4 [Secale cereale].	55859456	520

Secale cereale	30K allergen.	75140047	16
Secale cereale	Major BAKER'S ASTHMA allergen SEC C 1.	75198875	26
Sesamum indicum	2S albumin [Sesamum indicum].	13183175	153
Sesamum indicum	7S globulin [Sesamum indicum].	13183177	585
Sesamum indicum	2S albumin precursor [Sesamum indicum].	5587323	148
Sinapis alba	allergen sin a 1.0104 [Sinapis alba].	1009434	145
Sinapis alba	allergen sin a 1.0105 [Sinapis alba].	1009436	145
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Sinapis alba	Allergen Sin a 1 precursor (Sin a 1) [Contains: Allergen sin a 1	51338758	145
Sinapis alba	major allergen Sin a 1 [Sinapis alba].	7545129	145
Solanum tuberosum	Aspartic protease inhibitor 11 (Cathepsin D inhibitor (PD))	124148	188
Solanum tuberosum	Patatin B1 precursor (Potato tuber protein).	129641	377
Solanum tuberosum	patatin.	169500	386
Solanum tuberosum	Cysteine protease inhibitor 1 precursor (PCPI 8.3) (P340) (P34021).	20141344	222
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Solanum tuberosum	aspartic proteinase inhibitor [Solanum tuberosum].	21413	217
Solanum tuberosum	unnamed protein product [Solanum tuberosum].	21510	386
Solanum tuberosum	patatin [Solanum tuberosum].	21512	386
Solanum tuberosum	patatin [Solanum tuberosum].	21514	386
Triticum aestivum	hypothetical 11.8K protein - wheat	100794	106
Triticum turgidum	alpha-amylase inhibitor, tetrameric, chain (M5 precursor - durum	100834	168
Triticum aestivum	profilin [Triticum aestivum].	1008443	141
Triticum aestivum	profilin [Triticum aestivum].	1008445	140
Triticum aestivum	profilin [Triticum aestivum].	1052817	138
Triticum aestivum	gamma-gliadin precursor [Triticum aestivum].	1063270	279
Triticum aestivum	triosephosphat isomerase [Triticum aestivum].	11124572	253
Triticum aestivum	allergenic peptide=low-molecular-weight glutenin chain [wheat,	1168171	30
Triticum aestivum	Endogenous alpha-amylase/subtilisin inhibitor (WASI).	123975	180
Triticum aestivum	alpha-gliadin [Triticum aestivum].	1304264	259
Triticum aestivum	IgE-binding polypeptide of major allergen (N-terminal) [wheat,	1311642	16
Triticum aestivum	agglutinin isolectin A precursor.	170666	212
Triticum turgidum	wheat germ agglutinin.	170668	186
Triticum aestivum	agglutinin isolectin D precursor.	170670	213
Triticum aestivum	gamma gliadin precursor.	170702	302
Triticum aestivum	gamma gliadin B precursor.	170708	291
Triticum aestivum	alpha-type gliadin precursor protein.	170710	318
Triticum aestivum	pre-alpha/beta gliadin A-II.	170712	291
Triticum aestivum	pre-alpha/beta gliadin A-V.	170716	319
Triticum aestivum	alpha/beta gliadin precursor.	170718	313
Triticum aestivum	alpha/beta gliadin precursor [Triticum aestivum].	170720	286
Triticum aestivum	pre-alpha/beta gliadin A-I.	170722	262
Triticum aestivum	pre-alpha/beta gliadin A-IV.	170724	297
Triticum aestivum	pre-alpha/beta gliadin A-III.	170726	282
Triticum aestivum	alpha-type gliadin.	170728	186
Triticum aestivum	gamma-gliadin B-I precursor [Triticum aestivum].	170730	304
Triticum aestivum	gamma-gliadin.	170732	323
Triticum aestivum	gamma gliadin B-III.	170734	244
Triticum aestivum	gamma-gliadin.	170736	251
Triticum aestivum	gamma-gliadin.	170738	327
Triticum urartu	gliadin.	170740	296
Triticum aestivum	HMW glutenin subunit Ax2* [Triticum aestivum].	170743	815
Triticum aestivum	serpin [Triticum aestivum].	1885350	399
Triticum aestivum	unnamed protein product [Triticum aestivum].	21673	307
Triticum aestivum	unnamed protein product [Triticum aestivum].	21701	145
Triticum aestivum	CM 17 protein precursor [Triticum aestivum].	21711	143
Triticum aestivum	unnamed protein product [Triticum aestivum].	21713	168
Triticum aestivum	high molecular weight glutenin subunit 1Ax1 [Triticum aestivum].	21743	830
Triticum aestivum	high molecular weight glutenin subunit 10 [Triticum aestivum].	21751	648

Triticum aestivum	unnamed protein product [Triticum aestivum].	21755	286
Triticum aestivum	unnamed protein product [Triticum aestivum].	21757	296
Triticum aestivum	unnamed protein product [Triticum aestivum].	21761	286
Triticum aestivum	unnamed protein product [Triticum aestivum].	21765	313
Triticum aestivum	seed storage protein (154AA) [Triticum aestivum].	21769	154
Triticum aestivum	unnamed protein product [Triticum aestivum].	21773	307
Triticum aestivum	unnamed protein product [Triticum aestivum].	21779	660
Triticum aestivum	unnamed protein product [Triticum aestivum].	21783	356
Triticum aestivum	unnamed protein product [Triticum aestivum].	21793	39
Triticum turgidum	precursor (AA -24 to 119) [Triticum turgidum subsp. durum].	21916	143
Triticum turgidum	CM2 protein [Triticum turgidum subsp. durum].	21920	145
Triticum turgidum	unnamed protein product [Triticum turgidum subsp. durum].	21926	295
Triticum turgidum	LMW glutenin [Triticum turgidum subsp. durum].	21930	285
Triticum aestivum	HMW glutenin subunit 1By9 [Triticum aestivum].	22090	705
Triticum turgidum	tetrameric alpha-amylase inhibitor 16 kDa subunit, CM16* [Triticum	244610	18
Triticum aestivum	27K protein [Triticum aestivum].	30793446	203
Triticum aestivum	Allergen C-C.	3913017	27
Triticum aestivum	pollen allergen (group II) [Triticum aestivum].	4007852	122
Triticum aestivum	putative pollen allergen precursor [Triticum aestivum].	40644792	178
Triticum aestivum	putative group V allergen [Triticum aestivum].	40644794	119
Triticum aestivum	putative major allergen Phl p 5 [Triticum aestivum].	40644796	231
Triticum aestivum	pollen allergen homolog [Triticum aestivum].	4099919	271
Triticum aestivum	alpha-gliadin.	473876	287
Triticum aestivum	pollen allergen Tri a 4 [Triticum aestivum].	55859458	518
Triticum aestivum	pollen allergen Tri a 4 [Triticum aestivum].	55859460	518
Triticum aestivum	putative gamma-gliadin [Triticum aestivum].	62484809	285
Triticum aestivum	putative LMW-glutenin subunit [Triticum aestivum].	62550933	326
Triticum aestivum	putative omega-gliadin [Triticum aestivum].	63252971	375
Triticum aestivum	glutenin [Triticum aestivum].	736319	838
Triticum aestivum	Gliadin omega-5.	75139902	32
Triticum turgidum	16K protein.	75140060	10
Triticum aestivum	LMM glutenin 1.	75219081	285
Triticum aestivum	LMM glutenin 3.	75317968	373
Triticum urartu	unknown protein.	806315	106
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886963	229
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886965	261
Triticum aestivum	low molecular weight glutenin [Triticum aestivum].	886967	276
Triticum aestivum	unnamed protein product [Triticum aestivum].	897811	101
Triticum aestivum	pollen allergen-like protein [Triticum aestivum].	972513	118
Vitis sp.	Nonspecific lipid-transfer protein P2 (LTP P2).	462717	38
Vitis sp.	Nonspecific lipid-transfer protein P3 (LTP P3).	462718	37
Vitis sp.	Nonspecific lipid-transfer protein P4 (LTP P4).	462719	37
Zea mays	Nonspecific lipid-transfer protein precursor (LTP) (Phospholipid	128388	120
Zea mays	Zm13.	1588669	170
Zea mays	beta-expansin 1a precursor (Pollen allergen Zea m 1) (Zea m 1).	20138191	269
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	group 3 pollen allergen [Zea mays].	33188338	120
Zea mays	pectate lyase homolog [Zea mays].	405535	438
Zea mays	Bet v 1 allergen [Zea mays].	54111527	154
Zea mays	Pectate lyase homolog.	75221515	104

Other contact allergens

Species	Comments	GI #	AA
Acanthamoeba castellanii	Acanthamoeba Castellani Profilin Ia.	2781014	125
Acanthamoeba castellanii	Chain B, Crystal Structure Of Acanthamoeba Castellani Profilin Ii,	9257090	125
Equus caballus	latherin [Equus caballus].	20143977	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.	11517601	131
Hevea brasiliensis	beta-1,3-glucanase.	1184668	374
Hevea brasiliensis	Pro-hevein precursor (Major hevein) [Contains: Hevein (Allergen Hev b 1)].	123062	204
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	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 Hevea 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	enolase, isoform 1 [Hevea brasiliensis].	9581744	445
Hevea brasiliensis	enolase, isoform 2 [Hevea brasiliensis].	9581746	445
Methanococcus maripaludis	Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal	45047603	217
Nicotiana tabacum	beta-expansin-like protein [Nicotiana tabacum].	12330698	273
Nicotiana tabacum	villin 1 [Nicotiana tabacum].	57283137	559
Nicotiana tabacum	villin 2 [Nicotiana tabacum].	57283139	520
Nicotiana tabacum	Polcalcen Nic t 1 (Calcium-binding pollen allergen Nic t 1).	59798467	84
Nicotiana tabacum	Polcalcen Nic t 2 (Calcium-binding pollen allergen Nic t 2).	59798468	86
Plasmodium falciparum	conserved protein [Plasmodium falciparum 3D7].	23505219	171
Styela plicata	major allergen [Styela plicata].	58257626	126

Nematodes and worms

Species	Comments	GI #	AA
Acanthocheilonema viteae	ladder protein [Acanthocheilonema viteae].	4102959	131
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	Tropomyosin (Allergen Ani s 3).	14423976	284
Anisakis simplex	21k allergen [Anisakis simplex].	31339067	194
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	putative nucleosome binding protein [Anisakis simplex].	6065744	321
Anisakis simplex	paramyosin [Anisakis simplex].	8117843	869
Anisakis simplex	paramyosin isoform [Anisakis simplex].	8453086	473
Ascaridia galli	fatty acid binding protein [Ascaridia galli].	3152922	135
Ascaris suum	allergen [Ascaris suum].	159653	395
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].	2735100	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	polyprotein allergen/antigen [Ascaris suum].	2970629	1095
Ascaris suum	major allergen ABA-1=TBA-1 allergen homolog {N-terminal} [Ascaris	299550	68
Brugia malayi	venom allergen antigen-like protein 1 [Brugia malayi].	13095442	220
Brugia malayi	major allergen [Brugia malayi].	13310414	227
Brugia malayi	larval allergen [Brugia malayi].	24711753	248
Dictyocaulus viviparus	DVA-1 polyprotein precursor (Antigen 1) (Allergen 1) (Nematode	2498317	1557
Dirofilaria immitis	venom allergen antigen 5-like protein [Dirofilaria immitis].	2245508	221
Heterodera glycines	secreted venom allergen-like protein vap2 [Heterodera glycines].	13447461	212
Heterodera glycines	venom allergen-like protein [Heterodera glycines].	14211968	212
Heterodera glycines	vap-1 [Heterodera glycines].	14326230	215
Heterodera glycines	probable polyprotein allergen Hgg-14 [Heterodera glycines].	18677166	288
Litomosoides carinii	ladder protein [Litomosoides carinii].	4102911	132
Loa loa	ladder protein [Loa loa].	4102951	132
Loa loa	LL20 15kDa ladder antigen.	414553	588
Meloidogyne incognita	secreted protein MSP-1 [Meloidogyne incognita].	4102596	231
Necator americanus	ancylostoma secreted protein 1 precursor [Necator americanus].	3396070	424
Necator americanus	calreticulin [Necator americanus].	3687326	403
Onchocerca volvulus	activation-associated secreted protein-2 [Onchocerca volvulus].	11762066	224
Onchocerca volvulus	myosin-like antigen.	159881	343
Onchocerca volvulus	vespid allergen antigen homolog [Onchocerca volvulus].	2796175	220
Onchocerca cervicalis	ladder protein [Onchocerca cervicalis].	4102953	133
Onchocerca volvulus	beta-galactoside-binding lectin.	433317	280
Onchocerca volvulus	activation-associated secreted protein-1 [Onchocerca volvulus].	5868902	220
Schistosoma japonicum	22.6 kDa tegumental antigen [Schistosoma japonicum].	2739154	191
Schistosoma japonicum	hypothetical protein, putative Profilin/allergen [Schistosoma	29841461	129
Setaria cervi	ladder protein [Setaria cervi].	4102957	133
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290388	152
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290390	90
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290392	128
Strongyloides stercoralis	IgG and IgE immunoreactive antigen recognized by sera from patients	2290394	144
Strongyloides stercoralis	IgG immunoreactive antigen [Strongyloides stercoralis].	2801529	156
Strongyloides stercoralis	allergen polyprotein homolog [Strongyloides stercoralis].	2801531	95
Stylonychia lemnae	unnamed protein product [Stylonychia lemnae].	10142	104
Toxocara canis	TBA-1 precursor [Toxocara canis].	1731859	140
Toxocara canis	ladder protein [Toxocara canis].	4102955	133
Toxocara canis	Allergen TBA-1.	74827032	36
Trichostrongylus colubriformis	aspartyl protease inhibitor precursor [Trichostrongylus	28274792	228
Wuchereria bancrofti	translationally controlled tumor protein-like protein [Wuchereria	14700054	181
Wuchereria bancrofti	vespid allergen antigen homolog [Wuchereria bancrofti].	4324680	220
Wuchereria bancrofti	vespid allergen antigen homolog [Wuchereria bancrofti].	4704758	220
Wuchereria bancrofti	cuticular endochitinase [Wuchereria bancrofti].	7673688	504

Appendix 2. FASTA sequence alignments of Cry2Ab2 protein
against AD6 database

!!SEQUENCE_LIST_1.0

(Peptide) FASTA of: cry2ab2_820.pep from: 1 to: 827 May 1, 2006 16:40

Cry2Ab2_820

TO: AD6: * Sequences: 1,511 Symbols: 333,422 Word Size: 2

Databases searched:
Monsanto, Release 1.0, Released on 6Mar2006, Formatted on 6Mar2006

Scoring matrix: GenRunData:blossum50.cmp
Variable pamfactor used
Gap creation penalty: 12 Gap extension penalty: 2

Histogram Key:
Each histogram symbol represents 3 search set sequences
Each inset symbol represents 1 search set sequences
z-scores computed from opt scores

z-score	obs	exp
(=)	(*)	(*)
< 20	4	0.==
20	0	0:
22	0	0:
24	0	0:
26	0	0:
28	0	0:
30	3	2:*
32	11	8:==*
34	23	22:=====*
36	39	45:=====*
38	77	74:=====*
40	97	103:=====*
42	155	126:=====*
44	123	139:=====*
46	101	141:=====*
48	138	135:=====*
50	111	124:=====*
52	100	109:=====*
54	78	93:=====*
56	86	78:=====*
58	67	64:=====*
60	74	52:=====*
62	51	41:=====*
64	38	33:=====*
66	38	26:=====*
68	25	20:=====*
70	21	16:=====*
72	15	13:=====*
74	7	10:=====*
76	5	8:=====*
78	7	6:=====*
80	3	5:=====*
82	6	4:=====*

84	2	3:*
86	3	2:*
88	1	2:*
90	1	1:*
92	0	1:*
94	0	1:*
96	0	1:*
98	0	0:
100	0	0:
102	1	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:

Joining threshold: 38, opt. threshold: 26, opt. width: 16, reg.-scaled

The best scores are:

AD6:GI-4538529	Begin: 2	End: 51	init1	initn	opt	z-sc E(1506)...
! Cop c1 allergen [Coprinus comatus]	68	72	103.5	0.89		
AD6:GI-38206325	Begin: 174	End: 229				
! Paramyosin isoform [Anisakis simplex]	39	39	74	90.4	4.8	
AD6:GI-38206325	Begin: 139	End: 172				
! Arginine 3 allergen SMIPP-S Yv5026E07...	40	40	68	88.7	5.9	
AD6:GI-704758	Begin: 111	End: 146				
! vespid allergen cotton homolog [Mu...]	35	35	66	87.0	7.3	
AD6:GI-5640550	Begin: 207	End: 263				
! class IV chitinase [Cryptomeria jap...]	52	52	67	86.1	8.2	
AD6:GI-385535	Begin: 121	End: 295				
! pectate lyase homolog [Zea mays]	35	35	70	86.0	8.3	
AD6:GI-4240803	Begin: 177	End: 323				
! putative latex protein allergen [Or...]	40	40	69	84.9	9.6	
AD6:GI-21104587	Begin: 99	End: 236				
! expansin Os-EXP2 [Oryza sativa (ja...)]	46	46	65	84.6	10	
\\End of List						

cry2ab2_820.pep
AD6:GI-4538529

gi|4538529|emb|CAB9376.1| Cop c1 allergen [Coprinus comatus]

SCORES Init1: 68 Initn: 68 Opt: 72 z-score: 103.5 E(1506) 0.89
>AD6:GI-4538529
Initn: 68 init1: 68 opt: 72 z-score: 103.5 E(1506) 0.89
Smith-Waterman score: 72; 32.7% identity in 52 aa overlap
(138-189:2-51)

cry2ab2_820. RLNTDTLARNVAELTGLQANVEEFNRQVDFLNPRNVAFLSITSSVNSQCHFFSRLEP
GI-4538529
RFLPSSSHLN PQHLPWLHPAPVLLPAPFO
110 120 130 140 150 160
170 180 190 200 210 220
cry2ab2_820. FQMGYQLLLPLFAQAANLHLSPFRDVLNADENGISAATLRTYRDYLNKTYRDSNYC

Product Characterization Center

SCORES	Init1: 35	Initn: 35	Opt: 66	z-score: 87.0	E(): 7.3
--------	-----------	-----------	---------	---------------	----------

CTY2ab2_820. ISGVFLVVRNEDLRRLPHUHEININASPSTPGGARGAYWVSVINRKNHIAHVENGSMIH
||| : : : : :
GI-0405535 NPIDRCRWCRDAWTDRKLAQAOCFGRHTVGGAAGKLAVVRDPSDDMIIPKRGTLRH
100 110 120 130 140 150

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cultivar-group))

SCORES      Init1: 46      Initn: 46      Opt: 65      z-score: 84.6      E(): 10
>>>AD6:GI-21104587
      initn: 46      init1: 46      opt: 65      z-score: 84.6      expect(): 10
      Smith-Waterman score: 84:      25.2% identity in 151 aa overlap
      (330-473:94-226)

      300      310      320      330      340      350
cry2ab2_820. LYSLFQVNSVYLVNGFGSARLSNTFFNIUGLPGSTTTTHALLAARVNVSGGSSGDIG-AS
GI-21104587 TAALSTLVFNDGACGSCYELRCDDNGQWCLFGSVTVTAINLCPFYA---LPNDGGWCHN
      70      80      90      100      110      120

      360      370      380      390      400      410
cry2ab2_820. PFQWQNFNCSTFLPPLLPFTFVRSWLDGSDREGVATVNNWQTESFETTLGRSGAFTARGN
      :      :      :      :      :      :
GI-21104587 PPRPHFD-----MAEF-----AFELQGVYRAGIVPVSYRVPCKVG-GIR---FTINGH
      130      140      150      160

      420      430      440      450      460      470
cry2ab2_820. SNYPFDYFIRNTSGVPLVWNEOLR-----RPLHYNEIRNIASPGSTPGGARAYMSVH
      :      :      :      :      :      :
GI-21104587 S-VFNLVLVTNVAG-PGDVQSVSIKSGSTGTGQPMRSNWGMQNSYLDGQSLSPQAVAS
      170      180      190      200      210      220

      480      490      500      510      520      530
cry2ab2_820. NRKNNHVAVHENGSMIHLAPNDYTGFTISPHATQVNNQRTIFSEKFGNQGDSLRFQEN
      230      240      250

GI-21104587 TGRKUTSNVNVVPAGWQGTGEGGQF
      260

! Distributed over 1 thread.
! Start time: Mon May 1 16:40:13 2006
! Completion time: Mon May 1 16:40:16 2006

! CPU time used:
! Database scan: 0:00:00.2
! Post-scan processing: 0:00:00.0
! Total CPU time: 0:00:00.3
! Output File: cry2ab2_820.ADM

```

```

! Distributed over 1 thread.
! Start time: Mon May 1 16:40:13 2006
! End time: Mon May 1 16:40:16 2006
! Completion time: Mon May 1 16:40:16 2006
! CPU time used: 0.000000
! Database scan: 0.000000
! Post-scan processing: 0.000000
! Total CPU time: 0.000000
! Output File: cry2ab2.820.ABC

```

Appendix 3. Search for immunologically relevant sequences in the Cry2Ab2 protein

allergensearch -infile=cry2ab2_820.pep -infile2=AD6:* -
outfile=cry2ab2_820.allergensearch -windowsize=8

Query sequence(s): cry2ab2_820.pep
Search sequence(s): AD6:*
Window size: 8

cry2ab2_820.allergensearch Mon May 1 16:38:32 2006

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! Q45709 bacillus thuringiensis (subs...	225	287	336	356.5	6e-14	! P17969 bacillus thuringiensis (subs...	97	282	299.8	8.7e-11	
! XN5:Y08920_1 Begin: 70 End: 646						! X17123_1 Begin: 51 End: 389					
! Y08920 Bacillus thuringiensis B.thu...	205	267	336	356.5	6e-14	! X17123 Bacillus thuringiensis Bacil...	97	282	299.8	8.7e-11	
! XN5:C1IA BACTX Begin: 70 End: 646						! XN5:C1DA BACTA Begin: 54 End: 321					
! Q45752 bacillus thuringiensis (subs...	205	267	336	356.5	6e-14	! P19415 bacillus thuringiensis (subs...	159	286	299.4	9e-11	
! XN5:C8BA BACUK Begin: 76 End: 658						! XN5:C0BA BACTY Begin: 18 End: 651					
! Q45705 bacillus thuringiensis (subs...	209	251	338	354.7	7.5e-14	! Q87905 Bacillus thuringiensis (subs...	93	125	281	298.5	1e-10
! XN5:U04365_1 Begin: 76 End: 658						! XN5:C1GB BACTZ Begin: 58 End: 598					
! U04365 Bacillus thuringiensis Bacil...	209	251	338	354.7	7.5e-14	! Q9az26 Bacillus thuringiensis (subs...	191	191	285	298.3	1e-10
! XN5:AAK6742 Begin: 70 End: 646						! XN5:X13233_1 Begin: 41 End: 610					
! Aak6742 bacillus thuringiensis. cr...	205	267	334	354.3	7.9e-14	! X13233 Bacillus thuringiensis B. th...	128	168	284	297.4	1.2e-10
! XN5:Q9F08 Begin: 70 End: 646						! XN5:C1AE BACTL Begin: 41 End: 610					
! Q9F08 bacillus thuringiensis. cryI...	226	288	334	354.3	7.9e-14	! Q03748 Bacillus thuringiensis (subs...	120	160	283	296.1	1.4e-10
! XN5:O85796 Begin: 70 End: 646						! XN5:M65252_1 Begin: 41 End: 610					
! Q85796 bacillus thuringiensis (subs...	205	267	333	353.3	9e-14	! M65252 Bacillus thuringiensis Bacil...	120	160	283	296.1	1.4e-10
! XN5:X62821_1 Begin: 70 End: 646						! XN5:M84650_1 Begin: 24 End: 239					
! X62821 Bacillus thuringiensis B.thu...	201	263	332	352.2	1e-13	! M84650 synthetic construct Syntheti...	114	158	277	295.2	1.5e-10
! XN5:C1ID BACTU Begin: 70 End: 646						! XN5:C3AA BACTT Begin: 39 End: 286					
! Q9xdl1 bacillus thuringiensis. pest...	206	267	328	348.0	1.8e-13	! P07130 Bacillus thuringiensis (subs...	114	158	277	294.6	1.7e-10
! XN5:U04367_1 Begin: 65 End: 277						! XN5:Q9S6N9 Begin: 47 End: 294					
! U04367 Bacillus thuringiensis Bacil...	242	271	331	347.5	1.9e-13	! Q9S6N9 bacillus thuringiensis. cry3...	114	158	277	294.5	1.7e-10
! Q45707 bacillus thuringiensis (subs...	242	271	331	347.5	1.9e-13	! XN5:M22472_1 Begin: 47 End: 294					
! XN5:C9EA BACTA Begin: 76 End: 651						! M22472 Bacillus thuringiensis B.thu...	114	158	277	294.5	1.7e-10
! Q9znl9 bacillus thuringiensis (subs...	152	183	326	342.1	3.8e-13	! XN5:AF363025_1 Begin: 68 End: 303					
! XN5:C1BE BACTU Begin: 73 End: 637						! AF363025 Bacillus thuringiensis sub...	206	233	281	293.7	1.9e-10
! Q85805 bacillus thuringiensis. pest...	193	217	324	339.4	5.4e-13	! XN5:AAK51084 Begin: 68 End: 303					
! XN5:AF077326_1 Begin: 73 End: 637						! AAK51084 bacillus thuringiensis (su...	206	233	281	293.7	1.9e-10
! AF077326 Bacillus thuringiensis Bac...	193	217	324	339.4	5.4e-13	! XN5:U031527_1 Begin: 32 End: 598					
! XN5:U04368_1 Begin: 65 End: 277						! U31527 Bacillus thuringiensis Bacil...	153	209	280	293.0	2.1e-10
! U04368 Bacillus thuringiensis Bacil...	231	260	319	334.7	9.8e-13	! XN5:C1JB BACTU Begin: 32 End: 598					
! XN5:C7AB BACUK Begin: 65 End: 277						! Q45716 bacillus thuringiensis. pest...	153	209	280	293.0	2.1e-10
! Q45708 bacillus thuringiensis (subs...	231	260	319	334.7	9.8e-13	! XN5:X06711_1 Begin: 68 End: 303					
! XN5:Q9S603 Begin: 61 End: 597						! X06711 Bacillus thuringiensis B.th...	206	233	280	292.6	2.2e-10
! Q9S603 bacillus thuringiensis. delt...	156	257	313	332.9	1.2e-12	! XN5:C1BA BACTX Begin: 66 End: 303					
! XN5:AF042733_1 Begin: 61 End: 597						! P0S517 Bacillus thuringiensis (subs...	206	233	280	292.6	2.2e-10
! AF042733 Bacillus thuringiensis Bac...	156	257	313	332.9	1.2e-12	! XN5:U04191_1 Begin: 41 End: 610					
! XN5:C0AA BACTP Begin: 74 End: 287						! U04191 Bacillus thuringiensis Bacil...	128	168	278	291.0	2.7e-10
! Q9x597 bacillus thuringiensis (subs...	156	156	317	332.4	1.3e-12	! XN5:A09398_1 Begin: 41 End: 610					
! XN5:AF122897_1 Begin: 74 End: 287						! A09398 Bacillus thuringiensis B.thu...	128	168	278	291.0	2.7e-10
! AF122897 Bacillus thuringiensis sub...	156	156	317	332.4	1.3e-12	! XN5:C1AB BACTK Begin: 41 End: 610					
! XN5:Q45740 Begin: 70 End: 314						! P06578 bacillus thuringiensis (subs...	128	168	278	291.0	2.7e-10
! Q45740 bacillus thuringiensis. inse...	205	205	308	331.8	1.4e-12	! XN5:Q9F296 Begin: 41 End: 610					
! XN5:C9DA BACTP Begin: 76 End: 612						! Q9F296 bacillus thuringiensis. delt...	128	168	278	291.0	2.7e-10
! O06014 Bacillus thuringiensis (subs...	156	257	313	328.1	2.3e-12	! XN5:M13898_1 Begin: 41 End: 610					
! XN5:C8AA BACUK Begin: 75 End: 301						! M13898 Bacillus thuringiensis B.thu...	128	168	278	291.0	2.7e-10
! Q45704 bacillus thuringiensis (subs...	154	181	302	316.5	1e-11	! XN5:D00117_1 Begin: 41 End: 610					
! XN5:U04364_1 Begin: 75 End: 301						! D00117 Bacillus thuringiensis Bacil...	128	168	278	291.0	2.7e-10
! U04364 Bacillus thuringiensis Bacil...	154	181	302	316.5	1e-11	! XN5:X04698_1 Begin: 41 End: 610					
! XN5:AF093107_1 Begin: 67 End: 463						! X04698 Bacillus thuringiensis Bacil...	128	168	278	291.0	2.7e-10
! AF093107 Bacillus thuringiensis Bac...	148	148	294	312.8	1.6e-11	! XN5:M17263_1 Begin: 41 End: 610					
! XN5:O87654 Begin: 67 End: 463						! M17263 Bacillus thuringiensis B.thu...	128	128	277	289.9	3.1e-10
! O87654 bacillus thuringiensis. delt...	148	148	294	312.8	1.6e-11	! XN5:Q9AM83 Begin: 41 End: 610					
! XN5:CRAA BACUH Begin: 49 End: 386						! Q9AM83 bacillus thuringiensis serov...	128	168	276	289.1	3.4e-10
! Q9x597 bacillus thuringiensis (subs...	184	184	295	311.8	1.9e-11	! XN5:C1DB BACTU Begin: 54 End: 321					
! XN5:AB023293_1 Begin: 49 End: 386						! Q45747 bacillus thuringiensis. pest...	152	176	275	287.8	4e-10
! AB023293 Bacillus thuringiensis Bac...	184	184	295	311.8	1.9e-11	! XN5:AAK48937 Begin: 54 End: 321					
! XN5:C7AA BACTU Begin: 65 End: 274						! Aak48937 bacillus thuringiensis. in...	152	176	275	287.8	4e-10
! Q03749 bacillus thuringiensis. pest...	223	223	297	311.3	2e-11	! XN5:L32019_1 Begin: 32 End: 597					
! XN5:A07236_1 Begin: 65 End: 274						! L32019 Bacillus thuringiensis Bacil...	150	203	275	287.7	4.1e-10
! A07236 Bacillus thuringiensis B.thu...	223	223	297	311.3	2e-11	! XN5:C1TA BACTU Begin: 32 End: 597					
! XN5:A07234_1 Begin: 43 End: 381						! Q45738 bacillus thuringiensis. pest...	150	203	275	287.7	4.1e-10
! A07234 Bacillus thuringiensis B.thu...	97	97	282	299.9	8.5e-11	! XN5:CJAA BACTY Begin: 74 End: 648					
! XN5:C3BA BACTO Begin: 51 End: 389						! O32307 bacillus thuringiensis (subs...	135	135	270	287.1	4.4e-10

! U28801	Bacillus thuringiensis Bacil...	148	177	252	262.9	9.7e-09
TXNS:C1KA_BACTM	Begin: 73 End: 636	148	177	252	262.9	9.7e-09
! Q45714	Bacillus thuringiensis (subs...	148	177	252	262.9	9.7e-09
TXNS:X13353_1	Begin: 79 End: 609	128	168	251	262.1	1.1e-08
! X13353	Bacillus thuringiensis Bacil...	128	168	251	262.1	1.1e-08
TXNS:C1AA_BACTM	Begin: 79 End: 609	128	168	251	262.1	1.1e-08
! P02965	Bacillus thuringiensis (subs...	128	168	251	262.1	1.1e-08
TXNS:C1AD_BACTA	Begin: 41 End: 609	151	192	251	262.1	1.1e-08
! Q03744	Bacillus thuringiensis (subs...	151	192	251	262.1	1.1e-08
TXNS:M73250_1	Begin: 41 End: 609	151	192	251	262.1	1.1e-08
! M73250	Bacillus thuringiensis Bacil...	151	192	251	262.1	1.1e-08
TXNS:X39103_1	Begin: 54 End: 246	206	206	245	260.8	1.3e-08
! X39103	synthetic construct Artificial...	206	206	245	260.8	1.3e-08
TXNS:X96682_1	Begin: 54 End: 246	206	206	245	259.3	1.5e-08
! X96682	Bacillus thuringiensis B.thu...	206	206	245	259.3	1.5e-08
TXNS:M12661_1	Begin: 41 End: 611	128	168	248	259.1	1.6e-08
! M12661	Bacillus thuringiensis B.thu...	128	168	248	259.1	1.6e-08
TXNS:Q95514	Begin: 41 End: 609	128	160	248	258.9	1.6e-08
! Q95514	Bacillus thuringiensis. inse...	128	160	248	258.9	1.6e-08
TXNS:X13620_1	Begin: 54 End: 246	206	206	245	258.6	1.7e-08
! X13620	Bacillus thuringiensis Bacil...	206	206	245	258.6	1.7e-08
TXNS:Q91877	Begin: 54 End: 246	208	208	247	257.8	1.9e-08
! Q91877	Bacillus thuringiensis. toxi...	208	208	247	257.8	1.9e-08
TXNS:AF215647_1	Begin: 54 End: 246	208	208	247	257.8	1.9e-08
! AF215647	Bacillus thuringiensis Bac...	208	208	247	257.8	1.9e-08
TXNS:A27531_1	Begin: 41 End: 609	151	192	246	256.8	2.1e-08
! A27531	Bacillus thuringiensis B.thu...	151	192	246	256.8	2.1e-08
TXNS:C1IC_BACTE	Begin: 54 End: 246	206	206	245	255.7	2.5e-08
! P05518	Bacillus thuringiensis (subs...	206	206	245	255.7	2.5e-08
TXNS:M73253_1	Begin: 54 End: 246	206	206	245	255.7	2.5e-08
! M73253	Bacillus thuringiensis Bacil...	206	206	245	255.7	2.5e-08
TXNS:A117675_1	Begin: 15 End: 565	128	128	237	252.8	3.6e-08
! A117675	synthetic construct Synthe...	128	128	237	252.8	3.6e-08
TXNS:C1EG_BACTU	Begin: 12 End: 257	192	192	242	252.6	3.7e-08
! Q45446	Bacillus thuringiensis. pest...	192	192	242	252.6	3.7e-08
TXNS:U03472_1	Begin: 41 End: 591	128	128	237	252.5	3.7e-08
! U03472	synthetic construct Synthe...	128	128	237	252.5	3.7e-08
TXNS:U03306	Begin: 41 End: 591	128	128	237	252.4	3.7e-08
! Q32306	Bacillus thuringiensis. delt...	128	128	237	252.4	3.7e-08
TXNS:Y09787_1	Begin: 41 End: 591	128	128	237	252.4	3.7e-08
! Y09787	Bacillus thuringiensis B.thu...	128	128	237	252.4	3.7e-08
TXNS:X07518_1	Begin: 54 End: 591	200	200	239	249.3	5.6e-08
! X07518	Bacillus thuringiensis Bacil...	200	200	239	249.3	5.6e-08
TXNS:U09872_1	Begin: 41 End: 591	128	128	237	247.2	7.3e-08
! U09872	Bacillus thuringiensis Bacil...	128	128	237	247.2	7.3e-08
TXNS:U87793_1	Begin: 41 End: 591	128	128	237	247.2	7.3e-08
! U87793	Bacillus thuringiensis. subs...	128	128	237	247.2	7.3e-08
TXNS:C1AC_BACTK	Begin: 41 End: 591	128	128	237	247.2	7.3e-08
! P05068	Bacillus thuringiensis (subs...	128	128	237	247.2	7.3e-08
TXNS:U043606_1	Begin: 41 End: 590	128	128	231	246.2	8.3e-08
! U043606	Bacillus thuringiensis Bacil...	128	128	231	246.2	8.3e-08
TXNS:Q045721	Begin: 41 End: 590	128	128	231	246.2	8.3e-08
! Q045721	Bacillus thuringiensis. cryi...	128	128	231	246.2	8.3e-08
TXNS:Q45737	Begin: 41 End: 590	128	128	231	246.1	8.6e-08
! Q45737	Bacillus thuringiensis. cryi...	128	128	231	246.1	8.6e-08
TXNS:AF081248_1	Begin: 41 End: 609	128	157	235	245.1	9.6e-08
! AF081248	Bacillus thuringiensis Bac...	128	157	235	245.1	9.6e-08
TXNS:C1AG_BACTU	Begin: 41 End: 609	128	157	235	245.1	9.6e-08
! Q95515	Bacillus thuringiensis. pest...	128	157	235	245.1	9.6e-08
TXNS:Q95485	Begin: 41 End: 590	128	128	231	244.8	1e-07
! Q95485	Bacillus thuringiensis. inse...	128	128	231	244.8	1e-07
TXNS:X07423_1	Begin: 11 End: 264	142	166	233	243.3	1.2e-07
! X07423	Bacillus thuringiensis Bacil...	142	166	233	243.3	1.2e-07
TXNS:C4BA_BACTI	Begin: 11 End: 264	142	166	233	243.3	1.2e-07

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142	166	233	243.3	1.2e-07	! M12662 Bacillus thuringiensis (subs...	69	101	173	183.7	0.0002
141	165	232	242.2	1.4e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
140	164	231	241.9	1.4e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
139	163	230	240.9	1.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
138	162	229	239.8	1.9e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
137	161	228	238.8	2.8e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
136	160	227	237.8	2.8e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
135	159	226	236.8	2.8e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
134	158	225	235.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
133	157	224	234.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
132	156	223	233.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
131	155	222	232.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
130	154	221	231.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
129	153	220	230.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
128	152	219	229.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
127	151	218	228.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
126	150	217	227.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
125	149	216	226.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
124	148	215	225.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
123	147	214	224.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
122	146	213	223.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
121	145	212	222.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
120	144	211	221.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
119	143	210	220.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
118	142	209	219.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
117	141	208	218.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
116	140	207	217.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
115	139	206	216.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
114	138	205	215.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
113	137	204	214.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
112	136	203	213.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
111	135	202	212.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
110	134	201	211.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
109	133	200	210.8	3.7e-07	TXNS:X07082_1 Begin: 11 End: 264	TXNS:CAAA_BACTI	Begin: 68 End: 296			
108	132	199	209.8	3.7e-07</						

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cry2ab2_820. LITGLQANVEEFNROVDNPNRNNAVPLSITSSVNTMOQLFNRLPQFOMOGYQLLLPL 180
C2AB_BACTK LITGLQANVEEFNROVDNPNRNNAVPLSITSSVNTMOQLFNRLPQFOMOGYQLLLPL 170

cry2ab2_820. FAQANLHLSFIRVDILNDEWGISAAATLRYDYLKNTYRDYSNYCINTYQSAFAGLNT 240
C2AB_BACTK FAQANLHLSFIRVDILNDEWGISAAATLRYDYLKNTYRDYSNYCINTYQSAFAGLNT 230

cry2ab2_820. RLHDMLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGPQOTQSTTSQDWPEL 300
C2AB_BACTK RLHDMLEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGPQOTQSTTSQDWPEL 290

cry2ab2_820. YSLFQVNSVNLNGFSGARLNTFPNIVGLPGSTTTTHALLAARNYSGMISGSGPQASPF 340
C2AB_BACTK YSLFQVNSVNLNGFSGARLNTFPNIVGLPGSTTTTHALLAARNYSGMISGSGPQASPF 330

cry2ab2_820. NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNWQTESFETTLGLRSGAFTARGNSN 420
C2AB_BACTK NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNWQTESFETTLGLRSGAFTARGNSN 410

cry2ab2_820. YFPDYFIRNLSGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHA 480
C2AB_BACTK YFPDYFIRNLSGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHA 470

cry2ab2_820. VHEGSMIHLAPNDYTGFTTISPIHATQVNNOTRTFISEKFGNQGDSLRFQNNITARTYL 540
C2AB_BACTK VHEGSMIHLAPNDYTGFTTISPIHATQVNNOTRTFISEKFGNQGDSLRFQNNITARTYL 530

cry2ab2_820. RGNGNSVNLRLVSSIGNSTIRVTINGRVYATVNNVTNNNDGVNDNGARFSDINIGNVV 600
C2AB_BACTK RGNGNSVNLRLVSSIGNSTIRVTINGRVYATVNNVTNNNDGVNDNGARFSDINIGNVV 590

cry2ab2_820. ASSNSDVPDLINVTLSGTFQDLNMLVPTNISPLY 630
C2AB_BACTK ASSNSDVPDLINVTLSGTFQDLNMLVPTNISPLY 620

cry2ab2_820.pcp
TXNS:AF200816_1

Description: AF200816 Bacillus thuringiensis Bacillus thuringiensis crystal protein (cry2) gene, complete cds.
Accession/ID: AF200816
=====General comments=====

LOCUS AF200816_1 (AF200816)

DEFINITION Bacillus thuringiensis crystal protein (cry2) gene, complete cds;

SCORES Init1: 3794 Initn: 3794 Opt: 3794 Z-score: 4034.6 E(): 8.1e-219
>TXNS:AF200816_1
Initn: 3794 Init1: 3794 opt: 3794 Z-score: 4034.6 expect(): 8.1e-219
Smith-Waterman score: 3794; 91.0% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820. MQAMDSVNLNGSRITTCDAVNVAAHDPFSFOHKSILDTVQKEWTEWKNHSHLYLDPVIGT 60
AF200816_1 MNSVNLNGSRITTCDAVNVVHDPFSFOHKSILDTVQKEWTEWKNHSHLYLDPVIGT 50

cry2ab2_820. VASFLLKKGVLGKRIILSELRLNLIFFPGSGTNLMQDILRETEKFLNQLNTDILARVNAE 120
AF200816_1 VASFLLKKGVLGKRIILSELRLNLIFFPGSGTNLMQDILRETEKFLNQLNTDILARVNAE 110

cry2ab2_820. LITGLQANVEEFNROVDNPNRNNAVPLSITSSVNTMOQLFNRLPQFOMOGYQLLLPL 180
AF200816_1 LITGLQANVEEFNROVDNPNRNNAVPLSITSSVNTMOQLFNRLPQFOMOGYQLLLPL 170

cry2ab2_820. FAQANLHLSFIRVDILNDEWGISAAATLRYDYLKNTYRDYSNYCINTYQSAFAGLNT 240
AF200816_1 FAQANLHLSFIRVDILNDEWGISAAATLRYDYLKNTYRDYSNYCINTYQSAFAGLNT 230

cry2ab2_820. RNLMELEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGPQOTQSTTSQDWPEL 300
AF200816_1 RNLMELEFRTYMLNVEFYVSIWLSFKYQSLVSSGANLYASGSGPQOTQSTTSQDWPEL 290

cry2ab2_820. YSLFQVNSVNLNGFSGARLNTFPNIVGLPGSTTTTHALLAARNYSGMISGSGPQASPF 360
AF200816_1 YSLFQVNSVNLNGFSGARLNTFPNIVGLPGSTTTTHALLAARNYSGMISGSGPQASPF 350

cry2ab2_820. NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNWQTESFETTLGLRSGAFTARGNSN 420
AF200816_1 NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNWQTESFETTLGLRSGAFTARGNSN 410

cry2ab2_820. YFPDYFIRNLSGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHA 480
AF200816_1 YFPDYFIRNLSGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHA 470

cry2ab2_820. VHEGSMIHLAPNDYTGFTTISPIHATQVNNOTRTFISEKFGNQGDSLRFQNNITARTYL 540
AF200816_1 VHEGSMIHLAPNDYTGFTTISPIHATQVNNOTRTFISEKFGNQGDSLRFQNNITARTYL 530

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CRY2ab2_820. YSLFQVNSVNLGFSGARLSTFPNVLGPGSTTHALLAARVNSGGISGDIASGPF 310 320 330 340 350 360
C2AD_BACTU YSLFQVNSVNLGFSGARLSTFPNVLGPGSTTHALLAARVNSGGITSGSISGNSF 300 310 320 330 340 350

cry2ab2_820. LTGLQANVEEFNRQVDNFLNPNRNAVPLSTSSVNTMQQLFLNRLPQFOMQGYQLLLPL

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C2AA_BACTK  LIGLQNTRENNQVQDNFLNPTONFVPLSITSSVNTMQQLFNRLPQFIQGYQLLLPL
120 130 140 150 160 170
cry2ab2_820  FQANLNSSTQVILNADENGISAATLRDYRLKNVTRDYNYNCINTYQSAFKGLNT
250 260 270 280 290 300
C2AA_BACTK  FQANLNLSPFIRLILADENGISATLRDYRLKNVTRDYNYNCINTYQAFRGLNT
180 190 200 210 220 230
cry2ab2_820  RLHDMLEFRTYMFENPFKXVSIWSEFQSLVSSGANLYASGSGPQQTOSTSQDWPFLL
240 250 260 270 280 290
C2AA_BACTK  RLHDMLEFRTYMFENPFKXVSIWSEFQSLVSSGANLYASGSGPQQTOSTSQDWPFLL
240 250 260 270 280 290
cry2ab2_820  YSLFOVNSYVINGFSGARLSNTFNIVGSGSTTHALLARVNSGSGISGDIASFPF
310 320 330 340 350 360
C2AA_BACTK  YSLFOVNSYVINGFSGARLSNTFNIVGSGSTTHALLARVNSGSGISGDIASFPF
300 310 320 330 340 350
cry2ab2_820  NONFNCSTFLPPLLTFFVRSWLDGSDREGVATVNTMOTESPETTLGNSGAFARGNSN
370 380 390 400 410 420
C2AA_BACTK  NONFNCSTFLPPLLTFFVRSWLDGSDREGVATVNTMOTESPETTLGNSGAFARGNSN
360 370 380 390 400 410
cry2ab2_820  YFPDYFIRNISGVPLVVRNEDLRRLHYNEIRNIASPSGTPGAGAYVSVHNRKNIIHA
430 440 450 460 470 480
C2AA_BACTK  YFPDYFIRNISGVPLVVRNEDLRRLHYNEIRNIASPSGTPGAGAYVSVHNRKNIIHA
420 430 440 450 460 470
cry2ab2_820  VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGOSLRFEQNTIARYTL
490 500 510 520 530 540
C2AA_BACTK  VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGOSLRFEQNTIARYTL
480 490 500 510 520 530
cry2ab2_820  RGNNGSNLYLRVSSISGNSTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
550 560 570 580 590 600
C2AA_BACTK  RGNNGSNLYLRVSSISGNSTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
540 550 560 570 580 590
cry2ab2_820  ASSNSDVPDLNVTLSNGTQFDLMNIMLVPTNISPLY
610 620 630
C2AA_BACTK  ASSNSDVPDLNVTLSNGTQFDLMNIMLVPTNISPLY
600 610 620 630
cry2ab2_820.pcp
TXN5:Q9S6N5
```

Description: Q9S6N5 bacillus thuringiensis. cry2aa protein. 6/2001
Accession/ID: Q9S6N5
ID Q9S6N5
AC Q9S6N5
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

SCORES Initl: 3706 Initn: 3706 Opt: 3714 z-score: 3949.5 E(): 4.4e-214

```
>>TXN5:Q9S6N5 (633 aa)
initn: 3706 opt: 3714 z-score: 3949.5 expect(): 4.4e-214
Smith-Waterman score: 3714; 87.3% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820  MQAMDSVINSGRITICDAYNVAADHPFQHKSLDTVQKEWTEKKNHSLYLDPIVGT
10 20 30 40 50 60
Q9S6N5  MNNVLNSGRITICDAYNVAADHPFQHKSLDTVQKEWTEKKNHSLYLDPIVGT
10 20 30 40 50

cry2ab2_820  VASFLKKVGSLSVGRKILSELRLNIPFSGSTNLMODILRETEFLNORLNTDTLARVNAE
70 80 90 100 110 120
Q9S6N5  VSSFLKKVGSLSVGRKILSELRLNIPFSGSTNLMODILRETEFLNORLNTDTLARVNAE
60 70 80 90 100 110

cry2ab2_820  LTGLQANVEEFNRQVDNPLNPNRNPVLSITSSVNTMQQLFNRLPQFIQGYQLLLPL
130 140 150 160 170 180
Q9S6N5  LTGLQANVEEFNRQVDNPLNPNRNPVLSITSSVNTMQQLFNRLPQFIQGYQLLLPL
120 130 140 150 160 170

cry2ab2_820  FQANLNLSPFIRLILADENGISATLRDYRLKNVTRDYNYNCINTYQSAFKGLNT
190 200 210 220 230 240
Q9S6N5  FQANLNLSPFIRLILADENGISATLRDYRLKNVTRDYNYNCINTYQSAFKGLNT
180 190 200 210 220 230

cry2ab2_820  YFPDYFIRNISGVPLVVRNEDLRRLHYNEIRNIASPSGTPGAGAYVSVHNRKNIIHA
250 260 270 280 290 300
Q9S6N5  YFPDYFIRNISGVPLVVRNEDLRRLHYNEIRNIASPSGTPGAGAYVSVHNRKNIIHA
240 250 260 270 280 290

cry2ab2_820  VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGOSLRFEQNTIARYTL
310 320 330 340 350 360
Q9S6N5  VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGOSLRFEQNTIARYTL
300 310 320 330 340 350

cry2ab2_820  RGNNGSNLYLRVSSISGNSTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
370 380 390 400 410 420
Q9S6N5  RGNNGSNLYLRVSSISGNSTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
360 370 380 390 400 410

cry2ab2_820  ASSNSDVPDLNVTLSNGTQFDLMNIMLVPTNISPLY
430 440 450 460 470 480
Q9S6N5  ASSNSDVPDLNVTLSNGTQFDLMNIMLVPTNISPLY
420 430 440 450 460 470

cry2ab2_820.pcp
TXN5:Q9S6N5
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cry2ab2_820. ASSNSDVLVDINVLNSGTQFDLMNIMLVPTNISPLY
Q9S6N5 ASDNVTNVLVDINVLNSGTQFDLMNIMLVPTNPPPLY
600 610 620 630
cry2ab2_820.pep
TXNS:Q9S6N4
Description: Q9S6N4 bacillus thuringiensis. cry2aa protein. 6/2001
Accession/ID: Q9S6N4
ID Q9S6N4 PRELIMINARY; PRT; 633 AA.
AC Q9S6N4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

SCORES Init1: 3694 Initn: 3694 Opt: 3702 z-score: 3936.7 E(): 2.3e-213
>>TXNS:Q9S6N4
initn: 3694 opt: 3702 z-score: 3936.7 expect(): 2.3e-213
Smith-Waterman score: 3702; 87.2% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820. MQAMDNSVLNSGRTTICDAYNVAADHPFSQHKSLDTVQKHWKNNHSLYLDPIVGT
Q9S6N4 MNVLSNRRTTICDAYNVAADHPFSQHKSLDTVQKHWKNNHSLYLDPIVGT
10 20 30 40 50 60
70 80 90 100 110 120
cry2ab2_820. VASFLKKVGSVLGKRLSELRLNLIFFSSGSLNLMQDILRETEKFLNQLNTDTLARVNAE
Q9S6N4 VSSFLKKVGSVLGKRLSELRLNLIFFSSGSLNLMQDILRETEKFLNQLNTDTLARVNAE
60 70 80 90 100 110
120 130 140 150 160 170
cry2ab2_820. LTGLQANVEEFNRQVDNPLAPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLDPL
Q9S6N4 LTGLQANVEEFNRQVDNPLAPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLDPL
120 130 140 150 160 170
180 190 200 210 220 230
cry2ab2_820. FAQAAHLHLSFTRDVLNDAEWGISAATLRTYRDYLNKNTYDYSNICYNTQSAFKGLNT
Q9S6N4 FAQAAHLHLSFTRDVLNDAEWGISAATLRTYRDYLNKNTYDYSNICYNTQSAFKGLNT
180 190 200 210 220 230
240 250 260 270 280 290
cry2ab2_820. RLHDMLEFRTYFLNVEFYVSIWSLFKYQSLVSSGANLYASGGPQQTSTQSDWFFL
Q9S6N4 RLHDMLEFRTYFLNVEFYVSIWSLFKYQSLVSSGANLYASGGPQQTSTQSDWFFL
240 250 260 270 280 290
300 310 320 330 340 350
cry2ab2_820. YSLFQVNSYLVNLSGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGDGTGASFF
Q9S6N4 YSLFQVNSYLVNLSGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGDGTGASFF
300 310 320 330 340 350
360 370 380 390 400 410
cry2ab2_820. NONFNCSSTLPLLTTPFVRSMLDSGSDREGVATVTNMQTESFETTLGLRSAGFTARGNSN
Q9S6N4 NONFNCSSTLPLLTTPFVRSMLDSGSDREGVATVTNMQTESFETTLGLRSAGFTARGNSN
360 370 380 390 400 410
```

```
Q9S6N4 NHFNCSSTLPLLTTPFVRSMLDSGSDREGVATVTNMQTESFETTLGLRSAGFTARGNSN
360 370 380 390 400 410
cry2ab2_820. YFPDYFIRNISGVPLVRNEDLRPLHYNIRINIASPSGTPGGRAYVSVHRKNNIHA
Q9S6N4 YFPDYFIRNISGVPLVRNEDLRPLHYNIRINIASPSGTPGGRAYVSVHRKNNIHA
420 430 440 450 460 470
480 490 500 510 520 530
cry2ab2_820. VHEGNSMHLAPNDYTGFTISPIHATQVNNQTRTISEKFGNQGDSLRFEQNNITARYTL
Q9S6N4 VHEGNSMHLAPNDYTGFTISPIHATQVNNQTRTISEKFGNQGDSLRFEQNNITARYTL
480 490 500 510 520 530
540 550 560 570 580 590
cry2ab2_820. RGNNGSNLYLRVSSISGNTIRVTINGRVYVATNNTTNDGVNDMGARFSDINIGNV
Q9S6N4 RGNNGSNLYLRVSSISGNTIRVTINGRVYVATNNTTNDGVNDMGARFSDINIGNV
540 550 560 570 580 590
600 610 620 630
cry2ab2_820. ASSNSDVLVDINVLNSGTQFDLMNIMLVPTNISPLY
Q9S6N4 ASDNVTNVLVDINVLNSGTQFDLMNIMLVPTNPPPLY
600 610 620 630
cry2ab2_820.pep
TXNS:Q9RM89
Description: Q9RM89 bacillus thuringiensis. cry2a protein (fragment). 6/2001
Accession/ID: Q9RM89
ID Q9RM89 PRELIMINARY; PRT; 551 AA.
AC Q9RM89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

SCORES Init1: 3234 Initn: 3234 Opt: 3242 z-score: 3448.7 E(): 3.5e-186
>>TXNS:Q9RM89
initn: 3234 opt: 3242 z-score: 3448.7 expect(): 3.5e-186
Smith-Waterman score: 3242; 87.3% identity in 550 aa overlap
(6-555:2-551)

cry2ab2_820. MQAMDNSVLNSGRTTICDAYNVAADHPFSQHKSLDTVQKHWKNNHSLYLDPIVGT
Q9RM89 MNVLSNRRTTICDAYNVAADHPFSQHKSLDTVQKHWKNNHSLYLDPIVGT
10 20 30 40 50 60
70 80 90 100 110 120
cry2ab2_820. VASFLKKVGSVLGKRLSELRLNLIFFSSGSLNLMQDILRETEKFLNQLNTDTLARVNAE
Q9RM89 VSSFLKKVGSVLGKRLSELRLNLIFFSSGSLNLMQDILRETEKFLNQLNTDTLARVNAE
60 70 80 90 100 110
120 130 140 150 160 170
cry2ab2_820. LTGLQANVEEFNRQVDNPLAPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLDPL
Q9RM89 LTGLQANVEEFNRQVDNPLAPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLDPL
120 130 140 150 160 170
180 190 200 210 220 230
cry2ab2_820. YSLFQVNSYLVNLSGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGDGTGASFF
Q9RM89 YSLFQVNSYLVNLSGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGDGTGASFF
180 190 200 210 220 230
240 250 260 270 280 290
cry2ab2_820. NONFNCSSTLPLLTTPFVRSMLDSGSDREGVATVTNMQTESFETTLGLRSAGFTARGNSN
Q9RM89 NONFNCSSTLPLLTTPFVRSMLDSGSDREGVATVTNMQTESFETTLGLRSAGFTARGNSN
240 250 260 270 280 290
300 310 320 330 340 350
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~~FRASCHWELLSFIRBLLSADDEWGISAATLRTYRDVINYTRDYSNYCNYTOTAERGIT~~

cty2ab2_820. ~~RLHMDSEFTFLNMFVTSWINSFTYSLVSSGANLYASGGPQQTSTSDWPFLL~~
230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430 435 440 445 450 455 460 465 470 475 480 485 490 495 500 505 510 515 520 525 530 535 540 545 550 555 560 565 570 575 580 585 590 595 600 605 610 615 620 625 630 635 640 645 650 655 660 665 670 675 680 685 690 695 700 705 710 715 720 725 730 735 740 745 750 755 760 765 770 775 780 785 790 795 800 805 810 815 820 825 830 835 840 845 850 855 860 865 870 875 880 885 890 895 900 905 910 915 920 925 930 935 940 945 950 955 960 965 970 975 980 985 990 995

cry2ab2_820. YSLFQVNSNVLVNGFSGLSNTFPNI GLPQSSTTHALMARVNYSGGISGSDIGASPF
|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
YSLFQVNSNVLISGSITGRLSINFPNLGGPSPTTTLNSLARVNWSGVSYSGLICATNL

Q9RM69 300 310 320 330 340 350

```

cry2ab2_820.  NONFNCSTFLPPLLTFFVRSWLDGSDREGVATVNNOTESFETTLGRSAGFTSGNSN
370          380          390          400          410          420
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
NHNFNCSVLPLP:STIPVRSWLDSDTDREGVATSTNWOFSSTTSLRCAFSAGNSN
Q9RMB9

```

```

cry2ab2_820.      430      440      450      460      470      480
YFPDYFIRNIGSVPLAVNEQLRRPLHYNEIRINASPSTGGGARAYMSVVRKNKHAY
|||||
YFPDYFIRNIGSVPLAVNEQLTPLHYNOIRINISPSTGGGARAYLYSVHKNKHAY
|||||

```

```

cry2ab2_820.  VHENGSMIHLPADNYGTFTISPIHATOVNQTRTFSKFGNQGDSLRFEQNNITARTVL
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Q3RM89        ANENGTMHILAPEDYGTFTISPIHATOVNQTRTFSKFGNQGDSLRFEQNNITARTHL

```

cry2ab2_820. RQNGNSYNLYLRVSSIGNSTIRVTNGRVYATNVNTTNNDDGVNDNGARFSDINIGNV
 |||||
 Q9RM89 RQNGNSYNLYLRVSS

cry2ab2_820.pep
TXN5 : C2AC BACTU

Description: Q45743 bacillus thuringiensis. pesticidal crystal protein cry2ac

(insecticidal
Accession/ID: Q45743

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=====General comments=====
ID  C2AC BACTU          STANDARD:      PRT:  622 AA
```

AC Q45743; . . .

	C
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	C
	T
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	O
	O
	A
	C
	T
	L
	C
	P
	J.
	B
	H
	C
	-
	L
	R
	S
	F
	H
	E
	B
	C
	C
	C

SCORES INITI: 1948 INITH: 2654 OPT: 2294 Z-SCORE: 2439.7 E(): 5.5e-130
>>TXN5:C2AC BACTU (622 aa)

Smith-Waterman score: 3211; 77.8% identity in 634 aa overlap
 in1th: 2654 in1tl: 1548 opt: 2294 z-score: 2439.7 expect(): 5.5e-130

(6-637:2-622)

Year	10	20	30	40	50	60
MO	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MA	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MI	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MS	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
MT	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NE	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NH	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NJ	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NM	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
NY	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
OH	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
OK	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
OR	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
PA	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
RI	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
SC	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
SD	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
TN	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
TX	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
UT	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
VA	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
VT	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
WA	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
WI	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
WY	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000

CITYADZ_020. MQAMJNSVNSGRKIIICDAYINVAHADFFSFQRKSLDIVQKEWIEWKNHNSLYLDDPLVGI
|::||:| |::||:| |::||:| |::||:| |::||:| |::||:| |::||:| |::||:| |::||:| |::||:| |::||:|

C2AC_BACTU MNTVLNNGRNTTCHAHNVVAHDPPFSEHKSLNTIEKEWKWKRTDHSLYVAPIGT

cry2ab2_820. 70 80 90 100 110 120
 VASFLKKVGSIVGKRIILSEURNIPFGSTNIMODIILRETEKELNQRINTDTLARVNAE
 VGSFTLKKVGSIVGKRIILSEVONIIPFGSINIMODIILRETEKELNQRINTDTLARVNAE
 C2AC BACTU
 VGSFTLKKVGSIVGKRIILSEVONIIPFGSINIMODIILRETEKELNQRINTDTLARVNAE

ccy2ab_820. 130 140 150 160 170 180
 LTGLQANVEEFNRQVDNFPNPNNAVPLSTTSVNTMQLFLNPLQFQMGVQLLLPL
 LAGLQANVAEFNRQVDNFPNPNVPLAIIDSVNTLQGFLLSRLFOFOTGVQLLLPL
 C2AC BACTU

[illegible]

cry2ab2_820. RLHDLLEFTYTNFLNVPEYVISINSLFKYQSLLVSSGANLYASGGPQQTOSTFTSDWFFL
 |||||
 RLHDLLEFTYTNFLNVPEYVISINSLFKYQSLLVSSGANLYASGGPQQTOSTFTSDWFFL
 |||||
 C2AC_BACTU RLHDLLEFTYTNFLNVPEYVISINSLFKYQSLLVSSGANLYASGGP--TQSTAQWFFL

CN2AB2_820_YSLFQNSVNLGFGSARLSTFNPIVG-P-GSTTHALLAARNYSGGISGGIGAS
C2AC_BACTO_YSLFQNSVNLGSGARTTTFNPNGISLPVYNSTLHF--ARNINRGVGVSSRIGCA

6820. PFNONFNGSTFFPLLPFPVRSMLDGSOREGVAATVNWQSFETTLGRSGAFTARGN
CY2002 368 370 390 400 410

CGAC BACTU
NLAKONFNISLFILOTFPIRSMLDGSTGREGVAATSNWQSAFETLLDRFSIFASRGN
360 370 380 390 400 410

cry2ab_2826	SNFFPDTFTNISVPLVVNRD-----RRLPHYNRIINSPSTPGGAYAMVSYHVRKNNI	429	430	431	432	433	434	435	436	437
CZAC_BACTU	SNFPDFETRTNSGVGRISWADNPENFNEIRDI----GTT--AVASLVTYHKRNKI	429	430	431	432	433	434	435	436	437

~~cyt2ab2_820. HAVHENGSMHLIANDNDNGFTIDAHAFVNNQNTTSEKFGNQGDSLRFPQNNTTARY
:
YDHTGNTGTHLAPNDYTSTFPIHAWVMSITFTISIKYGNQGDLSRFLSPLNTARY~~

cry2ab2_820. TLGGNGSNLYLRYLVSSISGNSLTVRTINRVTATVACATNNDGVNDVNSAPSPDINGIG
 530 540 550 560 570 580
 C2AC_BACTU TLGGNGSNLYLRYLVSSISGNSLTVRTINRVTATVACATNNDGVNDVNSAPSPDINGIG
 530 540 550 560 570 580

crý2ab2_820.	WASSSDVPELDIVTLNSGTQFELNMLVPTNLSPPY	590	600	610	620
	: : : : : : :				
CZAC_BACTU	WASANTVPLDIQVTFENGQPELNMNMFVTNLPPIY	590	600	610	620

CRYZAU_020.pep
TXNS:X57252_3

Description: X57252 *Bacillus thuringiensis* B. thuringiensis plasmid DNA for cryIIIC operon and
Accession/ID: X57252
LOCUS X57252.3 [BTCRYIIIC]
DEFINITION B. thuringiensis plasmid DNA for cryIIIC operon and gene for cryIIIC
=====General comments=====

SCORES Initl: 1548 Initn: 2654 Opt: 2294 Z-score: 2439.7 E(): 5.5e-130
>>TXNS:X57252_3 (622 aa)
Initn: 2654 Initl: 1548 Opt: 2294 Z-score: 2439.7 expect(): 5.5e-130
Smith-Waterman score: 3211; 77.8% identity in 634 aa overlap
(6-637:2-622)

cry2ab2_820. MQAMDNSVLNSGRITTCIDAYNVAADHPFSEFOHKSIDTVQKEWTEWKKNNHSLYLDPVIGT 10 20 30 40 50 60
X57252_3 MNTVLNNGRNTTCHANNVVAADHPFSEFKSLNTEKEWKKRTHDSLYVAPIVGT 10 20 30 40 50
10 20 30 40 50 60

cry2ab2_820. VASFLKKVGSILVGRKILSELRLNLIPEPSSGNLMQDILRETEKFLNQRINTDTLARVNAE 70 80 90 100 110 120
X57252_3 VGSFLKKVGSILVGRKILSELRLNLIPEPSSGNLMQDILRETEKFLNQRINTDTLARVNAE 70 80 90 100 110 120
60 70 80 90 100 110

cry2ab2_820. LTGLQANVEEFNRQVDNPLNPNNAVPLSITSSVNTMQQLFLNRLPQFOMQGYQLLLPL 130 140 150 160 170 180
X57252_3 LAGLQANVAEPNRQVDNPLNPNNAVPLSITSSVNTMQQLFLNRLPQFOMQGYQLLLPL 130 140 150 160 170
120 130 140 150 160 170

cry2ab2_820. FAQAANLHLSFTRDVLNDAEWGISAATLRTYRDYLNKTYRDSYNCINTYOSAFKGLNT 190 200 210 220 230 240
X57252_3 FAQAANLHLSFTRDVLNDAEWGISAATLRTYRDYLNKTYRDSYNCINTYOSAFKGLNT 190 200 210 220 230
180 190 200 210 220 230

cry2ab2_820. RLHDMLEFRITYNFLNVEFYYSIWSLFKYQSLVSSGANLYASSGGPQQTQSFTSQDWFFL 250 260 270 280 290 300
X57252_3 RLHDMLEFRITYNFLNVEFYYSIWSLFKYQSLVSSGANLYASSGGPQQTQSFTSQDWFFL 250 260 270 280 290
240 250 260 270 280 290

cry2ab2_820. YSLFQVNSVNLGFSGRNLSTNFNIVGLP--GSTTHALLAARVNYSGGLSSDGIGAS 310 320 330 340 350
X57252_3 YSLFQVNSVNLGFSGRNLSTNFNIVGLP--GSTTHALLAARVNYSGGLSSDGIGAS 310 320 330 340 350
300 310 320 330 340 350

cry2ab2_820. PFNQNFNCSTFPLLPFPVRSWLDSDGREGVATVNWQTESFETTLGLRSGAFTARGN 360 370 380 390 400 410
X57252_3 NLNQNFNISTLFPPLFPVRSWLDSDGREGVATVNWQTESFETTLGLRSGAFTARGN 360 370 380 390 400 410
360 370 380 390 400 410

cry2ab2_820. SNFYDPDFIRNISGVPLVVRNEDLRRPLHYNEIRNIAFSPGTCGARAYMVSHNRKNNI 420 430 440 450 460 470
X57252_3 SNFYDPDFIRNISGVPLVVRNEDLRRPLHYNEIRNIAFSPGTCGARAYMVSHNRKNNI 420 430 440 450 460 470
420 430 440 450 460 470

480 490 500 510 520 530

cry2ab2_820. HAVHENGSMIHLAPNDYTGFTISPHATQVNNQTRTFISEKFGQGSLSRFEQNNTTARY 470 480 490 500 510 520
X57252_3 YDHTENGSMIHLAPNDYTGFTISPHATQVNNQTRTFISEKFGQGSLSRFEQNNTTARY 470 480 490 500 510 520

cry2ab2_820. TLRGNGNSYNYLRLRVSSIGNSITRTVINGRVYTATVNTTNNQGVNDGARGFSDINIGN 540 550 560 570 580 590
X57252_3 TLRGNGNSYNYLRLRVSSIGNSITRTVINGRVYTATVNTTNNQGVNDGARGFSDINIGN 540 550 560 570 580 590
540 550 560 570 580 590

cry2ab2_820. VVASNSDVPLDINVLNSGTQFQDLMNIMLVPTNISPLY 600 610 620 630
X57252_3 VVASANTNVPLDIQVTFNGNPOFELMNMIFVPTNLPLY 590 600 610 620
590 600 610 620

cry2ab2_820.pgp
TXNS:CIAA_PAEPP

Description: Q45358 *paenibacillus popilliae* (*Bacillus popilliae*). parasporal
crystal protein
Accession/ID: Q45358
=====General comments=====

ID CIAA_PAEPP STANDARD; PRT; 706 AA.
AC Q45358; . . .

SCORES Initl: 725 Initn: 1195 Opt: 1032 Z-score: 1096.7 E(): 3.5e-55
>>TXNS:CIAA_PAEPP (706 aa)
Initn: 1195 Initl: 725 Opt: 1032 Z-score: 1096.7 expect(): 3.5e-55
Smith-Waterman score: 1364; 38.8% identity in 665 aa overlap
(1-637:72-706)

cry2ab2_820. MQAMDNSVLNSGRITTCIDAYNVAADHPFSE 10 20 30
CIAA_PAEPP DGISDDLICLDPIYNNNNNDNAICDELGLTIPIDNNITCTDFT---PINVMTDPPF-- 50 60 70 80 90
50 60 70 80 90

cry2ab2_820. QHKSIDTVQKEWTEWKKNNHSLYLDPVIGTVASFLKKVGSILVGRKILSELRLNLIPEPSS 40 50 60 70 80 90
CIAA_PAEPP RKKSTQELTRETEWTEWKKNNHSLYLDPVIGTVASFLKKVGSILVGRKILSELRLNLIPEPSS 40 50 60 70 80 90
100 110 120 130 140 150

cry2ab2_820. TNLMDILRETEKFLNQRINTDTLARVNAELTGLQANVEEFNRQVDNPLNPNNAVPLSI 100 110 120 130 140 150
CIAA_PAEPP SLTMEELRATEQYVQGERLDTANRVSQELVGLKNNLITFDNDQVEDFLQNRVIGISFLAI 160 170 180 190 200 210
160 170 180 190 200 210

cry2ab2_820. TSSVNTMQQLFLNRLPQFOMQGYQLLLPLFAQAANLHLSFTRDVLNDAEWGISAATLR 160 170 180 190 200 210
CIAA_PAEPP IDSINTMQQLFVNRPLPQFQVGYQLLLPLFAQAATLHLTFLRDVLIINADEWNIPTAQLN 220 230 240 250 260 270
220 230 240 250 260 270

cry2ab2_820. TYRDYLNKTYRDSYNCINTYOSAFKGLNTR--LHDMLEFRITYNFLNVEFYYSIWSLFPK 220 230 240 250 260
CIAA_PAEPP TYTRYFKEYTAESYNSALSTYDDGFRFFRYFRNTLEDMLQFKFTMTNALDLVSLSLK 280 290 300 310 320 330
280 290 300 310 320 330

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[illegible]

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cry2ab2_820. VASSNSDVLINVT-LSNGTOFDLMNIMLVPTNISPLY
CICA_PAEPP FVSQTARELOQSGATSSSPLDMMILIPINDVPLY
cry2ab2_820.pcp
TXN5:CIBA_PAEPP

Description: P57091 paenibacillus popilliae (bacillus popilliae). parasportal
crystal protein
Accession/ID: P57091
=====General comments=====
ID CIBA_PAEPP STANDARD; PRT; 675 AA.
AC P57091;

SCORES Init1: 693 Initn: 1213 Opt: 965 z-score: 1025.8 E(): 3.1e-51
>>TXN5:CIBA_PAEPP (675 aa)
Initn: 1213 Init1: 693 Opt: 965 Z-score: 1025.8 expect(): 3.1e-51
Smith-Waterman score: 1388; 38.4% identity in 670 aa overlap
(1-637:30-675)

cry2ab2_820.
CIBA_PAEPP MNNGNALSRTALTPTNNKVISGLVTLNGLPPIDNNIICSGNEMPI---NVTRKNPF--
cry2ab2_820. QHKSIDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLGKRIILSELRNLIFFSGS
CIBA_PAEPP RKRTOEFIREWTEWKNSESPFTAPIGVVTSITLLEALKQVQSLLMTLLNTLFFNNS
cry2ab2_820. TNLMDILRETEKELNORLNTDTLARVNAELTGLQANVEEFNQVDNLFNPNRAVLSI
CIBA_PAEPP TSTMEILRATEQYVQEQDVTWNRVSGEGLKKNLRTFNQDIDDFLQNRVSIPTAM
cry2ab2_820. TSVNTMQQLFLNLPQFQMGVQLLLPLFAQAAHLHSFIRDVILNADEMGISAATLR
CIBA_PAEPP IDSINTMQQVFNRLPQFQLSDYQLLLPLFAQAGATLHLTFIRDIIINAGEWNIPEAQLN
cry2ab2_820. TYRDLVKNYTDVSNYCINTYQSAFKGL---NTRLHDMLEFRYTMFLNVEFVSIWLSFK
CIBA_PAEPP TKRRLKQYVAQYSNVALSTYEGAFRFRYPATLENMLOKFTFTMLNVLVLSLSLK
cry2ab2_820. YQSLVSSGANLYASGSGPOQTSFTSDWPFLYSLFQVNSNVNLFNGFSGARLNTFPNI
CIBA_PAEPP YNWLXISANLYNIGNKNVEGEVSIWFFNSYQTKNSNLTSLVSGVGAIRWYLYNT
cry2ab2_820. VGLPGSTTHALLAARVNYSGGISDGIGAS-----PF-----NONFNC
CIBA_PAEPP --FFGEYIODNLNIIASVYGVGVGPKIGVQLSTTELDKQIKQAGAGMTGLDLSFNC
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AF017416_1 120 130 140 150 160 170
ATAKVFUNSNLQRLPQFEIAGYEGVISISLTQMCITLHGLKKGILAGSDWGTFPE
cry2ab2_820 210 220 230 240 250 260
KYLTRDYLKATRDYNYCNITQSAF-KGLNTRHDMLEFRYMFNLFVYVSIWLSF
AF017416_1 180 190 200 210 220 230
DRSLISQFNRYVEVATMMGLYSERGLLAKNLNEALNFRNWCISLYVPFSEAWLL
cry2ab2_820 270 280 290 300 310 320
KYSQSLVSSGANDNASGSGQOQFQWPF-FLASLPVSNVNLVANG--FSGARLSNT
AF017416_1 240 250 260 270 280 290
RYEGTKLENTLSLW-NFVG-EDGGILHDMKGLYKLLMGSATNRLANVRFNYSFSDT
cry2ab2_820 330 340 350 360 370 380
FENIVGLPGSTTTHALLAARVNYSGGISGDIS--ASPFQFNCSTFLPLLPFVRWS
AF017416_1 300 310 320 330 340 350
-QGTIHRNIGLGHPTNGEQPTGWNIGRGLRGSANVSELEITKVEQEI-----TY
cry2ab2_820 390 400 410 420 430 440
LDSGDRGVATVNMQTESFETILGRSAGF--TARGNSNYPF--YFIRNI-----
AF017416_1 360 370 380 390 400 410
NNKGDSHSIVPA-NTRNEILTATVPITADPFKTDINRWYFSQGLYSNNYKEDDRVI
cry2ab2_820 440 450 460 470 480 490
--SGVPLVVRNEDLRRPLHNEIRNI--ASPSGTP--GGARAYMVSVHNRKNNIHAVHENG
AF017416_1 410 420 430 440 450 460
LNSRVPGGIPSNRLEYDGY--IRAVSACPRNVPLSYNNHLYLTLYNLEVDATQNT-I
cry2ab2_820 490 500 510 520 530 540
MIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGD-----SLAPEQN
AF017416_1 470 480 490 500 510 520
IVGFSFNNTKSPYARNSHYLSATNDAYVIPALQFATVSDRSFLEDTPDQATDGSIKFET
cry2ab2_820 550 560 570 580 590 600
--NTTARYTLRGNNGSNYLLRVSSI--GNSTIRVTNGRVYATNVT-----TTNN
AF017416_1 530 540 550 560 570 580
VLGNEAKYSIRLN-TGFNTATRYRLVIRFKATAFLAAGIRVRSQSGNNRLLGGIPVEGN
cry2ab2_820 600 610 620 630 640 650
DG-VNDNGARPSDINGNVASNSDVPDLNVLNLSGTFQFLMIMILVPTNISPLY
AF017416_1 590 600 610 620 630 640
SGWDYITDSFTFDNLGITASTNAFFSIDSD-GVNASQOQWLSKLILVKDFVNNSGFRN
AF017416_1 650 660 670 680 690 700
QVPLAPVVIARCPNTFFVSNNTSSGEGYQYNDNQNNTSSGEGYQYQYNDNQNNTSSGEGY
cry2ab2_820.pep
TXNS:CBBB_BACTV
Description: Q92IUS bacillus thuringiensis (subsp. medellin). pesticidal
crystal protein cry
Accession/ID: Q92IUS
-----General comments-----
ID CBBB_BACTV STANDARD; PRT: 750 AA.
AC Q92IUS;

SCORES Init1: 149 Initn: 251 Opt: 371 z-score: 393.4 E(): 5.3e-16
>>TXNS:CBBB_BACTV (750 aa)
Initn: 251 Init1: 149 Opt: 371 z-score: 393.4 expect(): 5.3e-16
Smith-Waterman score: 403; 22.3% identity in 619 aa overlap
(58-629:35-633)
cry2ab2_820 30 40 50 60 70 80
FSFOHKSLLTVQKEWTEKWNKNKXNLDLPVITVASFLKKVSLGKRLSELNRLIFF
CBBB_BACTV 10 20 30 40 50 60
SFNVLANNNWSSFFLPFNSKIEPISAPALIAPAPIAKYLATALAKWAKQGFALKESEIFF
cry2ab2_820 90 100 110 120 130 140
SGSTNLMDILRETEKEFLNQRLNTDTLARVNAELTGLQANVEFNQVDNFLNPNRNPV
CBBB_BACTV 70 80 90 100 110
GNETATMEKVRLEVTILNQTLQTDRAVTKAEYEGFHLGKVFDTYVSO-----STFTF
cry2ab2_820 150 160 170 180 190 200
LSITSSVNTMQLFLNRLPQFQMGYOQLLLPLFAQANLHLGFIRDVILNADENGISAA
CBBB_BACTV 120 130 140 150 160 170
ATAKTHFLANSLLIQRLPEPEIAGYEGVISISLTQMCITLHGLKKGILAGSDWGTFPE
cry2ab2_820 210 220 230 240 250 260
ILRTYRDYLNKVTDRYDNYCINTYQSAF-KGLNTRHDMLEFRYMFNLFVYVSIWLSF
CBBB_BACTV 180 190 200 210 220 230
LMSLSLCQFNRYVNEYNRMGLYSIEFGRLAKNLNEALNFRNWCISLYVPFSEAWLL
cry2ab2_820 270 280 290 300 310 320
KYSQSLVSSGANDNASGSGQOQFQWPF-FLASLPVSNVNLVANG--FSGARLSNT
CBBB_BACTV 240 250 260 270 280 290
RYEGTKLENTLSLW-NFVG-EDGGILHDMKGLYKLLMGSATNRLANVRFNYSFSDT
cry2ab2_820 330 340 350 360 370 380
FENIVGLPGSTTTHALLAARVNYSGGISGDIS--ASPFQFNCSTFLPLLPFVRWS
CBBB_BACTV 300 310 320 330 340 350
-QGTIHRNIGLGHPTNGEQPTGWNIGRGLRGSANVSELEITKVEQEI-----TY
cry2ab2_820 390 400 410 420 430 440
LDSGDRGVATVNMQTESFETILGRSAGF--TARGNSNYPF--YFIRNI-----
CBBB_BACTV 360 370 380 390 400 410
NNKGDSHSIVPA-NTRNEILTATVPITADPFKTDINRWYFSQGLYSNNYKEDDRVI
cry2ab2_820 440 450 460 470 480 490
--SGVPLVVRNEDLRRPLHNEIRNI--ASPSGTP--GGARAYMVSVHNRKNNIHAVHENG
CBBB_BACTV 410 420 430 440 450 460
LNSRVPGGIPSNRLEYDGY--IRAVSACPRNVPLSYNNHLYLTLYNLEVDATQNT-I
cry2ab2_820 490 500 510 520 530 540
MIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGD-----SLAPEQN
CBBB_BACTV 470 480 490 500 510 520
IVGFSFNNTKSPYARNSHYLSATNDAYVIPALQFATVSDRSFLEDTPDQATDGSIKFET
cry2ab2_820 550 560 570 580 590 600
--NTTARYTLRGNNGSNYLLRVSSI--GNSTIRVTNGRVYATNVT-----TTNN

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CBBA_BACTJ      QATI-----HRENIHVLPF--YNGGTTIGWINGRSGLSFFCSNLEIKIWKQEIY
               300       310       320       330       340       350

cry2ab2_820.    LDGSDREGVATVTNNQTESPETTLGLRSQAF--TARNSNYF-PD-YFIRNI-----
               390       400       410       420       430
CBBA_BACTJ      NDKGSFNSTVPAA-T-RNEILTATVPTSDAPFEKTADINWKYFSPGLYSGWNLIKFDITVT
               360       370       380       390       400

               440       450       460       470       480
cry2ab2_820.    --SGVLIVVNEDLRPLHYNEIRNI-ASPSGTFGGARAYVWSVHNKKNIIHAVHENGSM
               |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
CBBA_BACTJ      LKSRRPSTIIPSNILKYDDYY--IRAVSACPKGVSLAYNHDEFLTITTYNKLEYDAFTQTII
               410       420       430       440       450       460

               490       500       510       520       530       540
cry2ab2_820.    IHLRPDYTGTFISPIHATOVNNQTRFISEKEGNGDSLPEQN-----NTTARYLRLG
               |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
CBBA_BACTJ      VGFSPDNTKFYPRNSHYLUSTIDDAYVIPALQFSTVSDRSFLEDTPQAOTDGSIKFDTIV
               470       480       490       500       510       520

               550       560       570       580       590
cry2ab2_820.    NGNSYNLYLRVSSIGNSTR---VTINGRVYTATNVNTTINDGVNDN-GARFSNDING
               |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
CBBA_BACTJ      LGNEAKYSIRLTNGFTATFRYLRIIFKAPARLAAGIRVRSCNSGNKLGGIPVEGNSG
               530       540       550       560       570       580

               600       610       620       630
cry2ab2_820.    NVVASNSDVPLDLINTLNSGTQFDLMNLMLVPTNISPLY
               :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CBBA_BACTJ      WDIYITDSPTFDLDGITTSYNNAFSDSDGVNASQQWLSKLLVKESSTFTQIPLKPY
               590       600       610       620       630       640

cry2ab2_820.pep
TXN5:X86902_1

Description: X86902 Bacillus thuringiensis B.thuringiensis cryIIb gene. 3/1996
Accession/ID: X86902
LOCUS        X86902_1 [BTCRYIIIB]
DEFINITION   B.thuringiensis cryIIb gene.
DATE         20-MAR-1996 . . .

SCORES      Initl: 144      Inltln: 252      Opt: 369      z-score: 391.5 E(): 6.7e-16
              >TXN5:X86902_1
              Inltln: 252 Initl: 144 Opt: 369 Z-score: 391.5 expect(): 6.7e-16
Smith-Waterman score: 400; 22.2% identity in 594 aa overlap
(58-621:35-611)

cry2ab2_820.    FSFOHKSLDVTQKEWTENWKKNNHSLYLDPIVGTVASFLLKKVGSLVGRKRILSERNLIPP
               30       40       50       60       70       80
X86902_1        NFNTTEINNMFPMYNGRLSPLESLAPALIAVAPIAKYLATALAWKVQKGFAKLKSEIFF
               10       20       30       40       50       60

               90       100       110       120       130       140
cry2ab2_820.    SGSTNMULDLRETEKFINQRINLTTLARVNAELTGLQANVEEFNRQVDNPLPNNAVYP
               |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
X86902_1        GNPATMDKRIEVOQLDRLQDRVKILEGEYKG---IIDVSKVPTDVIQVQSFKETG
               70       80       90       100       110       120

               150       160       170       180       190       200

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CRY2AB2_820. LSITSSVNTWQQLNRLPQFMQGYQLLLPLFAQAANHLSEFIRVDILNADENGISAA
X86902_1 TANKLFFTSNQL-LSRDPFETAGYEGVISLFTQMCTFHLGLKDLGILAGSANGFAPA
CRY2AB2_820. TLRVYDLKNTDYANKCINTYQAF-KGLNTHLDMLEFRTYMLFVYVSIWLSF
X86902_1 DKDALLCONRNEYNELMWYISKEFGRKARKLALNFRMCLSYVFFPSEWLSL
CRY2AB2_820. KYQSLVSSGANLYASGSGQOQSFTSDWP-FLYSLFQVNSNYLN-FCGRLSNT
X86902_1 RYEGTKLENTLSLW-NFVG-ESINNLSNDWIGALYKLMGAPNORLNKNNYSYFSDT
CRY2AB2_820. FPNIVGLPSTITHALLAARVNYSGGIS-SGDIGASPMQ-NFNCSTLPPLTTPRSM
X86902_1 QATIT-HRENIHGLVLT---YNGFTITIGWINGRESSPSCSNESEYKIKYITY
CRY2AB2_820. LDGSDREGVATVNTWQESFETTLGLRSGAF--TARGNSNYP-PO-YFERN
X86902_1 NDRGGSNFSIVPAAT-RNEILTATVTSADPEPKTADINWKYFSPGLYSGWIKRQDTAT
CRY2AB2_820. --SGVPLVVRNEDLRPLHYNEIRNI-ASPSGTGPGARAYMVSVHNRKNNIHAVHENGSM
X86902_1 LKSRVPSIIPSNILKYDDY--IRAVSACPKGVSLAYNHDFLTLTYNKLEYDAPTQNI
CRY2AB2_820. IHLAPNDYGTISPIHATQVNNQTRTFISEKFGNOGDSLRPQN-----NTARYTURG
X86902_1 VGFSPDNKSFYRNSHYLSITDDAYVIFALQFSTVSDRFLSDTDPQATDGSIKFTDV
CRY2AB2_820. NGNSYNLRLVSSIGNSTIR---VTINGRVYATVNTVNTTNDGVNDN-GARFSDINIG
X86902_1 LGNEAKYSIRLNTGNTATRYRLIIRFKAPAEALAGIRVRSQNSGNNKLLGCPVEGNSG
CRY2AB2_820. NVVASNSDVLIDNVLNLSGTQFDMLNMLVPTNISPLY
X86902_1 WDIYDTSFTDDLGITTSNTNAFFSIDSDGVNASQOQWYLSKILVKRESSFTQIPLKPY
CRY2AB2_820. pep
TXN5:CBAA_BACTI

Description: P21256 bacillus thuringiensis (subsp. israelensis), pesticidal
crystal protein
Accession/ID: P21256
ID CBAA_BACTI
AC P21256;
STANDARD;
PR: 643 AA.
General comments:=====

SCORES Initl: 147 Initn: 315 Opt: 361 z-score: 384.0 E(): 1.8e-15
>TXN5:CBAA_BACTI (643 aa)
Initn: 315 Initl: 147 Opt: 361 z-score: 384.0 E(): 1.8e-15
Smith-Waterman score: 422; 25.2% identity in 636 aa overlap
(59-636:35-641)
CRY2AB2_820. FSQHKSLDTVQKEWTEWKNHNSLYLDPIVGVASFLKLVGSLVGRKILSELNLIFF
CBAA_BACTI SLDITLSIVNETDPLFYNNYTEPIAPALIAVAPIAQYLATAICKWAAKAAPSKVLSLFF
CRY2AB2_820. SGSTNLMODILRETEKFLNORLNTDTTLARVNABLTGLQANVEEFNRQVDNPLAPNNAV
CBAA_BACTI GSQPATWEKVRTEVELINQKLSQDRVNILNAEYRGLIEVSDVDAIKQ---PGFT--P
CRY2AB2_820. LSITSSVNTWQQLNRLPQFMQGYQLLLPLFAQAANHLSEFIRVDILNADENGISAA
CBAA_BACTI ATAKGYFLNLSGALIQRLPQEPVQYEGVSIALFTQMCTLHLTLKXGILAGSANGFQA
CRY2AB2_820. TLRVYDLKNTDYANKCINTYQAFKGL-NTRLHDMLEFRTYMLFVYVSIWLSF
CBAA_BACTI DVDSFKLNFQKVDYRTLRMXYTEEFGRCKVSLKDLGTLFRNMCNLYVFPFAEAWLSM
CRY2AB2_820. KYQSLVSSGANI--YASGSGPQOQTSFTSDWP-FLYSLFQVNSNYLN----GFSGAR
CBAA_BACTI RYEGTKLENTLSLW-NFVG-ESINNLSNDWIGALYKLMGAPNORLNKNNYSYFSDT
CRY2AB2_820. TARGNSNYPDYFIRNISGVPLVR--NEULRPLHYNARNIASPSGTGPGARAYMVS
CBAA_BACTI TIPPNLAYDGYIIRAIACACPRGVSLAYNHDLIT-ITNIEE-YDFT-----FNIR
CRY2AB2_820. VHNKNNIHAVHENGSMIHLAPNDYGTISPIHATQVNNQTRTFISEKFGNOGDSLRPQN
CBAA_BACTI VGFAPDNTKDFYSKSHVLSLTND--SYVLPALQFAEYSD--RSFLEDTPQATDGSIKFTDV
CRY2AB2_820. EON--NTARYTLRGN-----GNSYNLRLVSSIGN--STIRV-----TINGRVYATVNW

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cry2ab2_820. SGSGPQQTQSFTSQDW-----PFLYSLFQVNSYV-----LNGPFGARL-SNTFPNIVG

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CGCTTGGGCGG      300    310    320    330    340    350
AGGAGATACGGVANGHNSGGGVITLSTGLGFGFVFNFNLTALAFWGNQAVVANGDNRNL
cry2ab2_820..LPGSTTTTHALLAAR-VNYSGGISGGDI---GASPFNQFNCSITELPLLP---FVRSLW

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[illegible]

cry2ab2_820. DSGSDREGVATVNWQTESFETTLGL-RSGAFTARGNSNFFPDYFIRNISGVPLVWRNED

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																													
1990	420	430	440	450	460	470	480	490	500	510	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	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	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410

CITYABZ_820.
LKRPLHNEIKNIASPSGIPGGAKAYMVSVHNKKNNIHAVHENGSMHLAPNDXIGFII
: : : : :
YNHILSYMLINGETFGQKRGYSFAETHSSVDRYNTI--VPDKIVQIPAVKTNDLVGANII
CUBA BACUH

[illegible]

510	520	530	540	550
-----	-----	-----	-----	-----

cry2ab2_820. NSTIRVT-INGRVYVYATN-----VNTT-----TNNGDNGDNGARFSDINICNVVASSNSDV
 560 570 580 590 600
 KGPFGT---GGDLTKUEYERFD---SLRLKLIASMTFAIRKIRVASNISQGMNINIGYQ
 530 540 550 560 570
 CUBA_BACUH

```

CUBA_SALCH      580      590      600      610      620      630
FFIFNLPIKSLKIDELAEFEQVQVDSIYLSISGGGFSLSSNLDWGNFSGVFIILDKLIEF

cry2ab2_820..  610      620      630
PLDINVTLSNGTGQFDLMNIMLVPNTISPLY
|||...|..

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cr2ab2.820.pep
TVNS·GGTA·VLCCT
640 650 660 670 680

Description: Q45733 bacillus thuringiensis (subsp. tolworthi). pesticidal crystal protein cr
Accession/ID: Q45733
=====General comments=====

```

AC      Q45733; . . .
SCORES   Intrl: 148      Intron: 178      Opt: 344      Z-score: 361.1 E( ): 3.3e-14
>TXNS: CSCA, BACTO
Intron: 178, intrl: 148 Opt: 344 Z-score: 361.1 exact(1): 3.3e-14

```

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cry2ab2_820. FOHKSLOTGKTEWKKNNHSLYDPIGVCTVASFLLKKVSLVGRKILSE---LNNLIF
30      40      50      60      70      80
Smtn-waterman score: 344: 25.1% identity in 558 aa overlap
(60-580:75-600)

```

C9CA_BAC10 Y L Q M I D E D Y I D S Y I N F S L S I S G R D A V Q I A L T V V G R I L G A L G V P F F S G Q I V S F Y Q F L E N I L T W

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```

Description: Q45709 bacillus thuringiensis (subsp. entomocidus). pesticide
crystal protein
Accession/ID: Q45709
=====General comments=====
ID C11B_BACTE STANDARD; PRT; 719 AA.
AC Q45709; . . .

SCORES      Init1: 225      Initn: 287      Opt: 336      Z-score: 356.5 E(): 6e-14
>>IAXN3:C11B_BACTE
Initn: 287 Init1: 225 Opt: 336 Z-score: 356.5 expect(): 6e-14
Smith-Waterman score: 353; 21.9% identity in 607 aa overlap
(57-634;70-646)

cry2ab2_820. PPSFOHKS LDTQGEWTEWKKNNHSLYLDPIGVGTWASFLKKVGSVGKRIISLENLNLI
30 40 50 60 70 80
cry2ab2_820. EDYLRMSEHSDIPFVSASTIGTIGIGIACKILGTIGVFPFGAQIASLYS--FILGEL---W
40 50 60 70 80 90

cry2ab2_820. PPSGNTLMQDIURETEKFLNQRNLNTDILARVNAELTIGQANVEEFNRQVDFNPNRNVAV
90 100 110 120 130 140
cry2ab2_820. PKGKSO--WEIFMEHVEEITNOKILTYARNKALSDLRGLGDAVALYSHLESLESVENNRNTR
100 110 120 130 140 150

cry2ab2_820. PLSIT--SSVNTWMOQLFLNLPFCOMOGYQLLLPLPQAQANHLHSFIROVILNADWGVIS
150 160 170 180 190 200
cry2ab2_820. ARS-VKRNQYIALELFWOKLPSFAVGEEVPLPLPYAQANHLHLDRQASTIFGKEWGLS
160 170 180 190 200 210

cry2ab2_820. AATATYRDYKKNRDIYSNYCI---NTYQSAFKGLNTR-LHDMLEFRTYMFNLYNVEYVS
210 220 230 240 250 260
cry2ab2_820. ASQSTLNQROVERSDYSDHCIKWYNTGLNLRGTNAKSWRYNOFRKDMTLMVLDLVA
220 230 240 250 260 270

cry2ab2_820. IWSERKYSLLVSS--AND---YASSEGR-QOTQFTSQDMPLYSLFQVSNVYLVNGFS
270 280 290 300 310
cry2ab2_820. LFPSSYDLNWPNTTSQLEWYDAIGTWNQNFASFTW---YN---NNAPSFSAIE
280 290 300 310 320

cry2ab2_820. GARLSTNFPNIVGLSGTSTHANA---AFNYVGG--SSSDIG-ASPNNQNFNCST
320 330 340 350 360
cry2ab2_820. AAVTFS--PHLLDFLEKVIYISLSRSTQYWNKNGVLESRPFGGANTSTQGSTNT
330 340 350 360 370 380

cry2ab2_820. FLPLLPFPVRSWLDGSDREGVATVNNQTESF-ETTLGLRSGATAGANNYFQYTM
370 380 390 400 410 420
cry2ab2_820. SINVTIQTFSRDVRYRTESLAGNLFLTQPVNGVPRVDFPKSTLPIQDSTLPIGLY--
390 400 410 420 430 440

cry2ab2_820. RNISGVPLVVRNEDLRRPLHNEIRNITASPSGTGPGARINYSVHNRKNMIA--YENGCS
430 440 450 460 470 480 490
cry2ab2_820. ---AGVGTQJQSENELPPTTGQPNFYNSYHRL--SHIGLISASHVKALVYSWYTHRSMD
450 460 470 480 490 500 510 520 530 540 550

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cry2ab2_820. MIH-LAPNDYTGFTISPIHATQVNNQTRFISEKFGNQGLRFEQNNTIARYTLRNGN
CL1B_BACTE RNTIEPNSITQIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RTNTGTGDIRVNIN
500 510 520 530 540 550
cry2ab2_820. S-----YNLYLRVSSIGNSTIRVTINGRVYATNVNTTNNQDNGARSDINIGNVV
550 560 570 580 590 600
CL1B_BACTE PPFARQYRVRIRYASTTDLQFHSINGKAINQGNFSATMNR--GEDLDYKTFR--TIGFTT
560 570 580 590 600
cry2ab2_820. FLPPLLTPFVRSLDSDREGVAIVTNWQTESF--ETTLGLRSGAFTARGNSNYFPDYPFI
610 620 630
CL1B_BACTE PFSFSDVQSTFTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTLFTSTNP
620 630 640 650 660
CL1B_BACTE RGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQIHIERNM
670 680 690 700 710
cry2ab2_820.pep
TXNS:Y08920_1
Description: Y08920 Bacillus thuringiensis B.thuringiensis cryv gene; 159.
10/1996
Accession/ID: Y08920
LOCUS Y08920_1 [BICRV159]
DEFINITION B.thuringiensis cryv gene; . .
=====General comments=====
>TXNS:Y08920_1
initn: 267 initl: 205 opt: 336 z-score: 356.5 E(): 6e-14
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820. PFSQHKSLDVTQKEWTEWKKNHSLYLDPIVGVASFLKKVGLVGRILSELRLNLI
30 40 50 60 70 80
Y08920_1 EPCLKXSEYENVEPFSASTIQTGIGIAGKILGTLPVFPAGQVSLYS--FILGEL---W
40 50 60 70 80 90
cry2ab2_820. PGSGNLMDILRETEKFLNORLNTDILARVNAELTGLQANVEFNROVDNPLFNNAV
90 100 110 120 130 140
Y08920_1 PKGK--NWEIPEWHEVREIINQKISTYARKKALDGLKGLDALAVYHDSLESWGNRNTR
100 110 120 130 140 150
cry2ab2_820. PLISIT--SSVNTMOOLFNLRLPQFMQGYQLLLPLFAQAANLHLSFIRDVINADWGIS
150 160 170 180 190 200
Y08920_1 ARSVVRSQYIALELMFVKLPFSFAVSGEEVLLPIYQAANLHLLLDASIFGKEWGLS
160 170 180 190 200 210
cry2ab2_820. AAILATYRDYLUKNYTRDYSNYCINTYQSAFKGL--NTRLHML---EFRTYMLFNVEYS
210 220 230 240 250 260
Y08920_1 SSEISTFYNRQVERAGDYSDCHVKWYKYSTGLNNLRGTNAESWVRYNQFRDRMTLMLVLDA
220 230 240 250 260 270
cry2ab2_820. IWSLFKYQSLVLSSGANL---YASGSGFQQTQ-SFTSQDWPFLYSLFQVNSVNLNGFS
270 280 290 300 310
```

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Y08920_1 LFPSTDMYPIKTTAQTRVYDAIGTVHPHPSFTSTTW---YN-----NNAPSPSAIE
280 290 300 310 320
cry2ab2_820. GARLSNTFFNIVGLPGSITTHALLA-----ARVNYSGG--ISSGDIGAS--PFNQNFNCST
320 330 340 350 360 370 380
Y08920_1 AAVRN--PHLLDFLEQVTIYSLLSRWSNTQYMNWMMGHKLEFRTIGTGLNISTOGSTNT
330 340 350 360 370 380
cry2ab2_820. FLPPLLTPFVRSLDSDREGVAIVTNWQTESF--ETTLGLRSGAFTARGNSNYFPDYPFI
370 380 390 400 410 420
Y08920_1 SINPVLTPFTSRDVRITESLAGNLFLTQPVNGVPRVDFHMKFVTHPIASDNFYYPGY--
390 400 410 420 430 440
cry2ab2_820. RNISGVFLVVRNEDLRRPLHYNEIRNIASPSGTPGAGAYMVSVHNEKNNIHA--VHENG
430 440 450 460 470 480
Y08920_1 ---AGICTQLQDSENELPPEATGQPNYESYSHRL--SHIGLISASHVKALVYSWTHRSAD
450 460 470 480 490
cry2ab2_820. MIH-LAPNDYTGFTISPIHATQVNNQTRFISEKFGNQGLRFEQNNTIARYTLRNGN
490 500 510 520 530 540
Y08920_1 RTNTEPNSITQIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RTNTGTGDIRVNIN
500 510 520 530 540 550
cry2ab2_820. S-----YNLYLRVSSIGNSTIRVTINGRVYATNVNTTNNQDNGARSDINIGNVV
550 560 570 580 590 600
Y08920_1 PPFARQYRVRIRYASTTDLQFHSINGKAINQGNFSATMNR--GEDLDYKTFR--TIGFTT
560 570 580 590 600
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLNMIMLVPTNISPLY
610 620 630
Y08920_1 PFSFLDVSQSTFTIGAMNFFSSGNEVYIDRIEFVPEVVEYAEYDFEKAQEKVTLFTSTNP
610 620 630 640 650 660
Y08920_1 RGLKTDVKDYHIDQVSNLVESLSEDFYLDKRELFELVYKAKQIHIERNM
670 680 690 700 710
cry2ab2_820.pep
TXNS:CL1A_BACTK
Description: Q45752 bacillus thuringiensis (subsp. kurstaki). pesticidal
crystal protein cry
Accession/ID: Q45752
=====General comments=====
ID CL1A_BACTK STANDARD; PRT; 719 AA.
AC Q45752; Q45750; Q45751; Q45756; P71092; . . .
SCORES Initl: 205 Initn: 267 Opt: 336 z-score: 356.5 E(): 6e-14
>TXNS:CL1A_BACTK
initn: 267 initl: 205 opt: 336 z-score: 356.5 expect(): 6e-14
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820. PFSQHKSLDVTQKEWTEWKKNHSLYLDPIVGTVASFLKKVGLVGRILSELRLNLI
30 40 50 60 70 80
Y08920_1 EPCLKXSEYENVEPFSASTIQTGIGIAGKILGTLPVFPAGQVSLYS--FILGEL---W
40 50 60 70 80 90
```

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CIIA_BACTK BDCINSEYANVFVSASTIQTGIGIAGKILGTLGVPFAGQVSLYS-FILGEL-70 80 90
cry2ab2_820 90 100 110 120 130 140
CIIA_BACTK PKG-NONEIFNADPEINOKISTARNWLDLGLGDALAYHDSLESWGNINR 150 160 170 180 190 200
cry2ab2_820 150 160 170 180 190 200
CIIA_BACTK ARSVKSOXIALELMFVONPSTAVSCGUPYIYAQANHLILLRDASIFGKENGLS 210 220 230 240 250 260
cry2ab2_820 210 220 230 240 250 260
CIIA_BACTK AATLRTYRDYLNKTYRDSNYCINTYOSAKG-NTRJLML-270 280 290 300 310 320
cry2ab2_820 270 280 290 300 310 320
CIIA_BACTK LFPSTYQMPKTKTAQLTREYIDALGTVHPHPSFTITW-330 340 350 360 370 380
cry2ab2_820 330 340 350 360 370 380
CIIA_BACTK GARLSNIFNIVGLPGSTTHALLA-390 400 410 420 430 440
cry2ab2_820 390 400 410 420 430 440
CIIA_BACTK SINFVLPTSDRDYRTESLAGNLFLTQPVNGVRVDFHWKFTVTHIASDNFYFPGY-450 460 470 480 490
cry2ab2_820 450 460 470 480 490
CIIA_BACTK ---AGICTOLQSDSENELPPEATGQPNYESYSHL-500 510 520 530 540 550
cry2ab2_820 500 510 520 530 540 550
CIIA_BACTK RNTIEFNSTIQIPL--VKAFNLSSGAAVVRGPGFTG-GDILR-RINTGTGDIRVIN 560 570 580 590 600
cry2ab2_820 560 570 580 590 600
CIIA_BACTK PPFQRYRIRIYASTDLOQHTSINKAINOGNFSATMNR-GEGLDYKTFR-TVGTFT 610 620 630 640 650
cry2ab2_820 610 620 630 640 650
CIIA_BACTK ASSNSVDPLDINV--TLNSGTQFDLMNLVPTNISPLY 660 670 680 690 700
cry2ab2_820 660 670 680 690 700
CIIA_BACTK PFFFLDQSTFTIIGAWNFSSGNEVYIDRIEFVFEVTEAEYDFEKAQKVALTSTNP 710 720 730 740 750
cry2ab2_820 710 720 730 740 750
CIIA_BACTK RGLKTDKDYHIDQVSNLVSLSDEFYLDQKRELFEIVKYAKQLHIERN 760 770 780 790 800
cry2ab2_820 760 770 780 790 800

cry2ab2_820 pep
TXN5:C8BA_BACUK
Description: Q45705 bacillus thuringiensis (subsp. kumamotoensis). pesticidal
crystal protei
Accession/ID: Q45705
ID C8BA_BACUK
AC Q45705;
General comments: STANDARD; PRT; 1169 AA.
SCORES Initl: 209 Inltn: 251 Opt: 338 z-score: 354.7 E(): 7.5e-14
>TXN5:C8BA_BACUK
Initl: 251 Inltn: 209 Opt: 338 z-score: 354.7 expect(): 7.5e-14
Smith-Waterman score: 338; 21.3% identity in 596 aa overlap
(57-632:76-658)
cry2ab2_820. PFSQHKSLDTQKWEWTKNNHSLYLDPIVGTASFL-LKKVGSLYGKRIILSELNLI
C8BA_BACUK LKMSAGNVSEYVPGSPVEFLSEQDAVKAIDIVGKLLTGLGVPFVGPVIVS--LYTOLLIDIL
cry2ab2_820. PFSGSTNLMDQILFRETQKFLNRLNLTDLARVNAELTGLQANVEEFNQVDNFL-NPNRN
C8BA_BACUK MESKQSQWEIFMEQVEELINOKIAEYARNKALSELGLGNVQVLYLTALAEWKENENG
cry2ab2_820. AVPLSITSSVMQQLFNLRLPOFQMGYQLLLPLFAQANLHLSFIRDVILNADWGI
C8BA_BACUK RLRLVNRVRFELDSSTQYMPFSFRVTFVFFLVVTYMAANLHLLLRDASIFGEWGL
cry2ab2_820. SAATPTVRYDVAADRDYSNYSINWOSA---FKGLNTRLH-DMLEFTYMLNVEYV
C8BA_BACUK SSTITNNTNOMKLRDPSGCVRWYSGDKKSGSAKQWIDINQFRREMTLTVLDVV
cry2ab2_820. SIWSLFYQSLVSSGNNLYVSGSGFQSTSDQMPYLSLFOVNSVYVNLNGFSGARL
C8BA_BACUK ALFNSYDTRTYPLATTAOL---TRSVYTDKAGVYFNIGSWDKRPSFSEIEKAAIRP
cry2ab2_820. SMTFNIVGLPGSTTHALLAR-VNYSGG--SSQDIG-ASFFONKFCSTPAPPITP
C8BA_BACUK PHVFDYITGLTVYTKRSFTSDRYMRVWAGHOISYKHSITSTFTOMSTONLOST-SN
cry2ab2_820. FVRSWLDGSDREGVATVINWQTESFE-TTILGRSNGFTARGNSYFFVYRNSGV
C8BA_BACUK PFTYIDYIKLSGALLDIYVPGYTYTFPGMPETEFFVWNLNNTKTLTKPASKDI
cry2ab2_820. VVRNED--LRRLPHYNEIRNIASPSGTGPGAR-AYMVSVHNRKNNIHAVHENGSMHLAP

Product Characterization Center

[illegible]

cr:y2ab2_820. PFSQHKSLDTQKEWTEWKNHNSLYLDPVTGTVASFLKKKVGSLGKRIISLRNLIF
EDCLKSEYENPFVFSASTIOTGIGACKILGTGVPFAGOVASLYS-FILGEL---W

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cry2ab2_820. 90 100 110 120 130 140
PSSTNMDILRETEKFNQKNTDTLARVNAELTGLQANVEEPNQVDNPLNPNNAV
AAK66742 100 110 120 130 140 150
PAGKQWELTQCHPSEIINQKISTYANKALTDLKLGDALAVYHDSLESWGRNNTIR

cry2ab2_820. 150 160 170 180 190 200
PLSIT-SSVNTMOQELNRLPFOVQKQVQLLLPFAQANLHLSFIRDVILNADWEGIS
AAK66742 160 170 180 190 200 210
ARSVKSQVIALELMFQKNSFAVSGEPFLPIYQAQANLHLLLRDASIFGKEWGLS

cry2ab2_820. 210 220 230 240 250 260
AATLRTYRDYLNKNTDYNSNYCINTQCAFGL-NTRLHML---EPRTYMFNLNVEYVS
AAK66742 220 230 240 250 260 270
SSLSITFYNRQVERAGDISDHCWKVYSTGLNNRGNNAESWVRNQFQDMTLMVLDLIA

cry2ab2_820. 270 280 290 300 310 320
IWSLFYQSLVSSGANL---YASGSGPQQTQ-SFTSQDMFSLYSFQVNSVNLNGFS
AAK66742 280 290 300 310 320 330
LFPSYDTQWPIKITTAAQLTRVYTDAGTVHPHPSFTTWTW---YN---NAPSPSAIE

cry2ab2_820. 330 340 350 360 370 380
GARLSNTFNNVGLPGSTTHALLA-----ARVNSGG--ISSGDIQAS-PFNQNFNGST
AAK66742 330 340 350 360 370 380
AAVRN--PHLLDFLEQVITYLSLSRWSTQYMNMMGGHKL-EFTTIGTLNTSTQSTNT

cry2ab2_820. 390 400 410 420 430 440
FLPPLPTPVRSMWLDGSDREGVATVNMWQTESF-ETTLGLRSGAFTAGNSNVPDYFI
AAK66742 390 400 410 420 430 440
SINPVLPTSDVDVYTESLAGLNELFTHPVNGVRVDFHWKFTVTHIASDNFYFGI--

cry2ab2_820. 450 460 470 480 490 500
RNISGVPVLRNEDLRPLHNEIRNIAASPGTGGARAYMVSVHNRKNIIHA-VHENG
AAK66742 450 460 470 480 490 500
---AGIGTQLODSENELPPEATQPNYESYSHRL--SHIGLISASHVKALVYSWTHRSAD

cry2ab2_820. 510 520 530 540 550 560
MIH-LAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFQEQNTTARTYURNGN
AAK66742 510 520 530 540 550 560
RTWTFEISITQIDP--VKAFNLSSGAAVVRGPGFTG-GDILR--RINTGTGDIRVNIN

cry2ab2_820. 570 580 590 600 610 620
S-----YNLIRVSSIGNSTIRVYATVNTVNTTNDGVNDGNGARFSDINIGNVV
AAK66742 570 580 590 600 610 620
PPFAQRYRIRYASITDLOFHTSINGKAINGNFSATMNR-GEDLDYKTFR--TVGFTT

cry2ab2_820. 630 640 650 660 670 680
ASSNSDVLIDNV---TNSGTQFDLMNIMLVPTNISPLY
AAK66742 630 640 650 660 670 680
PFSLDVOSTFTIGAWNFSSGNEVIDRIEFVFPVEVTEYAEYDFEKAQKVTALFTSTNP

cry2ab2_820. 690 700 710 720 730 740
RGLKTDVYDHYDQVSNLVLESLSDEFYLDKELFEIVKAKOHIERNM
AAK66742 690 700 710 720 730 740

cry2ab2_820.pep
TXN5:Q9F0P8

Description: Q9F0P8 bacillus thuringiensis. cryii. 6/2001
Accession/ID: Q9F0P8
ID Q9F0P8 PRELIMINARY; PRT; 719 AA.
AC Q9F0P8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

====General comments=====

SCORES Init1: 226 Initn: 288 Opt: 334 Z-score: 354.3 E(): 7.9e-14
>TXN5:Q9F0P8
Initn: 288 Init1: 226 Opt: 334 Z-score: 354.3 expect(): 7.9e-14
Smith-Waterman score: 349; 21.7% identity in 608 aa overlap
(57-634:70-646)

cry2ab2_820. 30 40 50 60 70 80
PFSFOHKSLOTVQKEMTEWKNNHSLYLDPIVGTVASFLKKKVGSLGVKRLISLRLNLI
Q9F0P8 40 50 60 70 80 90
EDFLMSEHESIDPFVSASTIQTGTGIGTAGKILGTGVFPAGQIASLYS-FILGEL----W

cry2ab2_820. 90 100 110 120 130 140
PGSNTNMQDILRETEKFNQKNTDTLARVNAELTGLQANVEEPNQVDNPLNPNNAV
Q9F0P8 90 100 110 120 130 140 150
PKGSKQ-WEIFMEHVEBELIDQKISTYARNIALADLKLGDALAVYHDSLESWIKNNAR

cry2ab2_820. 150 160 170 180 190 200
PLSIT-SSVNTMOQELNRLPFOVQKQVQLLLPFAQANLHLSFIRDVILNADWEGIS
Q9F0P8 150 160 170 180 190 200 210
ATSKYCYTAMELFVQKPSFAVSGEVEFLPIYQAQANLHLLLRDASVFGKEWGLS

cry2ab2_820. 210 220 230 240 250 260
AATLRTYRDYLNKNTDYNSNYCINTQCAFGL-NTRLHML---EPRTYMFNLNVEYVS
Q9F0P8 210 220 230 240 250 260 270
NSQISTFNNRQVERAGDISDHCWKVYSTGLNNRGNNAESWVRNQFQDMTLMVLDLIA

cry2ab2_820. 270 280 290 300 310 320
IWSLFYQSLVSSGANL---YASGSGPQQTQ-SFTSQDMFSLYSFQVNSVNLNGFS
Q9F0P8 270 280 290 300 310 320
LFPSYDTLVPIPIKITTAAQLTRVYTDAGTVHPHPSFTTWTW---YN---NAPSPSAIE

cry2ab2_820. 320 330 340 350 360 370 380
GARLSNTFNNVGLPGSTTHALLA-----ARVNSGG--ISSGDIQAS-PFNQNFNGST-
Q9F0P8 320 330 340 350 360 370 380
SAVRN--PHLLDFLEQVITYLSLSRWSTQYMNMMGGHKL-EFTTIGTLNTSTQSTNT

cry2ab2_820. 390 400 410 420 430 440
FLPPLPTPVRSMWLDGSDREGVATVNMWQTESF-ETTLGLRSGAFTAGNSNVPDYFI
Q9F0P8 390 400 410 420 430 440
TSINPVLPTSDVDVYTESLAGLNELFTHPVNGVRVDFHWKFTVTHIASDNFYFGI--

cry2ab2_820. 450 460 470 480 490 500
RNISGVPVLRNEDLRPLHNEIRNIAASPGTGGARAYMVSVHNRKNIIHA-VHENG
Q9F0P8 450 460 470 480 490 500

```
Q9F0P8  ----AGVCTQLQDSENELPETTQGPVYESYSHRL--SHIGLISASHVKALVYSWTHRSA
          450      460      470      480      490
cry2ab2_820. SMIH-LAPNDYTGFTTSPHATQVNNQTRFISEKFGNQDLSLRFQNNITARTYLRGNG
          490      500      510      520      530      540
Q9F0P8  DRNTIEPNSITQIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RNTGTGFDIRVNI
          500      510      520      530      540      550
cry2ab2_820. NS-----YNLRLVSSIGNSTRVINGRVYATNNTVNTINDGNDNGARPSDINIGNV
          550      560      570      580      590
Q9F0P8  NPPFAQRYRVAIRVASTTDLQPHTSINGKAINQGNFSATMNR--GEDLDYKTFR--TVGFT
          560      570      580      590
cry2ab2_820. VASSNSDVPDLINV---TLNSGTQFDLMNMLVPTNISPLY
          600      610      620      630
Q9F0P8  TPFSFSDVQSFTTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKVTLFTSTN
          610      620      630      640      650      660
Q9F0P8  PRGLKTDVKYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQIHIERNM
          670      680      690      700      710
cry2ab2_820.pcp
TXN5:O85796

Description: O85796 bacillus thuringiensis (subsp. kurstaki). insecticidal
protein. 9/2001
Accession/ID: O85796
ID O85796 PRELIMINARY;
AC O85796; . . .

=====General comments=====
PRT: 719 AA.

SCORES  Initl: 205  Initn: 267  Opt: 333  Z-score: 353.3 E(): 9e-14
>TXN5:O85796
Initn: 267 Initl: 205 Opt: 333 Z-score: 353.3 expect(): 9e-14
Smith-Waterman score: 362; 21.6% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820. PFSQHKSLDTVQKEMTKNNHSLYLDPIVGTVASFLKKVGLVGRKILSELNLI
          30      40      50      60      70      80
O85796  EDCLKMSYEVENVEFFVSASTIQTGIGIAGKILGTLPVPFAGQVASLYS-FILGEL---W
          40      50      60      70      80      90

cry2ab2_820. PGSTNLMQDLIRETEKFNQRLNTDTLARVNAELTGLQANVEEFNRQVDNPLNPNNAV
          90      100      110      120      130      140
O85796  PKGK-NQWEIFMEHVEEIIQKISTYARNKALTDLKGSLDALAVYHDSLESWGVRNNR
          100      110      120      130      140      150

cry2ab2_820. PLSIT-SSVNTMQQLFLNLPQFMQGYQLLLPLFAQANLHLSFIRVILNADENGIS
          150      160      170      180      190      200
O85796  ARSVKQSYIALELMFVQKLPSPASGVEFLLPIYAAANLHLLLRDASIFKNGLS
          160      170      180      190      200      210

cry2ab2_820. AATLTARYDLKNVTRDYSNYCINTYQSAFKGL-NTRLHDML---EFTRYMFLNVEVVS
          210      220      230      240      250      260
O85796  SSEISTFYNRQVERAGDYSRHCVKVYSGISGLNLRGNTNAESWVRYNQFRDMLVLDLVA
          210      220      230      240      250      260
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220      230      240      250      260      270
cry2ab2_820. IWSLFKYQSLLYSSGANI---XASGSGPQQTQ-SFTSQDWPFLYSLFQVNSNYVLNGFS
          270      280      290      300      310      320
O85796  LFTSYDTQWPIKTKTAQLTRVYTDALGTGHPHPSTFTTW---YN-----NNAPSFSAIE
          280      290      300      310      320
cry2ab2_820. GARLSNTFFNVLGPGSTTHALLA-----ARVNYSGG--ISSGDIGAS-PFNQNFNCST
          320      330      340      350      360
O85796  AAVRN--PHLLDLEQVITYSLLSRMSNTQYMNWGGHKLEFRTIGTGLNISTQGSTNT
          330      340      350      360      370      380
cry2ab2_820. FLPELLTPFVRSWLDSGSDREGVATVNTQTESF-ETTLGLRSGAFTARGNSNYFPDYFI
          370      380      390      400      410      420
O85796  SINPVTLPFTRSDVRYTESLAGNLNLTQPVNGVRVDFHMKFVTHFIASDNFYYPGY--
          390      400      410      420      430      440
cry2ab2_820. RNISGVLVVRNEDLRRLHYNEIRNIASGTPGAGARAYMVSVHNNKNIHA--VHENG
          430      440      450      460      470      480
O85796  ---AGICTQLQDSENELPEATGPVYESYSHRL--SHIGLISASHVKALVYSWTHRSAD
          450      460      470      480      490
cry2ab2_820. MIH-LAPNDYTGFTTSPHATQVNNQTRFISEKFGNQDLSLRFQNNITARTYLRG--
          490      500      510      520      530      540
O85796  RTNTEPNSITQIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RNTGTGFDIRVNIK
          500      510      520      530      540      550
cry2ab2_820. ---GNSYNLRLVSSIGNSTRVINGRVYATNNTVNTINDGNDNGARPSDINIGNV
          550      560      570      580      590      600
O85796  PPFPAQRYRVAIRVASTTDLQPHTSINGKAINQGNFSATMNR--GEDLDYKTFR--TVGFTT
          560      570      580      590      600
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLMNMLVPTNISPLY
          610      620      630
O85796  PFSFLDVGQSTFTIGAWNFSSGNEVYIDRIEFVPEVVEYEAEDPEKAQEKVTLFTSTNP
          610      620      630      640      650      660
O85796  RGLKTDVKYHIDQVSNLVESLSDFFYLDEKRELFEIVKAKQHLIERNM
          670      680      690      700      710

cry2ab2_820.pcp
TXN5:X62821_1

Description: X62821 Bacillus thuringiensis B.thuringiensis cryV gene for
delta-endotoxin. 5/1
Accession/ID: X62821
=====General comments=====
LOCUS  X62821_1 [BTRVY]
DEFINITION  B.thuringiensis cryV gene for delta-endotoxin. . .
SCORES  Initl: 201  Initn: 263  Opt: 332  Z-score: 352.2 E(): 1e-13
>TXN5:X62821_1
Initn: 263 Initl: 201 Opt: 332 Z-score: 352.2 expect(): 1e-13
Smith-Waterman score: 361; 21.7% identity in 607 aa overlap
(57-634:70-646)
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390      400      410      420      430      440
cry2ab2_820.  IKNISGVLVVRNEDLRRLPHLYNEIRNIASPSGTPGAGRAYMVSVHNNKNNIHA-VHENG
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C11D_BACTU    ---AGIGTQLODSENELPETTGQPNYESYSHRL--SHIGLISASHVKALVSWTHRSA
               450      460      470      480      490

cry2ab2_820.  SMHILAPNDVGTFTSPIHATOVNQHTFTFISEKFGNQGDSLRFQNNNTIARYTLRNGN
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C11D_BACTU    DRTNTNSD-SITQIPLVKAFNLPDGSASVVRGPGFTG-GDIL--QRTNTGTGDIRVNIIN
               500      510      520      530      540      550

cry2ab2_820.  S-----YNLYRVSSIGNSTIRVTINGRVYATNVTNTTNDGVDNGAREFSIDINIGNV
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C11D_BACTU    PFAQRVRLIRVASTINLEFHTSINGKAINQGNFSATMNR-GEGLDYKAFRTVGTTPF
               560      570      580      590      600      610

cry2ab2_820.  610      620      630
               ASSNSDVLQINV-TLNSGTQFDLMNIMLVPTNISPLY
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C11D_BACTU    SFSNAQSTFTTIGAWFSLGNVEYIDRIEFVFEVTEYAEYDLKKAQDEITAMFTSTNLR
               620      630      640      650      660      670

C11D_BACTU    LKTNVTCHIDQVSNLVSLSDEFYLDKRELPEIVKYAKQLNIERNM
               680      690      700      710

cry2ab2_820.pcp
TXNS:U04367_1

Description: U04367 Bacillus thuringiensis Bacillus thuringiensis dakota HD511
CryIII delta-e
Accession/ID: U04367
LOCUS      U04367.1 (BU04367)
DEFINITION Bacillus thuringiensis dakota HD511 CryIII delta-endotoxin gene. . .

SCORES      Initl: 242      Initn: 271      Opt: 331      z-score: 347.5 E(): 1.9e-13
>TXNS:U04367_1
            initn: 271 initl: 242 opt: 331 z-score: 347.5 expect(): 1.9e-13
Smith-Waterman score: 331; 26.5% identity in 215 aa overlap
(57-266:65-277)

cry2ab2_820.  PFSQHKSLDTQKTEWKKNNHSLYLDPIVGTIVASFLKKVGLGKRIELSELNLIF
               30      40      50      60      70      80
U04367_1      MNYQDFLSITEREQPEALASGNTAINTVSVTGATLSALGVPGASFTNFYL-KITGLLW
               90      100      110      120      130      140      150

cry2ab2_820.  PSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGLQANVEEFNRQVDFNLN-PNRNA
               160      170      180      190      200
U04367_1      PHNK-NIWDEFMTEVETLIEQIEQYARNKALAEGLGNLTIIYQQALEDWLNPPDPA
               210      220      230      240      250      260      270

cry2ab2_820.  VPLSITSSVNTMQOLFNLRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
               280      290      300      310      320      330
U04367_1      TITRVDRFRILLALFESYMPFSRVAGYEIPLLTVYQAANLHLLALDSTLYGDKWGFT
               340      350      360      370      380      390      400

cry2ab2_820.  WSLFKYQSLVSSGANLYASGSGPQQTOSTQSDWPFYLSLFQVNSNVYLVNGFSGARLS
               410      420      430      440      450      460      470
U04367_1      VFIIDPRYMSMETSTQLTREVYTDPISLISINPDIGPSFSQMENTAFRTPHLVLDLDEL
               480      490      500      510      520      530      540
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210      220      230      240      250      260
cry2ab2_820.  AATLRTYRDYLNKYTRYDSNYCYINTYQSFKGLNTRLDML----EFRTYMFNLVFEYVS
               : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
U04367_1      QNNIEENYNRQKHHSYSESNHCYKWNYSGLSLNGSTYEQWYNNYFRREMILMULDIAA
               270      280      290      300      310      320      330

cry2ab2_820.  IWSLFYKQSLVSSGANLYASGSGPQQTOSTQSDWPFYLSLFQVNSNVYLVNGFSGARLS
               340      350      360      370      380      390
U04367_1      VFIIDPRYMSMETSTQLTREVYTDPISLISINPDIGPSFSQMENTAFRTPHLVLDLDEL
               400      410      420      430      440      450      460

cry2ab2_820.pcp
TXNS:C7AB_BACUA
Description: Q45707 bacillus thuringiensis (subsp. dakota). pesticidal
crystal protein cry7a
Accession/ID: Q45707
ID      C7AB_BACUA      STANDARD; PRT; 1138 AA.
AC      Q45707; . . .

=====General comments=====
ID      C7AB_BACUA      STANDARD; PRT; 1138 AA.
AC      Q45707; . . .

=====General comments=====

SCORES      Initl: 242      Initn: 271      Opt: 331      z-score: 347.5 E(): 1.9e-13
>TXNS:C7AB_BACUA
            initn: 271 initl: 242 opt: 331 z-score: 347.5 expect(): 1.9e-13
Smith-Waterman score: 331; 26.5% identity in 215 aa overlap
(57-266:65-277)

cry2ab2_820.  PFSQHKSLDTQKTEWKKNNHSLYLDPIVGTIVASFLKKVGLGKRIELSELNLIF
               30      40      50      60      70      80
C7AB_BACUA    MNYQDFLSITEREQPEALASGNTAINTVSVTGATLSALGVPGASFTNFYL-KITGLLW
               90      100      110      120      130      140      150

cry2ab2_820.  PSGSTNLMQDILRETEKFLNQLRNTDTLARVNAELTGLQANVEEFNRQVDFNLN-PNRNA
               160      170      180      190      200
C7AB_BACUA    PHNK-NIWDEFMTEVETLIEQIEQYARNKALAEGLGNLTIIYQQALEDWLNPPDPA
               210      220      230      240      250      260      270

cry2ab2_820.  VPLSITSSVNTMQOLFNLRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
               280      290      300      310      320      330
C7AB_BACUA    TITRVDRFRILLALFESYMPFSRVAGYEIPLLTVYQAANLHLLALDSTLYGDKWGFT
               340      350      360      370      380      390      400

cry2ab2_820.  IWSLFYKQSLVSSGANLYASGSGPQQTOSTQSDWPFYLSLFQVNSNVYLVNGFSGARLS
               410      420      430      440      450      460      470
C7AB_BACUA    VFIIDPRYMSMETSTQLTREVYTDPISLISINPDIGPSFSQMENTAFRTPHLVLDLDEL
               480      490      500      510      520      530      540

cry2ab2_820.pcp
TXNS:C9EA_BACTA
```

Description: 09A01 bacillus thuringiensis (subsp. aizawai). pesticidal crystal protein cry2

Accession ID: Q92NL9

ID C9EA_BACTA

AC Q92NL9; STANDBY; PRT: 1150 AA.

SCORES Initl: 152 Intn: 183 Opt: 326 Z-score: 342.1 E(): 3.8e-13
>TXNS:C9EA_BACTA
Initn: 183 Initl: 152 Opt: 326 Z-score: 342.1 expect(): 3.8e-13
Smith-Waterman score: 326; 22.5% identity in 612 aa overlap
(57-632:76-651)

cry2ab2_820. PFSPQHSKSLDTYQKWTWKNNHSLYLDYVGVASLKKVGSVGVKRLSELRNLI

C9EA_BACTA LQYDGYTGSLINPLNSINPRDVLQGTINIGRNIGFVGFAGQV--TFYFDLQQL

cry2ab2_820. PFSGSTNMQDLIRETEKFLNQLNTDTLARVNAELTGLQANVEENRQNDPLN--PGR

C9EA_BACTA WPTNDNAWEAFMAQIEELIDQISQAVVRNALDLTGLHDYVEVLAADEWEPNGA

cry2ab2_820. AVLSITSSVTVMQOLFNLRLPOFW--QGYQ---LLLPFPAQANLHLSPFIRDLNAD

C9EA_BACTA RANL-VTQRFENLHTAFVTRMPSFGTGPQSGORDAVALTYVQAANLHLLKDAEYGA

cry2ab2_820. EWGISAATRTYRDLKNTYRDYSNICYOSAF---KGNTR-LHDMLERTYMFNLV

C9EA_BACTA RWGLQOQNLVFNQAQERTIYNHCVEIYRNGLEDVRGINTESMINVHRFRREMTLMA

cry2ab2_820. FEYVTSWLSFKYQSLVSSGANLYASGSGFQOTQSFISQDWPFLYS-----LFQVNSNY

C9EA_BACTA MDLVALFFPFYVNRQ-----YFGANPQLTREIYTD--PIVYNPPANQOICRRWGN

cry2ab2_820. VLVGSGARLSNTPFNVLPGSTTHALLAARVNSYGGISSG--DIGASFPNQFNCS

C9EA_BACTA PYNTFS--ELENAFIRPHL--FERLNRLTISRNRKYTAPTNTNSFLDYWSGHTLQSOHANN

cry2ab2_820. FLPPILLTFPVSRLDSDGSDREGVATVIMWOT--ESFETTLGRSGAFTAGSNVFPDYFI

C9EA_BACTA --P---TTVEISYQILTSNRLNTNGARALDSRANFNGLYANLYGVSSLNIFPFGVM

cry2ab2_820. RNTSGVPLVNRDLRR---PLHYNEIRNIASP-----SGTPGGARVAMVSVHNRQIN

C9EA_BACTA SEITNAANTCR-QDLITTEELPLENNF--NULLSHVTLFRNTTGGGFLATLGFVPTV--

cry2ab2_820. IHAHVHENGSMIHLAPNDYTGFTISP-IHATOVNNOTRTFISEKFGNGDSLRFPQNNITA

C9EA_BACTA --WTRDVDFTNITADR--ITQLPWSVASISGGTIVVKGPGFTG-GDILR--RTDGG

cry2ab2_820. RYTLRGNGS-----NLYLRVSSIGNSTIRVIINGRVYVATNNTTNDGVNDNGARF

C9EA_BACTA VGTITANYNAPLTOQYRILRLRYASTTSFVNLFVNNSAAGFTLPSTMAONGSLTYES--F

cry2ab2_820. SDINIGNVASSNSDVPDLINVTLN-SGTQFDLMNIMLPTNISPLY

C9EA_BACTA NLEVTHTIRFSQSDITILRLNIFPSSISQGVYVDKLEIPIPIPTREAEDELEDKAKAVAS

cry2ab2_820. LFTRTDGLQVNTDYQVQAAANLVCLSDQYGHDKMKMLEAVRAAKRLSRERNLQDP

TXNS:CLBE_BACTU

Description: 085805 bacillus thuringiensis. pesticidal crystal protein cryIb

Accession ID: 085805

ID CLBE_BACTU

AC 085805

General comments: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

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Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

Standard: PRT: 1227 AA.

[illegible]

Description: U04368 Bacillus thuringiensis Bacillus thuringiensis
Kumamotoensis H867 CryII
Accession/ID: U04368
LOCUS U04368.1 (1138 aa)
DEFINITION Bacillus thuringiensis Kumamotoensis H867 CryII delta-endotoxin

SCORES Initl: 231 Initn: 260 Opt: 319 Z-score: 334.7 E(): 9.8e-13
>>TXNS:U04368_1
Initn: 260 Initl: 231 Opt: 319 Z-score: 334.7 expect(): 9.8e-13
Smith-Waterman score: 319; 26.0% identity in 215 aa overlap
(57-266:65-277)

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 MNYQDFLSITEREQPEALASGNTAINTVSVTGATLSALGVFGASFIITFYLLKITGLLW
40 50 60 70 80

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 PHDK-NIWDEFTEVEITLIEQKIEQYARNKALAEGLGNNLTICQALDGLANPDPPA
90 100 110 120 130 140 150 160 170 180 190 200 210

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 TITRVIDRFRILDALFESYMPFRVAGYEIPLLTVYAQAANHLHALLRDLSTLYGDKWEFT
160 170 180 190 200 210

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 QNNIEENRQKHISEYNSHCYKWSGLSRLNGSTYEQWYNNFRFRMILMVLIDIAA
220 230 240 250 260 270

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 VFIYDPRMYSMETSTOLTREVYTDPISLISNPGIGSPFSQMENTAIRTPLHVDYLDL
280 290 300 310 320 330

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
U04368_1 VFIYDPRMYSMETSTOLTREVYTDPISLISNPGIGSPFSQMENTAIRTPLHVDYLDL
280 290 300 310 320 330

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
TXNS:C7AB_BACUK
Description: Q45708 Bacillus thuringiensis (subsp. kumamotoensis) . pesticidal
crystal protei
Accession/ID: Q45708
ID C7AB_BACUK
AC Q45708;

SCORES Initl: 231 Initn: 260 Opt: 319 Z-score: 334.7 E(): 9.8e-13
>>TXNS:C7AB_BACUK
Initn: 260 Initl: 231 Opt: 319 Z-score: 334.7 expect(): 9.8e-13
Smith-Waterman score: 319; 26.0% identity in 215 aa overlap
(57-266:65-277)

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
TXNS:C7AB_BACUK
Description: Q45708 Bacillus thuringiensis (subsp. kumamotoensis) . pesticidal
crystal protei
Accession/ID: Q45708
ID C7AB_BACUK
AC Q45708;

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
TXNS:C7AB_BACUK
Description: Q45708 Bacillus thuringiensis (subsp. kumamotoensis) . pesticidal
crystal protei
Accession/ID: Q45708
ID C7AB_BACUK
AC Q45708;

C7AB_BACUK MNYQDFLSITEREQPEALASGNTAINTVSVTGATLSALGVFGASFIITFYLLKITGLLW
40 50 60 70 80

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
C7AB_BACUK PHDK-NIWDEFTEVEITLIEQKIEQYARNKALAEGLGNNLTICQALDGLANPDPPA
100 110 120 130 140 150

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
C7AB_BACUK TITRVIDRFRILDALFESYMPFRVAGYEIPLLTVYAQAANHLHALLRDLSTLYGDKWEFT
160 170 180 190 200 210

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
C7AB_BACUK QNNIEENRQKHISEYNSHCYKWSGLSRLNGSTYEQWYNNFRFRMILMVLIDIAA
220 230 240 250 260 270

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
C7AB_BACUK VFIYDPRMYSMETSTOLTREVYTDPISLISNPGIGSPFSQMENTAIRTPLHVDYLDL
280 290 300 310 320 330

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
TXNS:C7AB_BACUK
Description: Q45708 Bacillus thuringiensis. delta-endotoxin (fragment). 6/2001
Accession/ID: Q45708
ID Q45708;
AC Q45708;
DT 01-MAY-2000 (MEMBLrel). 1.3 Created

SCORES Initl: 146 Initn: 155 Opt: 313 Z-score: 332.9 E(): 1.2e-12
>>TXNS:Q45708
Initn: 257 Initl: 156 Opt: 313 Z-score: 332.9 expect(): 1.2e-12
Smith-Waterman score: 313; 22.1% identity in 580 aa overlap
(57-592:61-597)

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
Q45708 LQTYGDDYTDPLINPNIYSVGKDVIVQGINVGLLSFCGPFSSQWNTVATYLLNSLW
40 50 60 70 80

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
Q45708 PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
90 100 110 120 130 140

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
Q45708 PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
90 100 110 120 130 140

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
Q45708 PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
150 160 170 180 190 200

Cry2ab2_820. PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
Q45708 PFSQHKSLDTVQKWTWKNNHSLYLDPIVGTVASFLFKKVGSLVKILSELNLIF
150 160 170 180 190 200

Final Report

Product Characterization Center

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cry2ab2_820.   WGISAALRTYRDYLKNTIRDSYNCLINTYQSAFGL--NTRLHDMLEFRYYFLNFLNVFYV
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    WGLNQIQIDQFSROOSLTQTYTHCVATYNDGLAELRGITTSWFKYQRYRREMTLITAM
210      220      230      240      250      260

cry2ab2_820.   STWSLFKYQSLLVSSGANLYASGSGPOOT-----SFTSQDWP-----FLYSLFQ
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    DLVALFFYYNL-----ROYPDGINQLIREVYTDPDIADFLEOPTQLCRSWYNINAPR
270      280      290      300      310      320      330

cry2ab2_820.   VNSNYVLNGPFGARGLSNTFPNIVGLP---GSTTHALLAARVNY-----SGGI
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    NHLNFSLVLENSLRPPHLPERLSNLQILVNYQTNGSAWRGSRVRYHYLHSSIIOEKSYGL
330      340      350      360      370      380      390

cry2ab2_820.   SSGDIGASPFENONF-----CSTFLPLPLLTPFVRSMLDSGSDREG-VATVTNNQTESF
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    LSDPVGGANINVQNNDIYOIIISOVSNFASPGVSSY-SVWDNIFYLSSGOVSGISGY-----
390      400      410      420      430      440      450

cry2ab2_820.   ETTGLGRGAFTARGNSYFDYFINIGSVLPVVRNEDRLPHNEIRNIASPSTGP
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    -TOGIPPAVCLOQRNSTDELPSL--NPEGD-IIRNYSHRLS-HITQVRFOATQSGSPS
440      450      460      470      480      490      500

cry2ab2_820.   GARAYMVSVHNKNHIHAVHENGSMHLPANDYTOFTISPHTAQVNNOTRFTISEKFN
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    TVSANLPFCVWTHRVDI--DNT-----ITANOITQLPL--VKAYELSSGATVKGPGFTG
490      500      510      520      530      540      550

cry2ab2_820.   QGDSLRFEPQNNNTARYTLRUGNSYNYLYLRVSSIGNSTRVINGVYATNVTNNTND
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    -GDVIR--RTNTG-----GFGA-----IRVSVTGPLTQYRIRFRVASTIDDFVFTRG
550      560      570      580      590      600      610

cry2ab2_820.   GYNDNGARS DINGVVASNSDVLDINVTLSGTFQDMMIMLVPTNISPLY
||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Q9S603    GTILLNFRTRTMWRQGESYVESYRTVEFTTFFNFTSQDIIRTSIQGLSGNGEYILD
590      600      610      620      630      640      650

cry2ab2_820.pep
TXNS-AF042733 1

```

Description: AF042733 *Bacillus thuringiensis* delta-endotoxin gene, par
Accession/ID: AF042733

LOCUS AF042733_1 [AF042733]

2003
AR042733-1 [AR042733]
DEFINITION *Bacillus thuringiensis* delta-endotoxin gene, partial cds. . . .

```
SCORES      Init1: 156      Initn: 257      Opt: 313      z-score: 332.9 E(): 1.2e-12
>>TXN5:AF042733.1      (645 aa)
```

```

TRAINING: AT 042/33.1
initn: 257 init1: 156 opt: 313 Z-score: 332.9 expect(): 1.2e-12
(645 d

```

Smith-Waterman score: 317; 22.1% identity in 580 aa overlap

[illegible]

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AF082731.1 GTTINR...
Initn: 156 Initn: 156 Opt: 317 Z-score: 332.4 E(1.3e-12)
Initn: 156 Initn: 156 Opt: 317 Z-score: 332.4 expect(1.3e-12)
Smith-Waterman score: 317; 24.5% identity in 216 aa overlap
(57-266:74-287)

cry2ab2_820.pap
TXN5:COAA_BACTF
Description: Q9X597 Bacillus thuringiensis (subsp. finitimus). pesticial
crystal protein cr
Accession/ID: Q9X597
=====
ID COAA_BACTF STANDARD; PRT: 163 aa
AC Q9X597

SCORES Initl: 156 Initn: 156 Opt: 317 Z-score: 332.4 E(1.3e-12)
>>TXN5:COAA_BACTF
Initn: 156 Initl: 156 Opt: 317 Z-score: 332.4 expect(1.3e-12)
Smith-Waterman score: 317; 24.5% identity in 216 aa overlap
(57-266:74-287)

cry2ab2_820. PFSQHKSLDTQKWEKKNHSLYLDPIVGTVASFL-LKKVGSIVGKRLSELNLI
COAA_BACTF LQSYGFENMDNFGSEPFIDASGAINAAGVGTGLGVPFAGALT--TFYQKLGFL
30 40 50 60 70 80 90 100
110 120 130 140 150 160
170 180 190 200 210 220

cry2ab2_820. AVPLSITSSVNTMQQLFLNRLPQFOMQGYQLLLPLFAQANLHLSFIRVDILNADWGI
COAA_BACTF AVRDVLRQWRILDGFFEQOMPFAVGFEVLLVYVYTOAANLHLSLRDAIYGAEWGL
170 180 190 200 210 220

cry2ab2_820. SAATLRTRYDLYKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLE---FRTYMLNVEYV
COAA_BACTF TPTNIDQNHTRLRHSAEYTDHCNVWNTGLKQLENSDAKSWFYQNRFRREMTLSLDVI
230 240 250 260 270 280

cry2ab2_820. SIMSLFKYQSLVSSGANLYASGSGPQQTQSTSDMPFLYSFLQVNSYVNLGFSGARL
COAA_BACTF ALFPAYDKMYPIPTNFQLTREVYTDVIGKIGRNSDHWYSANAFSFLNLESTLIRTPHV
270 280 290 300 310 320 330 340

cry2ab2_820.pap
TXN5:AF122897_1

Description: AF122897 Bacillus thuringiensis subsp. finitimus Bacillus
thuringiensis subsp. f
Accession/ID: AF122897
=====
LOCUS AF122897.1 [AF122897]
DEFINITION Bacillus thuringiensis subsp. finitimus Cry26Aa1 protein (cry26Aa1)

SCORES Initl: 156 Initn: 156 Opt: 317 Z-score: 332.4 E(1.3e-12)
>>TXN5:AF122897_1
Initn: 156 Initl: 156 Opt: 317 Z-score: 332.4 expect(1.3e-12)
Smith-Waterman score: 317; 24.5% identity in 216 aa overlap
(57-266:74-287)

cry2ab2_820. PFSQHKSLDTQKWEKKNHSLYLDPIVGTVASFL-LKKVGSIVGKRLSELNLI
AF122897_1 LQSYGFENMDNFGSEPFIDASGAINAAGVGTGLGVPFAGALT--TFYQKLGFL
30 40 50 60 70 80 90 100
110 120 130 140 150 160
170 180 190 200 210 220

cry2ab2_820. PFSGSTNLMDILRETEKFLNQLNTDTLARVNAELTGLQANVEEFNRQVDFNLPNRN-
AF122897_1 FPNNTKQWEEFMKQVEALIDEKISDAVNAKKAISELQGLVNNITLYTEALEELENKENP
110 120 130 140 150 160
170 180 190 200 210 220

cry2ab2_820. AVPLSITSSVNTMQQLFLNRLPQFOMQGYQLLLPLFAQANLHLSFIRVDILNADWGI
AF122897_1 AVRDVLRQWRILDGFFEQOMPFAVGFEVLLVYVYTOAANLHLSLRDAIYGAEWGL
170 180 190 200 210 220

cry2ab2_820. SAATLRTRYDLYKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLE---FRTYMLNVEYV
AF122897_1 TPTNIDQNHTRLRHSAEYTDHCNVWNTGLKQLENSDAKSWFYQNRFRREMTLSLDVI
230 240 250 260 270 280

cry2ab2_820. SIMSLFKYQSLVSSGANLYASGSGPQQTQSTSDMPFLYSFLQVNSYVNLGFSGARL
AF122897_1 ALFPAYDKMYPIPTNFQLTREVYTDVIGKIGRNSDHWYSANAFSFLNLESTLIRTPHV
270 280 290 300 310 320 330 340

cry2ab2_820.pap
TXN5:Q45740
Description: Q45740 Bacillus thuringiensis. insecticidal crystal protein
(crystal fragment).
Accession/ID: Q45740
=====
ID Q45740 PRELIMINARY; PRT: 81 aa
AC Q45740

SCORES Initl: 205 Initn: 205 Opt: 308 Z-score: 331.8 E(1.1e-12)
>>TXN5:Q45740
Initn: 205 Initl: 205 Opt: 308 Z-score: 331.8 expect(1.1e-12)
Smith-Waterman score: 317; 26.3% identity in 251 aa overlap
(57-297:70-314)

cry2ab2_820. PFSQHKSLDTQKWEKKNHSLYLDPIVGTVASFL-LKKVGSIVGKRLSELNLI
Q45740 EDCLKISEVENVEPFVASTIQTGTSIAGKILGLVGFPAQVASYLS-FFNGEN-----
30 40 50 60 70 80 90
100 110 120 130 140
150 160 170 180 190 200

cry2ab2_820. PFSGSTNLMDILRETEKFLNQLNTDTLARVNAELTGLQANVEEFNRQVDFNLPNRN-
Initn: 205 Initl: 205 Opt: 308 Z-score: 331.8 expect(1.1e-12)
Smith-Waterman score: 317; 26.3% identity in 251 aa overlap
(57-297:70-314)

```
Q45740 PKGK-NONEIFMEHVEEIIINQKISTYARNKALTDLKGGLDALAVHESLESVWGNKXNTR
      100      110      120      130      140      150
cry2ab2_820. PLISITSS-VNTMOQLFLNRLPQFMQGYQLLLFLFAQAANHLSEFIRDVILNADEWGIS
      150      160      170      180      190      200
Q45740 ARSVKSGVIALELMFVKLPSPFVSGEVELLPPIYAQAANHLHLLRLDASIFGKEWGLS
      160      170      180      190      200      210
cry2ab2_820. AATLRTYRDYLNKYNTRYDYSNYCINTYQSAFKGL-NTRLHDMLEFRFTYMFLNVFEYV
      210      220      230      240      250      260
Q45740 SSEISTFYNRQVERAGDYSCHCVKYSTGLNLRGTNAESWVRYNQFRKDMTLMVLDLVA
      220      230      240      250      260      270
cry2ab2_820. IWSLFKYQSLVSSGANL---YASGSGP-QQTQSFTSQDWPPFLYSLFQVNSYVNLGFS
      270      280      290      300      310
Q45740 LPPSDTLVYIKTKTSQLTREVTDAIGTVHPNASEASTTWYNNNAPSESTIESAVRNRP
      280      290      300      310      320      330
cry2ab2_820. GARLNTFPNIVGLPGSTTTHALLAARVNYSGISSGDIASFPNQNCSTFLPPLTP
      320      330      340      350      360      370
Q45740 HLLDLEQVITYISLSEWSNTQYMMNMGHRLERFTIGGMLNTSTQGS
      340      350      360      370      380
cry2ab2_820.pcp
TXN5:C9DA_BACTP
Description: O06014 bacillus thuringiensis (subsp. japonensis). pesticidal
crystal protein c
Accession/ID: O06014
=====General comments=====
ID C9DA_BACTP STANDARD; PRT; 1169 AA.
AC O06014; . . .
SCORES Initl: 156 Initn: 257 Opt: 313 z-score: 328.1 E(): 2.3e-12
>>TXN5:C9DA_BACTP
initn: 257 initl: 156 opt: 313 z-score: 328.1 expect(): 2.3e-12
Smith-Waterman score: 317; 22.1% identity in 580 aa overlap
(57-592:76-612)
cry2ab2_820. PFSFQHKSLDTPQKEMTEWKKNNHSLYLDPTVGTVASFLKKYGLVGRKILSELRLNLF
      30      40      50      60      70      80
C9DA_BACTP LQTYGSDYTDPLNPLNLSVSGKDVIOGINIVGRLLSFFGFPSSQW-VTVYVILLNSLW
      50      60      70      80      90      100
cry2ab2_820. PGSTNLMQDLIRETEKFLNRLTDLARVNAELTGLQANVEEFNRQVDNPLN-PRNRA
      90      100      110      120      130      140
C9DA_BACTP PDSENSVMDAFMERVEELIDQKISEAVKGRALDDLTGLQVNYLYVEALDEWLNRNGAR
      110      120      130      140      150      160
cry2ab2_820. VPLSITSSVNTMOQLFLNRLPQFM---QGYQLLLFLFAQAANHLSEFIRDVILNADE
      150      160      170      180      190      200
C9DA_BACTP ASL-VSQRFNLDLSFTQFMPSFGSGSQNYATILLFVYAQAANHLHLLRLDADYIGAR
      170      180      190      200      210      220
cry2ab2_820. 210 220 230 240 250 260
```

```
cry2ab2_820. WGISAAATLRTYRDYLNKYNTRYDYSNYCINTYQSAFKGL-NTRLHDMLEFRFTYMFLNVFEYV
      230      240      250      260      270      280
C9DA_BACTP WGLNQTDIDFHSRQCSLTQYTHNCVTAINOGLAELGTTAESWFKYQYRREMTLTAM
      230      240      250      260      270      280
cry2ab2_820. SIMSLFKYQSLVSSGANLYASGSGPQQTQ-----SFTSQDWMP-----FLYSLFQ
      270      280      290      300
C9DA_BACTP DLVALFFYNNL-----RQYPDGNTPOLTREVTDFIAFDPLEQPTTQLCRSWINPAPR
      290      300      310      320      330
cry2ab2_820. VNSNYVLNGSFSGARLNTFPNIVGLP---GSTTTHALLAARVNY-----SGGI
      310      320      330      340      350
C9DA_BACTP NHLNFSYLENSLIRPFLPERLSNLQILVNQYNTNGSAMRGRVRYHYLHSSIIQEKSYGL
      340      350      360      370      380      390
cry2ab2_820. SSGDIGASFPNQNFN-----CSTFLPPLLTPFVRSMLDSDREG-VATVTNQTESF
      360      370      380      390      400
C9DA_BACTP LSDPVGANINQVNDLIYQIIISQVSNFASPVGSSY-SVMDTFYLSGQVSGISGY-----
      400      410      420      430      440      450
cry2ab2_820. ETTGLRSGAFTARGNSVFPDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPG
      410      420      430      440      450      460
C9DA_BACTP -TQGGIPAVCLQQRNSTDELPSL---NPEGD--IIRNYSHRLS-HITQYRFQATQSSSPS
      460      470      480      490      500
cry2ab2_820. GARYMVSVNRRKNNIHVAHENGSMIHLAPNDYGTFTSPIHATQVNNQTRTFISEKFGN
      470      480      490      500      510      520
C9DA_BACTP TVSANLPTCVWTRHDVDL--DNT----ITANQITQLPL--VKAYELSSGATVVKGPGFTG
      510      520      530      540      550
cry2ab2_820. QGDSLRFQEQNNTTARTYTLRGNNGSNVLYLRVSSIGNSTIRVTINGRVYVATNTVNTTND
      530      540      550      560      570      580
C9DA_BACTP -GDVIR--RINTG-----GFGA-----IRVSVTGLTQRYAIRFRVASTIDDFVTRG
      560      570      580      590      600
cry2ab2_820. GVNDRGARFSDINIGNVWASSNSDVPLDINVLNSGTQFDLMNIMLVPTNISPLY
      590      600      610      620      630
C9DA_BACTP GTTINNFRTRTMNGQESRYESYRTVEFTTTFNFTQSODIIRTSIOGLSGNGEVYLDRI
      610      620      630      640      650      660
cry2ab2_820.pcp
TXN5:C8AA_BACUK
Description: Q45704 bacillus thuringiensis (subsp. kumamotoensis). pesticidal
crystal protei
Accession/ID: Q45704
=====General comments=====
ID C8AA_BACUK STANDARD; PRT; 1157 AA.
AC Q45704; . . .
SCORES Initl: 154 Initn: 181 Opt: 302 z-score: 316.5 E(): 1e-11
>>TXN5:C8AA_BACUK
initn: 181 initl: 154 opt: 302 z-score: 316.5 expect(): 1e-11
Smith-Waterman score: 302; 25.0% identity in 228 aa overlap
(57-279:75-301)
```


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©01
cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFLKKVGSVLGKRLSELNLIF
C8AA_BACUK YLXKWSGGENPFLFGNPFETFISSSTIQTGIGVGRILGALGVFPFASQIAS-FYSFIVGQLW
cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFLKKVGSVLGKRLSELNLIF
C8AA_BACUK YLXKWSGGENPFLFGNPFETFISSSTIQTGIGVGRILGALGVFPFASQIAS-FYSFIVGQLW
cry2ab2_820. PLSITSSVNTMOQL-FLNRLPQFQMGYQVLLPLPFAQANLHLSFTRDVLNADWGIS
C8AA_BACUK TRSVVSNQFIADLNFVSIIPFAVSGHEVILLVAVYAQAVNLHLLLRDASIFGEWGT
cry2ab2_820. AATLRTYRDYLNKNTDYNSYNTYQ---SAFKGLNTR-LHDMLEFRTYMLNVEFVVS
C8AA_BACUK PGEISRYNRQVOLTAEYSYDYCVKWKYKGLDKLGTTSKSWLNHYQFREMTEILVLDIVA
cry2ab2_820. IWSLFKYQSLVSSGANLYASGGPQQTQSFTSQDMWFLYSLFQVNSNYLVNFGSGARLS
C8AA_BACUK LFPNDYTHMYPIETTAQLTDRVDYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPP
cry2ab2_820. pep
TXNS:U04364_1
Description: U04364 Bacillus thuringiensis Bacillus thuringiensis
Accession/ID: U04364
LOCUS U04364.1 (BTU04364)
DEFINITION Bacillus thuringiensis P850C(a) CryIII
=====General comments=====

SCORES Initl: 154 Inltn: 181 Opt: 302 Z-score: 316.5 E(): 1e-11
>TXNS:U04364_1
Initltn: 181 Inltn: 154 Opt: 302 Z-score: 316.5 expect(): 1e-11
Smith-Waterman score: 302; 25.0% identity in 228 aa overlap
(57-278:75-301)

cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFLKKVGSVLGKRLSELNLIF
U04364_1 YLXKWSGGENPFLFGNPFETFISSSTIQTGIGVGRILGALGVFPFASQIAS-FYSFIVGQLW
cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFLKKVGSVLGKRLSELNLIF
cry2ab2_820. PSGSTNLMQDILRETEKFLNQLNLTDLARVNAELTGLQANVEEFNRQVDFNPNRNV
U04364_1 PFSKVDIWEIMEVIEELVDQKIEKYVKDKALAEKGLNLDVYQOQSLDLEWENRNDAR
cry2ab2_820. PLSITSSVNTMOQL-FLNRLPQFQMGYQVLLPLPFAQANLHLSFTRDVLNADWGIS
cry2ab2_820. pep
TXNS:U04364_1

U04364_1 TRSVVSNQFIADLNFVSIIPFAVSGHEVILLVAVYAQAVNLHLLLRDASIFGEWGT
cry2ab2_820. AATLRTYRDYLNKNTDYNSYNTYQ---SAFKGLNTR-LHDMLEFRTYMLNVEFVVS
U04364_1 PGEISRYNRQVOLTAEYSYDYCVKWKYKGLDKLGTTSKSWLNHYQFREMTEILVLDIVA
cry2ab2_820. IWSLFKYQSLVSSGANLYASGGPQQTQSFTSQDMWFLYSLFQVNSNYLVNFGSGARLS
U04364_1 LFPNDYTHMYPIETTAQLTDRVDYTDPIAFNIVTSTGFCNPWSTHSGILFYEVENNVRPP
cry2ab2_820. pep
TXNS:AF093107_1
Description: AF093107 Bacillus thuringiensis Bacillus thuringiensis
Accession/ID: AF093107
LOCUS AF093107.1 (AF093107)
DEFINITION Bacillus thuringiensis delta-endotoxin gene, partial cds.
=====General comments=====

SCORES Initl: 148 Inltn: 148 Opt: 294 Z-score: 312.8 E(): 1.6e-11
>TXNS:AF093107_1
Initltn: 148 Inltn: 148 Opt: 294 Z-score: 312.8 expect(): 1.6e-11
Smith-Waterman score: 304; 25.2% identity in 420 aa overlap
(57-428:67-463)

cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFL-LKKVGSVLGKRLSELNLIF
AF093107_1 LQVAGTSGSLNPLNLSNTRDVLQGTGINVGRVLGFLGVPPAGQLV--TFYTFLLNQL
cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFL-LKKVGSVLGKRLSELNLIF
AF093107_1 WFTNNNAWFAFQOIEELFQVSEFQVVRVLAALGTGHDYNEVLAALAEWLERPNGA
cry2ab2_820. PFSQKSLDVTQKENTWKKNNHSLYLDPIVGTVASFL-LKKVGSVLGKRLSELNLIF
cry2ab2_820. AVPLSITSSVNTMOQLFLNQLNLTDLARVNAELTGLQANVEEFNRQVDFNPNRNV
AF093107_1 RANLAFQRFEN-LHQLFVSPQSFSGGSGSERDAALITVYAQAVNLHLLLRDASIFGEWGT
cry2ab2_820. EMCISATLRTYRDYLNKNTDYNSYNTYQSAF--KGLNTR-LHDMLEFRTYMLNVEFVVS
AF093107_1 RGLMQGQINLYFNAQODRTQIYTHNCHVATTYNRGLENLRTNLSWYNVDFNPNRNV
cry2ab2_820. FRYVSIWLSLFKYQSLVSSGANLYASGGPQQTQSFTSQ---DMWFLYSLFQVNSNYLVNFGSGARLS
AF093107_1 MDLVA--LFFYNYL-----ROYNGANPOLTREIYTDVFNPNPANGLCREWENRNV

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[illegible]

Description: Q9S597 bacillus thuringiensis (subsp. higo). pesticial crystal protein cry27aa
Accession/ID: Q9S597
=====General comments=====

ID	CRAA	BACUH	STANDARD;	PRT;	826 AA.
AC	Q9S597				

```

SCORES      Init1: 184      Initn: 184      Opt: 295      z-score: 311.8 E(): 1.9e-11
>>TXNS:CRAA_BACU
Init1: 184      Initn: 184      Opt: 295      z-score: 311.8 expect(): 1.9e-11
Smith-Waterman score: 295;      23.5% identity in 353 aa overlap
(15-355:49-386)

```

```
cry2ab2_g20.      10      20      30      40
MQMDSVNSGRITTCADYN-VAHDFSFQHKSLDTQKENT
                  :::-::|::|::|::|::|::|
CRAA_BACOU        NCHMSGVPYRPHLPDQMYLNAHYKDWSLCKNKNPVGLTTPSEFWTLNGTVAAII
                20      30      40      50      60      70
```

```
cry2ab2_820. EWKKNHSLYLDPIVGTVAFLKKVKGLSKRIILSELNLIFFSGSTNLMDILLRETEK
      : |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
IVSVIAGILTAPV--SVTAGLITVLGA--GAAALLAGITPUIWPAATDNTFNKITDATEVE
```

[illegible]

```
cry2ab_820. NRPQFMQGQLLLPLFAQAANHLSFIRDVILNADEWGIS----AATLRTYRDYLK
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
CRAA RACIH FAMPALSMGPEVFVGIGAYAQAAHHILLFEGIAVDADOWNIARDPMHGAAGDLHYKEFL-
```

220 230 240 250 260 270
cry2ab2_820. NYTRDYSNYCINTYQSAFKGINLRHDMLEFRYTMFLANFVEYVSIWSLF--KYQSLILVSS

Description: A07236 Bacillus thuringiensis B.thuringiensis (strain PGS1245)
gene. 10/1993
Accession/ID: A07236

LOCUS A07236_1 [A07236]

DEFINITION B.thuringiensis (strain PGS1245) gene.

=====
General comments=====

SCORES Init1: 223 Initn: 223 Opt: 297 z-score: 311.3 E(): 2e-11
>>TXN5:A07236_1 (1138 aa)
Initn: 223 Init1: 223 Opt: 297 z-score: 311.3 expect(): 2e-11
Smith-Waterman score: 297; 25.0% identity in 212 aa overlap
(57-263:65-274)

cry2ab2_820. PFSFOHKS LDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKKGVSGVKRIILSELRLNIF
30 40 50 60 70 80
A07236_1 MNYQDFLSITEREQPEALASGNTAINTVSVTGATLSALGVPGASFTINFYL-KIAGLLW
40 50 60 70 80 90

cry2ab2_820. PSGSTNLMQDURETEKFLNORLNTDLARVNAELTGLQANVEEFNRQVDNFINRNRA-
90 100 110 120 130 140
A07236_1 PENG-KIMDEFTEVEALIDQKIEEYVRNKAIAEGLDGLSALDQYKALADWLQKDDPE
100 110 120 130 140 150

cry2ab2_820. VPLSITSSVNTWQQLFNRLPQFMQGYQLLLPLFAQAAHLHSFIRDVILNADWEGIS
150 160 170 180 190 200
A07236_1 AILSVATEFRIIDSLFEFSPKVTGYEIPLLTYAQAANLHALLRSTLYGKWF
160 170 180 190 200 210

cry2ab2_820. AATLRTYRDLYKNYTRDYSNYCINTYQSAFKGLNTRLDML---EFTYMFNLFYFYS
210 220 230 240 250 260
A07236_1 QNNIEENRQKRISEYSDHCTKWYNSGLSLRNGSTYEQWYNNFRPREMILMALDVA
220 230 240 250 260 270

cry2ab2_820. IWSLFKYQSLVSSCANLYASGSGPQQTQSFTSQDWPFLLYSLFQVNSNYLNGFSGARLS
270 280 290 300 310 320
A07236_1 VFFPHDPRYSMETSTQLTREVTDVPSLSISNPDIGPSFSQMENTAIRTPHLVDYLDL
280 290 300 310 320 330

cry2ab2_820.pep
TXN5:A07234_1

Description: A07234 Bacillus thuringiensis B.thuringiensis (strain PGS1208)
gene. 10/1993
Accession/ID: A07234

LOCUS A07234_1 [A07234]

DEFINITION B.thuringiensis (strain PGS1208) gene.

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General comments=====

SCORES Init1: 97 Initn: 97 Opt: 282 z-score: 299.9 E(): 8.5e-11
>>TXN5:A07234_1 (651 aa)
Initn: 97 Init1: 97 Opt: 282 z-score: 299.9 expect(): 8.5e-11
Smith-Waterman score: 283; 22.9% identity in 349 aa overlap
(40-360:43-381)

cry2ab2_820. NSGRITTCIDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLD----PIVGTVASF
10 20 30 40 50 60

A07234_1 KVTNSELPTNHQYPLADNPSTLEELNYKEFLRMTADNSTEVLDSSTVKDAVGTGISV
20 30 40 50 60 70

cry2ab2_820. LLKKVGLSVKGRILSELR-----NLIFPSGNTNMQDILRETEKFLNQRNLNTDLARV
70 80 90 100 110
A07234_1 VQOILG-VVGVFPAGALTIFYQSFLNAINWPSDA-DPWKAFMAQVEVLIDKKIEYAKSKA
80 90 100 110 120 130

cry2ab2_820. NAEITGLQANVEEFNRQVDNFINRNNAVPLSTISSVNTWQQLF-----LNRLPQFM
120 130 140 150 160 170
A07234_1 LAELQGLQNNFEDYVNALDSW--KKAEPVNLRRSRQDRIRLFSQAESHFRNMPSPFAV
140 150 160 170 180

cry2ab2_820. QGYQLLLPLFAQAAHLHSFIRDVILNADWEGISAATLRTYRDYKKNYTRDYSNYCINT
180 190 200 210 220 230
A07234_1 SKFEVLFLPTYAQAANTHLLIKDAQVFGWEGYSSDEIAEFYQRLKLTQOYTDHCNVW
190 200 210 220 230 240

cry2ab2_820. YQSAFKGLNTRLDML---EFTYMFNLFYFYSIMSLFKYQSLVSSGANLYASG---
240 250 260 270 280
A07234_1 YNVGLNSLRGSTYDAWVKFNPRPREMTLTVLDLIVLFPFYDVR--LYSKGVKTELTRDIF
250 260 270 280 290 300

cry2ab2_820. SQPQTQSFTSQDWPFYELFO-VNSNYLVNGFSGARLSNTF-PNIVGLPOSTTTHALLA
290 300 310 320 330 340
A07234_1 TDPFTLNAQYEGTPTFSSSIENSIRKPHLFYLRGIEFHTRLRP---GYSGKDSFNYWSG
310 320 330 340 350 360

cry2ab2_820. ARVNYSGISGSDIGASPNQNFNCSTFLPPLTPFVRSMWSDSGSDREGVATVNNQTES
350 360 370 380 390 400
A07234_1 NYVETRESIGSNUTITSPFYGDKSTIEPQKLSFDGQKVYRTIANTDIAAFPDKGIYGVGT
370 380 390 400 410 420

cry2ab2_820.pep
TXN5:C3BA_BACTO

Description: Pl7969 bacillus thuringiensis (subsp. tolworthi). pesticial

crystal protein cr

Accession/ID: Pl7969

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General comments=====

ID C3BA_BACTO STANDARD; PRT; 659 AA.

AC Pl7969; . . .

SCORES Init1: 97 Initn: 97 Opt: 282 z-score: 299.8 E(): 8.7e-11
>>TXN5:C3BA_BACTO (659 aa)
Initn: 97 Init1: 97 Opt: 282 z-score: 299.8 expect(): 8.7e-11
Smith-Waterman score: 283; 22.9% identity in 349 aa overlap
(40-360:51-389)

cry2ab2_820. NSGRITTCIDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLD----PIVGTVASF
10 20 30 40 50 60
C3BA_BACTO KVTNSELPTNHQYPLADNPSTLEELNYKEFLRMTADNSTEVLDSSTVKDAVGTGISV
30 40 50 60 70 80

Monsanto Company
Final Report
Product Characterization Center

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001 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 8650 8660 8670 8680 8690 8700 8710 8720 8730 8740 8750 8760 8770 8780 8790 8800 8810 8820 8830 8840 8850 8860 8870 8880 8890 8900 8910 8920 8930 8940 8950 8960 8970 8980 8990 9000 9010 9020 9030 9040 9050 9060 9070 9080 9090 9100 9110 9120 9130 9140 9150 9160 9170 9180 9190 9200 9210 9220 9230 9240 9250 9260 9270 9280 9290 9300 9310 9320 9330 9340 9350 9360 9370 9380 9390 9400 9410 9420 9430 9440 9450 9460 9470 9480 9490 9500 9510 9520 9530 9540 9550 9560 9570 9580 9590 9600 9610 9620 9630 9640 9650 9660 9670 9680 9690 9700 9710 9720 9730 9740 9750 9760 9770 9780 9790 9800 9810 9820 9830 9840 9850 9860 9870 9880 9890 9900 9910 9920 9930 9940 9950 9960 9970 9980 9990 10000 10010 10020 10030 10040 10050 10060 10070 10080 10090 10100 10110 10120 10130 10140 10150 10160 10170 10180 10190 10200 10210 10220 10230 10240 10250 10260 10270 10280 10290 10300 10310 10320 10330 10340 10350 10360 10370 10380 10390 10400 10410 10420 10430 10440 10450 10460 10470 10480 10490 10500 10510 10520 10530 10540 10550 10560 10570 10580 10590 10600 10610 10620 10630 10640 10650 10660 10670 10680 10690 10700 10710 10720 10730 10740 10750 10760 10770 10780 10790 10800 10810 10820 10830 10840 10850 10860 10870 10880 10890 10900 10910 10920 10930 10940 10950 10960 10970 10980 10990 11000 11010 11020 11030 11040 11050 11060 11070 11080 11090 11100 11110 11120 11130 11140 11150 11160 11170 11180 11190 11200 11210 11220 11230 11240 11250 11260 11270 11280 11290 11300 11310 11320 11330 11340 11350 11360 11370 11380 11390 11400 11410 11420 11430 11440 11450 11460 11470 11480 11490 11500 11510 11520 11530 11540 11550 11560 11570 11580 11590 11600 11610 11620 11630 11640 11650 11660 11670 11680 11690 11700 11710 11720 11730 11740 11750 11760 11770 11780 11790 11800 11810 11820 11830 11840 11850 11860 11870 11880 11890 11900 11910 11920 11930 11940 11950 11960 11970 11980 11990 12000 12010 12020 12030 12040 12050 12060 12070 12080 12090 12100 12110 12120 12130 12140 12150 12160 12170 12180 12190 12200 12210 12220 12230 12240 12250 12260 12270 12280 12290 12300 12310 12320 12330 12340 12350 12360 12370 12380 12390 12400 12410 12420 12430 12440 12450 12460 12470 12480 12490 12500 12510 12520 12530 12540 12550 12560 12570 12580 12590 12600 12610 12620 12630 12640 12650 12660 12670 12680 12690 12700 12710 12720 12730 12740 12750 12760 12770 12780 12790 12800 12810 12820 12830 12840 12850 12860 12870 12880 12890 12900 12910 12920 12930 12940 12950 12960 12970 12980 12990 13000 13010 13020 13030 13040 13050 13060 13070 13080 13090 13100 13110 13120 13130 13140 13150 13160 13170 13180 13190 13200 13210 13220 13230 13240 13250 13260 13270 13280 13290 13300 13310 13320 13330 13340 13350 13360 13370 13380 13390 13400 13410 13420 13430 13440 13450 13460 13470 13480 13490 13500 13510 13520 13530 13540 13550 13560 13570 13580 13590 13600 13610 13620 13630 13640 13650 13660 13670 13680 13690 13700 13710 13720 13730 13740 13750 13760 13770 13780 13790 13800 13810 13820 13830 13840 13850 13860 13870 13880 13890 13900 13910 13920 13930 13940 13950 13960 13970 13980 13990 14000 14010 14020 14030 14040 14050 14060 14070 14080 14090 14100 14110 14120 14130 14140 14150 14160 14170 14180 14190 14200 14210 14220 14230 14240 14250 14260 14270 14280 14290 14300 14310 14320 14330 14340 14350 14360 14370 14380 14390 14400 14410 14420 14430 14440 14450 14460 14470 14480 14490 14500 14510 14520 14530 14540 14550 14560 14570 14580 14590 14600 14610 14620 14630 14640 14650 14660 14670 14680 14690 14700 14710 14720 14730 14740 14750 14760 14770 14780 14790 14800 14810 14820 14830 14840 14850 14860 14870 14880 14890 14900 14910 14920 14930 14940 14950 14960 14970 14980 14990 15000 15010 15020 15030 15040 15050 15060 15070 15080 15090 15100 15110 15120 15130 15140 15150 15160 15170 15180 15190 15200 15210 15220 15230 15240 15250 15260 15270 15280 15290 15300 15310 15320 15330 15340 15350 15360 15370 15380 15390 15400 15410 15420 15430 15440 15450 15460 15470 15480 15490 15500 15510 15520 15530 15540 15550 15560 15570 15580 15590 15600 15610 15620 15630 15640 15650 15660 15670 15680 15690 15700 15710 15720 15730 15740 15750 15760 15770 15780 15790 15800 15810 15820 15830 15840 15850 15860 15870 15880 15890 15900 15910 15920 15930 15940 15950 15960 15970 15980 15990 16000 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150 16160 16170 16180 16190 16200 16210 16220 16230 16240 16250 16260 16270 16280 16290 16300 16310 16320 16330 16340 16350 16360 16370 16380 16390 16400 16410 16420 16430 16440 16450 16460 16470 16480 16490 16500 16510 16520 16530 16540 16550 16560 16570 16580 16590 16600 16610 16620 16630 16640 16650 16660 16670 16680 16690 16700 16710 16720 16730 16740 16750 16760 16770 16780 16790 16800 16810 16820 16830 16840 16850 16860 16870 16880 16890 16900 16910 16920 16930 16940 16950 16960 16970 16980 16990 17000 17010 17020 17030 17040 17050 17060 17070 17080 17090 17100 17110 17120 17130 17140 17150 17160 17170 17180 17190 17200 17210 17220 17230 17240 17250 17260 17270 17280 17290 17300 17310 17320 17330 17340 17350 17360 17370 17380 17390 17400 17410 17420 17430 17440 17450 17460 17470 17480 17490 17500 17510 17520 17530 17540 17550 17560 17570 17580 17590 17600 17610 17620 17630 17640 17650 17660 17670 17680 17690 17700 17710 17720 17730 17740 17750 17760 17770 17780 17790 17800 17810 17820 17830 17840 17850 17860 17870 17880 17890 17900 17910 17920 17930 17940 17950 17960 17970 17980 17990 18000 18010 18020 18030 18040 18050 18060 18070 18080 18090 18100 18110 18120 18130 18140 18150 18160 18170 18180 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 18290 18300 18310 18320 18330 18340 18350 18360 18370 18380 18390 18400 18410 18420 18430 18440 18450 18460 18470 18480 18490 18500 18510 18520 18530 18540 18550 18560 18570 18580 18590 18600 18610 18620 18630 18640 18650 18660 18670 18680 18690 18700 18710 18720 18730 18740 18750 18760 18770 18780 18790 18800 18810 18820 18830 18840 18850 18860 18870 18880 18890 18900 18910 18920 18930 18940 18950 18960 18970 18980 18990 19000 19010 19020 19030 19040 19050 19060 19070 19080 19090 19100 19110 19120 19130 19140 19150 19160 19170 19180 19190 19200 19210 19220 19230 19240 19250 19260 19270 19280 19290 19300 19310 19320 19330 19340 19350 19360 19370 19380 19390 19400 19410 19420 19430 19440 19450 19460 19470 19480 19490 19500 19510 19520 19530 19540 19550 19560 19570 19580 19590 19600 19610 19620 19630 19640 19650 19660 19670 19680 19690 19700 19710 19720 19730 19740 19750 19760 19770 19780 19790 19800 19810 19820 19830 19840 19850 19860 19870 19880 19890 19900 19910 19920 19930 19940 19950 19960 19970 19980 19990 20000 20010 20020 20030 20040 20050 20060 20070 20080 20090 20100 20110 20120 20130 20140 20150 20160 20170 20180 20190 20200 20210 20220 20230 20240 20250 20260 20270 20280 20290 20300 20310 20320 20330 20340 20350 20360 20370 20380 20390 20400 20410 20420 20430 20440 20450 20460 20470 20480 20490 20500 20510 20520 20530 20540 20550 20560 20570 20580 20590 20600 20610 20620 20630 20640 20650 20660 20670 20680 20690 20700 20710 20720 20730 20740 20750 20760 20770 20780 20790 20800 20810 20820 20830 20840 20850 20860 20870 20880 20890 20900 20910 20920 20930 20940 20950 20960 20970 20980 20990 21000 21010 21020 21030 21040 21050 21060 21070 21080 21090 21100 21110 21120 21130 21140 21150 21160 21170 21180 21190 21200 21210 21220 21230 21240 21250 21260 21270 21280 21290 21300 21310 21320 21330 21340 21350 21360 21370 21380 21390 21400 21410 21420 21430 21440 21450 21460 21470 21480 21490 21500 21510 21520 21530 21540 21550 21560 21570 21580 21590 21600 21610 21620 21630 21640 21650 21660 21670 21680 21690 21700 21710 21720 21730 21740 21750 21760 21770 21780 21790 21800 21810 21820 21830 21840 21850 21860 21870 21880 21890 21900 21910 21920 21930 21940 21950 21960 21970 21980 21990 22000 22010 22020 22030 22040 22050 22060 22070 22080 22090 22100 22110 22120 22130 22140 22150 22160 22170 22180 22190 22200 22210 22220 22230 22240 22250 22260 22270

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MSL No. 20307

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CRY2AB2_820. NYCINTYQSFAKGL-NTRLHMDLBFRTY---MFLNVFFYVSIWELF---KYQ-SLLVSSGG
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
COAA_BACTJ NYCVEVYTKGLNALGSAIDMLDFNSFRDMDTLAVLDLVAIFPNVFPVRYPLSTKLSLS
240 250 260 270 280 290

CRY2AB2_820. ANLVSGSGPQQTOSTSODMFFLYSLFQVNSNYVLNGFSG-AELSNTPFNVLGPGSTT
280 290 300 310 320 330
COAA_BACTJ RKLIVDPVGRDTSFSG--DW-----INTGRILANFLDERVDSPLSVKVMGDMT
300 310 320 330

CRY2AB2_820. --THALLAAARVNYSG--GISSGDIGA-----SPFNQFNCFSTFLPPLTFFVRSW
340 350 360 370 380
COAA_BACTJ IVTGAIDSYRPTSPGDRIGVMYGNINAFYHTGRTDVMVFRQTGD-TAYEDP--STFIENI
350 360 370 380 390

CRY2AB2_820. L--DSGSDREGVATVNMQTESFETTLGLRSGA-TARGNSNYFPDFIRNISGVPLVVR
390 400 410 420 430
COAA_BACTJ LVDDIYKILDLRAAAVSTIQG-AMDTTFGVSSSFFDGRNQLYQSN--KPYPSPLFITIT
400 410 420 430 450

CRY2AB2_820. -----NEDLRRLPHVNEIRNIASPTGCGARAYMVSVHNRKNIHIAVHENGSMIH
440 450 460 470 480
COAA_BACTJ FPGESSEGWANDYSHL-LCDVKKILODSSNICEGRSSLLS-HAWTHA--SLDRNNITIL-
460 470 480 490 500 510

CRY2AB2_820. LAPNDYTGFTTSPIHATOVNMOTRTFISEKFGNOGDSLRFQNNNTARYTLRNGNSYNL
490 500 510 520 530 540
COAA_BACTJ --PDEIT--QIPAVTAYELRGN--SVVAGPSGTGCDLVKMSYHVSFWFKYVGSCLKNYRV
520 530 540 550 560

CRY2AB2_820. YLRVSSIGNSTIRVTINGRVYATNVNTITNDNDGVNDGARFSDINTGNVYASSNSDPL
550 560 570 580 590 600
COAA_BACTJ RIRVASHGNCQFLMKRWPSTGVAPQWARHNVOGTFSNMYEAFKYLDFITITPEENNFF
570 580 590 600 610 620

CRY2AB2_820. DINVTLASGQFDLMNIMLVPNISPLY
610 620 630
COAA_BACTJ AFTIDLESQGDGLFDIKIEFIPVSGSAFEGYKQNIETKQAVNDLFIN
630 640 650 660 670

CRY2AB2_820.pap
TXN5:C1GB_BACTJ

Description: Q9za26 bacillus thuringiensis (subsp. wuhanensis). pesticidal
crystal protein c
Accession/ID: Q9ZA26
=====General comments=====
ID C1GB_BACTJ STANDARD; PRT; 1169 AA.
AC Q9ZA26; . . .

SCORES Init1: 191 Initn: 191 Opt: 285 Z-score: 298.3 E(): 1e-10
>>TXN5:C1GB_BACTJ
Init1: 191 Init1: 191 Opt: 285 Z-score: 298.3 expected(): 1e-10
Smith-Waterman score: 301; 22.4% identity in 577 aa overlap

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01-634:58-598)

cry2ab2_820. 30 40 50 60 70 80 90 100 110
C1GB_BACTZ FSGEVAETHLPLFSLLENFLPSSPAFLGLDPLWINGIFNEDOWSAFLRQVLELINQRIIT
cry2ab2_820. 128 138 148 158 168 178 188 198 208
C1GB_BACTZ TDILARVNAELTCLQNVVEFNQVFNGLN-PNRARVNISITSSVNMTOOLFNLRLPOFQ
C1GB_BACTZ EFARGQAIQRIYVGFGRSDEVTALAKNEMEDNDPASKENVRVFRITDDALLTGVELMA
cry2ab2_820. 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
C1GB_BACTZ MOGVQVLLPLPFAQANLHLSFIRDVILNDEWGISATLIVYEDYLNKTRKSNYCIN
C1GB_BACTZ IPGFELATISVVAQSANLHLALLADAVFGERGELTQININDLYSRUKNIRIDYNUHR
cry2ab2_820. 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
C1GB_BACTZ TYOSAFKGNLRLHDMLEFRYMFNVFVYVSWLSFKYQSLNSSANL-S-VASGS-
C1GB_BACTZ FYNIGLGNLNVIRPEYVRFQRELTISVLDLVALFPNYDIRTYPIPTPSLTRELYTDLT
cry2ab2_820. 290 300 310 320 330 340 350 360 370 380 390 400
C1GB_BACTZ GPQQTQSFTSQW---PFLYSLFQVNSNYVNG-FSGARLSNTEPNFIVGLP-GSTTIBAL
C1GB_BACTZ SPQAQAGYTLQDLVRLPRLMDPL--NRLIYTGEGYRIR-----HWAGHEVSSRTGWM
cry2ab2_820. 340 350 360 370 380 390 400
C1GB_BACTZ LAARVNSGGISGSDIGASPNQNFNCFTPLPLTPVRSMWDSG--SDREGVATVNM
C1GB_BACTZ TNIRFLYGTAAAT---AEP-TRFITPSIF--PGLNLPYRT-USAFIRDEFGANIIIRY
cry2ab2_820. 400 410 420 430 440 450 460 470 480 490 500
C1GB_BACTZ QTESFETITGL---RSGA--FTAGNSNYFPDYFIRNISGVPLVVRNDRPLHYNEIR
C1GB_BACTZ RT-SLVEGVGFQPNNGEQLYRVRGTLDSLQDLPLEGSS--LITEYSHRLCHVRFQSLR
cry2ab2_820. 460 470 480 490 500
C1GB_BACTZ NIAPSGTGGARAYMS-VHNRKNNIHAVHENG-SMIHL--AFNDYTGTISPITHATQV
C1GB_BACTZ N-APPLDY---ARVPMFSWTHRSATPTNTIDPDVITQIPLKAFNLHSGATVVRGFGTG
cry2ab2_820. 510 520 530 540 550 560 570 580 590 600 610 620
C1GB_BACTZ NNGRTTFISKFGNQGSRLFEQNTTARYTLRGNNSYNLIRVSSGINSIRVTINGER
C1GB_BACTZ GDILARTNA---GNFGQ-MEV---NITAPLSOR-----YVRIRYASTANLOFHISINGER
cry2ab2_820. 570 580 590 600 610 620
C1GB_BACTZ VYTATVNTITNDGVNDGARFSDINIGNVASSNSDVPLDINV-TLNSGTGTOFLMMIM
C1GB_BACTZ AINQANFPATMNS-GENLOSGRVAGFTTPTFTSDALSTFTIGAFSPSSNNEVYIDGIE
cry2ab2_820. 630
C1GB_BACTZ LVPTNISPLY

C1GB_BACTZ FVPAEVTFATESDQRAQAVNALFTSSNQIGLXTDVINVIDQVSNLVECLSDDEFCLDE
cry2ab2_820. pep
TXNS:X13233_1
Description: X13233 Bacillus thuringiensis B. thuringiensis CryIc1 gene for
entomocidal delta
Accession/ID: X13233
=====General comments=====

LOCUS X13233.1 [BTCRYIC1]
DEFINITION B. thuringiensis CryIc1 gene for entomocidal delta-endotoxin;
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SCORES Initl: 128 Initn: 168 Opt: 284 z-score: 297.4 E(): 1.2e-10
>TXNS:X13233_1
Initn: 168 Initl: 128 Opt: 284 z-score: 297.4 expect(): 1.2e-10
Smith-Waterman score: 290; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. 30 40 50 60 70 80
X13233_1 IPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLEF--VPGAGEVFLGLVDIIWGIF
cry2ab2_820. 90 100 110 120 130 140
X13233_1 SMLMODLRETEKFNQNLNDTLARVNAELTGL---QANVEEFNQVDNLFNENRA
X13233_1 GPSSNDALVQIQLINQRIEAFARQAIKRLGLESLNLYQIYAESFREWEADTNP---A
cry2ab2_820. 150 160 170 180 190 200
X13233_1 VPEISLSSATMQSFLNELPQFQMOGVQVLLPLPFAQANLHLSFIRDVILNDEWGIS
cry2ab2_820. 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
X13233_1 DEEMRQFNDMNSALTTAIPKAVQNVQVPLLSVVVQAANLHLSVLRDVSVFGQWGF
cry2ab2_820. 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
X13233_1 RATLRTVNLVNYTRDQSNVNYQSAK-GLNRLHDM---EFFRYMFLNVFEY
X13233_1 AATINSRYNDLTALIGNYTDHAFNAGLERVWCPDS--DWIRYMQPRRELTAVLDI
cry2ab2_820. 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
X13233_1 VSLPNYDSRTYPIRTVSOL-----TREAYTN--VLEN-FDGSFAGSGQIEGSI
cry2ab2_820. 320 330 340 350 360 370 380 390 400
X13233_1 LSNTFFNIVGLPGSTTTHALLAARVNSGGISGSDIGASPNQNFNCSTFLPPL---

cry2ab2_820. 380 390 400 410 420 430 440 450 460 470 480 490 500
X13233_1 RS---PHLMDILNSITITD-AHRGEYVW--SGHQIMASPVG--FSQREFTTHVATDEN
cry2ab2_820. 380 390 400 410 420 430 440 450 460 470 480 490 500
X13233_1 TPVFR--SWLDSGSDREGVATV--TNWQTESFETITGLRSGAFTARGNSNYFQVFPEN
cry2ab2_820. 350 360 370 380 390 400
X13233_1 AAPQORVAQLGGQVYRTLSLTLYRRPFNIGINNQLSVLDGTFEYAGTSSNLPFSAYVAK

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cry2ab2_820. AATLRTRDYLVKNYTRDYSNVCINTYOSAFK---GLNTRLHDMEL---EFTYMYFLNVFEY
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CIAE_BACTL VATINSYNDLIRLIGTYTDVAVRYMYNTGLERVMGPDGR--DWRYYNQFRRELTITVDI
190 200 210 220 230 240

cry2ab2_820. VSIMSLFKYQSLVSSGANL---YASGSGPQQTOSTSQWPELYSLFQVNSYLVJNGF
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
CIAE_BACTL VSLFPNYSKTYPIRYVSQLTREYITNPVLENFDGSGFGSAQRTEYQSIKRSFPHLMILMSI
250 260 270 280 290 300

cry2ab2_820. SGARLSNTFFNIVGLPGSTTTHALLAARVNSYGGISS---GDIGASPPNQNFNGSTFLP
320 330 340 350 360 370
CIAE_BACTL T-----LYTDAHGYYVWSGHOIMASVPVGSFPEFTPLPYGTMGNAAPORI-----VA
310 320 330 340 350

cry2ab2_820. PLITPFVRSMLDGSOREGVAIVTWQTESFETTLGLASGAFTARGNSYFPDYFIRNIS
380 390 400 410 420 430
CIAE_BACTL TVDSLEIDFPODNNVPFPGFGRSHRLSHVSMFRSGFSNVSVI-IRAMPFVSIHRSRAEFNN
410 420 430 440 450 460

cry2ab2_820. LAPNDYTGFTISPI-HATOVNNOTRTFISEKFGNCGDSLRFEONNITARTYLGRN-----
490 500 510 520 530 540
CIAE_BACTL IIPS--SQITQIPLTKSTNLSSGTSVVGKPGFTG-GDILRTSPQGIS--TLRVNITAPL
470 480 490 500 510

cry2ab2_820. GNSYNLRYVSSIGNSTIRVTINGRVYATNVNNTTNDGVNDGARFSDINGNVASS
550 560 570 580 590 600
CIAE_BACTL SQRYVRIRVASTNIQFHTSIDGRPINQGNFATMSSGQNLQSGS-FRTVGTFTTFPNFS
520 530 540 550 560 570

cry2ab2_820. NSDVPELDINV-TLNSGTQDLMNIMLPTNISPLY
610 620 630
CIAE_BACTL NGSSVFTLSAHVNSGNEVYIDRIEFPAVTFEAYDLERAQAEVNAALFTSPNIQLKT
580 590 600 610 620 630

cry2ab2_820. DVYTDHIDQVSNLVECLSDFECLDEKSEKVKHAKLSDERNLLQDPNFRGINQPPDR
640 650 660 670 680 690

cry2ab2_820.pep
TXNS:M65252_1

Description: M65252 Bacillus thuringiensis Bacillus thuringiensis alesti delta
Accession/ID: M65252
=====General comments=====
LOCUS M65252_1 [BACEN1AB]
DEFINITION Bacillus thuringiensis alesti delta endotoxin gene, complete cds.

SCORES Initl: 120 Initn: 160 Opt: 283 z-score: 296.1 E(): 1.4e-10
>TXNS:M65252_1 (1181 aa)

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cry2ab_820. 610 620 630
NSDVPIDINV-TLNSGTQFDLMNIMLVPTNISPLY
||: : : : :||: : : : :||: : : : :

```

M65252_1
640 DVTYHIDQVSNLVECLSD EFCJLDEKRELSEKVKHAKELSDERNLLQDPNFRGINRQDPDR
640 650 660 670 680 690

cry2ab2_820.pep
TXN5:M84650.1

Description: M84650 synthetic construct Synthetic Bacillus thuringiensis tenebrionis crystal
Accession/ID: M84650

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=====General comments=====
LOCUS      M84650.1 [SYNCRY3ATX]
DEFINITION Synthetic Bacillus thuringiensis tenebrionis crystal toxin (Cr
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SCORES Init1: 114      Initn: 158      Opt: 277      Z-score: 295.2 E(): 1.5e-10
>TXN5.W84560.1
Initn: 158 Init1: 114 Opt: 277 Z-score: 295.2 expect(): 1.5e-10
Initn-Waterman score: 277; 27.4% identity in 219 aa overlap
(160-266:24-239)

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cyabz_020 PQHSLDTQKEWTENKNNHSYLDPIVGTVASFLKKVCSLVGRILS---ERNULIF
MTADNNTALDSSSTTKDVIOKGISVGSDGLGVGFPFGGVALSVFYINFLATW

30 40 50 60 70 80 90 100

M65601

C#42852_820. PS-EDTAFMEQVBDLMKADYARNKALAEQLQJNNVDYVSALSSWKNQPNVSSR
 M84650_1 PS-EDTAFMEQVBDLMKADYARNKALAEQLQJNNVDYVSALSSWKNQPNVSSR

cry2ab2_820. VPI5 --TSSVNTDQ--LNRLPOMGCVOLL180 180 190 200
 M84650_1 NPHSQCRIRPFSQAESHKFNPSFATSGTVECLTYYQAANTHFLFLDKAQIYGEW
 120 130 140 150 160 170

[illegible]

260 270 280 290 300 310
EYVSIWLSFKYQSLVSSGANLYASGSGPQQTOSTGQMPFLYLFQVNSVYLVSSSS
: : : : :
DLIAFPYDVLRYPKVKETLRDVLDPDVGNNRGVSTTGNIEHFKQALFDYL
240 250 260 270 280 290

cry2ab2_820.pep
TXNS:C3AA_EACTT
Description: P07130 bacillus thuringiensis (subsp. tenebrionis), bacillus thuringiensis (subsp. tenebrionis), bacillus thuringiensis (subsp. tenebrionis)

Description: P07130 bacillus thuringiensis (subsp. tenebrionis), bacillus thuringiensis (subs
Accession/ID: P07130

Description: P07130 bacillus thuringiensis (subsp. tenebrionis), bacillus thuringiensis (subs
Accession/ID: P07130

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=====General comments=====
ID C3AA_BACTT STANDARD; PRT; 644 AA.
AC P07130; P21255; .

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 294.6 E(): 1.7e-10
>>TXNS:C3AA_BACTT (644 aa)
Initn: 158 initl: 114 opt: 277 z-score: 294.6 expect(): 1.7e-10
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:39-286)

cry2ab2_820. NSVLSGRITICDAYNVAADPFQHKSLDTQKWTWKNNHSLYLDP-----IV--
10 20 30 40 50
C3AA_BACTT HDTIKTENNEVPTNHVQYPLAETNPFTLEDLNKYEFRLMTADNTEALDSSITTKDVIQK
10 20 30 40 50
60 70 80 90 100 110
cry2ab2_820. G-TVASFLLKKVGLVGRKILS---ELRNLIFFSGSTNLMODILRETEKFLNRLNTDTL
10 20 30 40 50 60 70 80 90 100 110
C3AA_BACTT GISVGDLLGVGFPFGGALVSFYTNFTIWPFS--EDPWKAFMEQVEALMDQKIADYAK
70 80 90 100 110 120 130
60 70 80 90 100 110
cry2ab2_820. ARVNAELTGLQANVEEFNRQVDNFI--NPNRNAVPLS---ITSSVNTMQOLFNLRFQFQM
120 130 140 150 160 170
C3AA_BACTT NKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLELFSQAESHFNRSMPSFAI
130 140 150 160 170 180
60 70 80 90 100 110 120 130 140 150 160 170 180
cry2ab2_820. QYQOLLPLFPAQAANHLSTFIRDVILNADWGISAAFL--RTYRDYLNKNTDYNSYCNIN
180 190 200 210 220
C3AA_BACTT SGYEVLFTTYAQAAANTHLFLKDAQIYGEWGYEKEDIAEFYKQRLK-LTQEYTDHCVK
190 200 210 220 230 240
60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220
cry2ab2_820. TYQSAFKGL-NTRLHDMLEFRY---MFLNVEFYVSIWLFKYQSLLVSSGANLYASGSG
230 240 250 260 270 280
C3AA_BACTT WYNVGLDKLRGSSVESWVNFNRYREMTLVLDLIALFLYDVRLYPKEVKTETLRDVL
250 260 270 280 290 300
60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280
cry2ab2_820. PQQTQSFTSQDWPFYLSLFQVNSNYVLNGFSGARLSNTFPNIVGLFGSTTTTHALLAARVN
290 300 310 320 330 340
C3AA_BACTT DPIVGNNLRGYGTTFTSNIENIRKPHLFDYLHRIQPHTRFQPGYGYGNDSPNYWSGNYVS
310 320 330 340 350 360
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
cry2ab2_820.pep
TXNS:Q9S6N9

Description: Q9S6N9 bacillus thuringiensis. cry3aa protein. 6/2001
Accession/ID: Q9S6N9
=====General comments=====
ID Q9S6N9 PRELIMINARY; PRT; 652 AA.
AC Q9S6N9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 294.5 E(): 1.7e-10
>>TXNS:Q9S6N9 (652 aa)
Initn: 158 initl: 114 opt: 277 z-score: 294.5 expect(): 1.7e-10
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:47-294)
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=====General comments=====
ID C3AA_BACTT STANDARD; PRT; 644 AA.
AC P07130; P21255; .

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 294.5 E(): 1.7e-10
>>TXNS:M22472_1 (652 aa)
Initn: 158 initl: 114 opt: 277 z-score: 294.5 expect(): 1.7e-10
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:47-294)

cry2ab2_820. NSVLSGRITICDAYNVAADPFQHKSLDTQKWTWKNNHSLYLDP-----IV--
10 20 30 40 50
M22472_1 HDTIKTENNEVPTNHVQYPLAETNPFTLEDLNKYEFRLMTADNTEALDSSITTKDVIQK
20 30 40 50 60 70
60 70 80 90 100 110
cry2ab2_820. G-TVASFLLKKVGLVGRKILS---ELRNLIFFSGSTNLMODILRETEKFLNRLNTDTL
10 20 30 40 50 60 70 80 90 100 110
M22472_1 GISVGDLLGVGFPFGGALVSFYTNFTIWPFS--EDPWKAFMEQVEALMDQKIADYAK
20 30 40 50 60 70 80 90 100 110 120 130
60 70 80 90 100 110
cry2ab2_820. ARVNAELTGLQANVEEFNRQVDNFI--NPNRNAVPLS---ITSSVNTMQOLFNLRFQFQM
120 130 140 150 160 170
Q9S6N9 NKALAELOGLQNNVEDYVSALSSWQKNPVSSRNPHSQGRIRLELFSQAESHFNRSMPSFAI
140 150 160 170 180 190
60 70 80 90 100 110 120 130 140 150 160 170 180 190
cry2ab2_820. QYQOLLPLFPAQAANHLSTFIRDVILNADWGISAAFL--RTYRDYLNKNTDYNSYCNIN
180 190 200 210 220
Q9S6N9 SGYEVLFTTYAQAAANTHLFLKDAQIYGEWGYEKEDIAEFYKQRLK-LTQEYTDHCVK
200 210 220 230 240 250
60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250
cry2ab2_820. TYQSAFKGL-NTRLHDMLEFRY---MFLNVEFYVSIWLFKYQSLLVSSGANLYASGSG
230 240 250 260 270 280
Q9S6N9 WYNVGLDKLRGSSVESWVNFNRYREMTLVLDLIALFLYDVRLYPKEVKTETLRDVL
260 270 280 290 300 310
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
cry2ab2_820. PQQTQSFTSQDWPFYLSLFQVNSNYVLNGFSGARLSNTFPNIVGLFGSTTTTHALLAARVN
290 300 310 320 330 340
Q9S6N9 DPIVGNNLRGYGTTFTSNIENIRKPHLFDYLHRIQPHTRFQPGYGYGNDSPNYWSGNYVS
320 330 340 350 360 370
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
cry2ab2_820.pep
TXNS:M22472_1

Description: M22472 Bacillus thuringiensis B.thuringiensis cryC gene encoding
delta-endotoxin
Accession/ID: M22472
=====General comments=====
LOCUS M22472_1 [BACCRYC]
DEFINITION B.thuringiensis cryC gene encoding delta-endotoxin, 5' end; . . .

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 294.5 E(): 1.7e-10
>>TXNS:M22472_1 (652 aa)
Initn: 158 initl: 114 opt: 277 z-score: 294.5 expect(): 1.7e-10
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:47-294)
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M22472_1
GISTVQDLLEWGFPEGGALVSFTYFNLTIMPS--EDPWAKRMEQVEALMPOOKIADYAK
80 98 100 110 120 130
120 130 150 160 170 180 190 200 210 220
cy2ab2_820_ ANNAEELGLGKAAEFENRQNDLE-NPNRNAVPLS--ITSSVNTWQOLFNLRLPQOFOM
M22472_1 NKAAAEISGLQNNVEDYVSLSSWQNEPUSSRNPHUSQGRIRLEFSQAESHFNSPSFAT
140 150 160 170 180 190
180 190 200 210 220
cy2ab2_820_ QGYQLLELPLFAQANLKLSPIRDITADLWGISANTL-ETYRDYLNKNTRDYSNYCIN
M22472_1 SGYEVFLTTYAAQANTHLLLSAAQIYSEWQYKEIDAEVNSQK-LTQEYTDHCVK
200 210 220 230 240 250
230 240 250 260 270 280 290 300 310 320 330 340 350 360 370
cy2ab2_820_ TYQSAFAGKL-NTRLHDMLEFTY---MFLNPEFVSIVSHKPYQSLLVSGGALNLSGSG
M22472_1 WYNYGLDKLRGSSYESFVNFNRYRENTLTLDLALPLFLDYDLRYLVEYEVKLTETRLVLA
260 270 280 290 300 310
290 300 310 320 330 340 350 360 370
cy2ab2_820_ PQQTQSFTSQDWPFLYSLFQVNSVNLGFSGARLNTFNPVQSGSTTHDAAPV
M22472_1 DPIGVNNLRGCHYCTTFESIENIYRKPHLDYLRHQFTRTPQDPQYGGNDSTFNGSVNS
320 330 340 350 360 370
cy2ab2_820_ pep
TXNS:AF363025_1

Description: AF363025 Bacillus thuringiensis subsp. entomocidus Bacillus
thuringiensis subsp.
Accession/ID: AF363025
=====General comments=====
LOCUS AF363025.1 [AF363025]
DEFINITION Bacillus thuringiensis subsp. entomocidus delta-endotoxin Crv1

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cyy2ab2_820. SAATLRTYRDLKKNYTRYSNVCI---NTYQSAFKGLNT-RLHDMLEFRYMLNVLNVEFY
AF363025_1 TSQEIQRYYERQVERTRDYSDYCVWEYNTGINSRGTTNAAASWRYNQFRDLTLGLGVLDV
210 220 230 240 250 260

cyy2ab2_820. STWSLFKYQSLLVSSGANL---YASGSGPQQTQFTSQDPPFLYSLFQVNSNYVLNGFS
AF363025_1 ALFFSYDTRYPINTSAQLTRREVTDIGAATGV-NWASMMNMYNNPNSAIEAAAIKSP
270 280 290 300 310 320

cyy2ab2_820. GARLSNTFFNIVGLPGSTTTTHALLAARVNSYSGISSGDIGASPFNQFNQNCSTFLPLLLTP
AF363025_1 HLLDFLEQLTIIPASSRSMNTEHTMYRGTHTIOSRPIGGGLNTSTHGATNTSINPVTILRF
330 340 350 360 370 380

cyy2ab2_820.pgp
TXNS:AAK51084

Description: Aak51084 bacillus thuringiensis (subsp. entomocidus).
delta-endotoxin cryIb2. 6
Accession/ID: 000000
=====General comments=====
XO AAK51084 PRELIMINARY; PRI: 1228 AA.
AC AAK51084; . . .

SCORES Initi: 206 Initn: 233 Opt: 281 Z-score: 293.7 E(): 1.9e-10
>XFN:AAK51084
init0: 233 init1: 306 opt: 281 Z-score: 293.7 expect(): 1.9e-10
Smith-Waterman score: 285; 25.9% identity in 251 aa overlap
(56-297/56-303)

cyy2ab2_820. DPFQVHPSLDTVQRNTEPKNNHSLDLPFIVGTVASFLFKKYGSLVGRKILSELRLNI
300 310 320 330 340 350 360 370 380
AAK51084 EGMWIDPFVSASTWGTGINTAGRLGVGVFPAGQLASFY---SPLVGE-----L
50 60 70 80

cyy2ab2_820. PPSGSTWLMQDITETKPLQKQNTLTLNNSLTGLQANVEEFNRQVDNPLNPNNA
90 100 110 120 130 140
AAK51084 WPRGR-DQWEIFLEVEDINQOQVWAKATALARKQLGSSFPRAQOQSLDMLNRRDA
150 160 170 180 190 200

cyy2ab2_820. VPLSITSSVNTMOQL-FLNRLPQFQMGQQLLLLEFQANLHSTFISVILNADWGI
210 220 230 240 250 260
AAK51084 RTRSVLHTQVIALELDFLNMLPFAINQVPELWYTAQANLHLLLELDRFLPSEFGL
150 160 170 180 190 200

cyy2ab2_820. SAATLRTYRDLKKNYTRYSNVCI---NTYQSAFKGLNT-RLHDMLEFRYMLNVLNVEFY
AF363025_1 TSQEIQRYYERQVERTRDYSDYCVWEYNTGINSRGTTNAAASWRYNQFRDLTLGLGVLDV
210 220 230 240 250 260

cyy2ab2_820. STWSLFKYQSLLVSSGANL---YASGSGPQQTQFTSQDPPFLYSLFQVNSNYVLNGFS
AF363025_1 ALFFSYDTRYPINTSAQLTRREVTDIGAATGV-NWASMMNMYNNPNSAIEAAAIKSP
270 280 290 300 310 320

cyy2ab2_820.pgp
TXNS:AAK51084

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320      330      340      350      360      370
cry2ab2_820. GARLSTFNIUGLPGSTTHALLAARVNYSGISGGDIGASPNFQNCSTFLPLLTLP
AAK51084  HLDLFLEQUTIFASRRSNRMTWYRGHTIQSPIGGSLNTSTHGATNSINPVTIURF
330      340      350      360      370      380
cry2ab2_820.pcp
TXN5:U31527_1

Description: U31527 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (cryII) ge
Accession/ID: U31527
=====General comments=====
LOCUS      U31527_1 (BTU31527)
DEFINITION Bacillus thuringiensis delta-endotoxin (cryII) gene, complete cds;

SCORES      Initl: 153      Initn: 209      Opt: 280      Z-score: 293.0 E(): 2.1e-10
>>TXN5:U31527_1
Initn: 209 Initl: 153 Opt: 280 Z-score: 293.0 expect(): 2.1e-10
Smith-Waterman score: 325; 21.6% identity in 607 aa overlap
(54-634:32-598)

cry2ab2_820. AHDPFQHKSLDTVQKEWTWKNNHSLYLDLP--IVGTVASFLKKVGLVGRILSEL
30      40      50      60      70      80
U31527_1      EINNQOCIPYNCLSPNEEVLDDGERILDPLEVSMSLLQFLNNF--VPGGGFISGL
10      20      30      40      50

cry2ab2_820. RNLFFSGSTNLMQDILRETEKFLNQRINTDTLARVNAELTGL----QANVEEFNRQVDN
90      100      110      120      130
U31527_1      FDKINGALRPSDWELFLAQIEQLDQRIEATVRAKAIAELEGLGRSFQLYVEAFKEWEET
60      70      80      90      100      110

cry2ab2_820. FLNPNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRDVIL
140      150      160      170      180      190
U31527_1      ---PNTAARSRTVERFRIIDAQIEANIPFRIPGFVEPLLSVYAAQANHLHALLRDSVI
120      130      140      150      160      170

cry2ab2_820. NADWEMGISAATLRTYRDYLNKYTRDYSNICYOSAFK--GLNTRLHDM--EFTYMF
200      210      220      230      240      250
U31527_1      FGERWGLTTINVDIYNRQVKRIHEYSDHCVDYTKLELERLGFTSRAQWKIYNQFRRLT
180      190      200      210      220      230

cry2ab2_820. LNVFEVTSIWSLFRKYQLSVSSGANLYASGSPQQTOSTFSQDW---PLYSLFQVNSNY
260      270      280      290      300      310
U31527_1      LTVLDIVAVFPNYD-----GKLY-----PIQTKSELTRREIYTSVPVSEYYGAINNY
240      250      260      270      280

cry2ab2_820. VLNGFGALSNFTFNIUGLPGSTTHALLAARVNYSG--ISSGDIGASPNFQNCST
320      330      340      350      360
U31527_1      NONGIQTEFQIRQ--PHLMDFFNTMTYTSYNRRYNSWGLEMTAYFTGAGQVFSFPLAG
290      300      310      320      330      340

cry2ab2_820. FLPLPLTLP--VRSWLDSDSDREGVATVTNWQTESFETTLGRSGAFTARGNSNYFPDYFI
370      380      390      400      410      420
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350      360      370      380
U31527_1      TRGDAAPFNVRVND-----GIYRIL--SAPFYSAFLGTSLVLSRGEPMFA---L
350      360      370      380

cry2ab2_820. RNISGVPLV--VRNEDLRRLPHYNEIRNIASFSGTGGARAYMVSVHKNKNIHAVHENG
430      440      450      460      470      480
U31527_1      NNISPPSARYRNPGTVDLSVSIPPQDNSVPHRGSSSHLSHVTWRNSSPFIHWTHSAT
390      400      410      420      430      440

cry2ab2_820. MIHLAPNDYTGFTISPIHATQVNNQTRTFISERFGNQSLSRFEQNNTTARYTLRNGNS
490      500      510      520      530      540
U31527_1      TTNRINSDVIT-QIPMVKAYNLHAGATVVRGPGFTG--GDILRTSNGMV--TLRVDASA
450      460      470      480      490      500

cry2ab2_820. ----YNLRLRVSSIGNSTIRVTINGRVYATNVNTTNNNGVNDGNGARFSDINIGNVVA
550      560      570      580      590      600
U31527_1      VNRQRYRIRFRYAATSNFVFVVR--RGNLGVNGREIMKMTSTGEELKSASFV---LSEFIT
510      520      530      540      550      560

cry2ab2_820. SSN---SDVPLDINV--TLNSGTQFDLMIMLIMLPTNISPLY
610      620      630
U31527_1      PENFENQVPLQIEIOSLSPGGEVYLDKIEFIPADTTFEAEYDLERAQKAVNALFTSTNQ
570      580      590      600      610      620

U31527_1      RGLKTDVTDVHDQVSNLVECLSDFECLDEKRELSEKVKHAKRLSDERNLLODPNFTSIN
630      640      650      660      670      680

cry2ab2_820.pcp
TXN5:CIJB_BACTU
Description: Q45716 bacillus thuringiensis. pesticidal crystal protein cryIjb
(insecticidal)
Accession/ID: Q45716
=====General comments=====
ID      CIJB_BACTU      STANDARD;      PRT; 1170 AA.
AC      Q45716;

SCORES      Initl: 153      Initn: 209      Opt: 280      Z-score: 293.0 E(): 2.1e-10
>>TXN5:CIJB_BACTU
Initn: 209 Initl: 153 Opt: 280 Z-score: 293.0 expect(): 2.1e-10
Smith-Waterman score: 325; 21.6% identity in 607 aa overlap
(54-634:32-598)

cry2ab2_820. AHDPFQHKSLDTVQKEWTWKNNHSLYLDLP--IVGTVASFLKKVGLVGRILSEL
30      40      50      60      70      80
CIJB_BACTU      EINNQOCIPYNCLSPNEEVLDDGERILDPLEVSMSLLQFLNNF--VPGGGFTSGL
10      20      30      40      50      60

cry2ab2_820. RNLFFSGSTNLMQDILRETEKFLNQRINTDTLARVNAELTGL----QANVEEFNRQVDN
90      100      110      120      130
CIJB_BACTU      FDKINGALRPSDWELFLAQIEQLDQRIEATVRAKAIAELEGLGRSFQLYVEAFKEWEET
60      70      80      90      100      110

cry2ab2_820. FLNPNNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRDVIL
140      150      160      170      180      190
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©17

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CLJB_BACTU 120 130 140 150 160 170
---PNTAARSVTRPRIDIAQIEANIPSPRIGFEVPLLSVVAQAANHLALLRDSVI
200 210 220 230 240 250
cry2ab2_820. NAEWGISATITIVRDYKNTKTSNYCINTYOSAFK--GLNTRLHML--EERTYMF
CLJB_BACTU 180 190 200 210 220 230
FGWNGTITINVALYHRSUKRIHE--DRSDVTYKTELRLGFTSRAQWKINYQFREL
260 270 280 290 300 310
cry2ab2_820. LNVFEYSWISLFWOSLVSSGARD--SAGSPQOQTSFSDQM--PFYLSLFOVNSNY
CLJB_BACTU 240 250 260 270 280 290
LTVLIDIVAVFPNYD-----GKLY--POTKSELRLTNSPSEYVYGAINNY
320 330 340 350 360 370
cry2ab2_820. VLNGFSGARLSNTFENIVGLPGSTTTTHAL--RANVYSG--ISSGDIGASPNWNCST
CLJB_BACTU 290 300 310 320 330 340
NQNGIOTERIQ--PHLMDFNTMTYTSYNRRYWSGLEMTAYFTFAGQOVSPOLAC
370 380 390 400 410 420
cry2ab2_820. FLPELLTTP--VRSMLDSCSDREGVATVWQTESPETTLGLRSGRTAGNSNYPTTPI
CLJB_BACTU 350 360 370 380 390 400
TRGDAAPPENVSVD-----GIYRL--SAPFYSAPFLGTSVLGSRDEEFA--
430 440 450 460 470 480
cry2ab2_820. RNISGVPLV--VRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA VHENG
CLJB_BACTU 410 420 430 440 450 460
NNISPPESARYNPGTDSLSVSPQDNVPPHRRGSSHRLSHVTRMNSPIFHWTHRAT
490 500 510 520 530 540
cry2ab2_820. MIHLAPNDYGTFTISPIHATQVNNQRTIFSEKFGNOGDSLRFEQNNITARTVTLRNGNS
CLJB_BACTU 450 460 470 480 490 500
TTNRNSDVIT--QIPMKANLHAGATVVRGFGT--GDILRTSGMVV--TLRVDASA
510 520 530 540 550 560
cry2ab2_820. -----YNLYRVSSISGNTSTIRTVINGRVYATNVNTTNDGVNDGARFSOINIGNVVA
CLJB_BACTU 570 580 590 600 610 620
VRNORYRIRFRYAATSNFYFVR--RGNLGVNGREIMTKMTSGTELKSAGFV--LGEFIT
630 640 650 660 670 680
CLJB_BACTU 610 620 630 640 650 660
RYLKTVDVTHIDQVSNLVECLSDSEFCDEKRELSEKVKHAKRLSDERNLQDPNFTSIN
690 700 710 720 730 740
cry2ab2_820.pap
TXN5:X06711_1
Description: X06711 Bacillus thuringiensis B. thuringiensis cryA4 gene for
delta-endotoxin; d
Accession/ID: X06711
=====General comments=====
LOCUS X06711.1 [BTRCRYA4]
DEFINITION B. thuringiensis cryA4 gene for delta-endotoxin; . . .
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SCORES Initl: 206 Initn: 233 Opt: 280 z-score: 292.6 E(): 2.2e-10
>TXN5:X06711_1
Initn: 233 initl: 206 Opt: 280 Z-score: 292.6 expect(): 2.2e-10
Smith-Waterman score: 284; 25.9% identity in 251 aa overlap
(56-297:68-303)

cry2ab2_820. DPFSQHKSLDTQKWEKTEWKKNNHSLYLDPIVGTVASFLKKVGVKRIUSELRNLI
30 40 50 60 70 80
X06711_1 EGNINIDPFVSASTVQTGINIAGRIILGVLPFFAFQGLASFY---SFLVGE-----L
40 50 60 70 80

cry2ab2_820. PFGSTNLMODILRETEKELNQLNTDTLARVNAELTGLQANVEEFQVDNLFNPNRA
90 100 110 120 130 140
X06711_1 WPRGR--DWEIPLFHEVQELINQOITENARNALTALRLOGIGDSFRAYQOSLEDLENRDDA
90 100 110 120 130 140

cry2ab2_820. VPLSITSSVNTMOQL--FLNRLPQFOMQGYQLLLPLFAQAANHLHSFIRDVILNADWGI
150 160 170 180 190 200
X06711_1 RTRSVLYTQVIALELDFLNA MPLFAIRNQEVFLMVYAQAANHLHLLLRDASLFGSEFGL
150 160 170 180 190 200

cry2ab2_820. SAALRTYRDYLNKYTRDYSNYCI---NTYQSAFKGLNT--RLHDMLEFRTYMFNVFEYV
210 220 230 240 250 260
X06711_1 LQETQRYRQVETRDYSDYCVENWTGSLRGTNAASWVRYNQPRDLTGLGLDLV
210 220 230 240 250 260

cry2ab2_820. STWSLFKQSLVSSCANL--280 290 300 310
X06711_1 ALFPYDTPYPTNLSQUTREYVIDAIGATGV--NNASMNWNNNAPSFAIEAAAIRSP
270 280 290 300 310 320

cry2ab2_820. GRLSNTPFPNIVFLL--320 330 340 350 360 370
X06711_1 HLLDFQLLTFFSASSWVWV--HMTYNSHTPOSRRPIGGGLNTSTHGATNTSINPVTLR
330 340 350 360 370 380

cry2ab2_820.pap
TXN5:CIBA_BACTX
Description: P05517 bacillus thuringiensis (subsp. thurstani), and bacillus
thuringiensis (sub
Accession/ID: P05517
=====General comments=====
ID CIBA_BACTX STANDARD; PRT: 1228 AA
AC P05517; Q45731; . . .

SCORES Initl: 206 Initn: 233 Opt: 280 z-score: 292.6 E(): 2.2e-10
>TXN5:CIBA_BACTX
Initn: 233 initl: 206 Opt: 280 Z-score: 292.6 expect(): 2.2e-10
Smith-Waterman score: 284; 25.9% identity in 251 aa overlap
(56-297:68-303)

cry2ab2_820. DPFSQHKSLDTQKWEKTEWKKNNHSLYLDPIVGTVASFLKKVGVKRIUSELRNLI
30 40 50 60 70 80
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C1BA_BACTK  EGNNDPFFVASTVQTGINTAGRIILGVLPFAQLASFY-----SPLVE-----L
              40      50      60      70      80
cry2ab2_820.  PFGSGTNLMQDILRETEKFLNQLRLNTDLARVNAELTGLQANVEEFNRQVNFNPNRNA
              90      100     110     120     130     140
C1BA_BACTK  WPRGR-DQWEIFLEHVEQLNQIITENARNTALARIQLGDSFRAQQSLEDLENRDDA
              90      100     110     120     130     140
cry2ab2_820.  VLSITSSVNTMQOL-FLNELPQFMQGYQLLLPLFAQAANLHLSFIRDLVILNADWGI
              150     160     170     180     190     200
C1BA_BACTK  RTRSVLYTQYIALELDFLNAFLFAIRNQEVFLMWYQAQAANLHLLRLDASLFGSEFGL
              150     160     170     180     190     200
cry2ab2_820.  SAATLRTYRDYLNKYTRDYSNYCI--NTYQSAFKGINT-RLHDMLEFRTYMLNVEYV
              210     220     230     240     250     260
C1BA_BACTK  TSQELRTYRQVETRDYSDYCVWYNTGLNSURGNAAWRYNQFRDLTLGLVLDLV
              210     220     230     240     250     260
cry2ab2_820.  SIWSLFKYQSLVSSGANL----YASGGPQQTQFTSQDMPFLYSLFQVNSYVNLNGFS
              270     280     290     300     310
C1BA_BACTK  ALFPPSYDRTYPTINTSAQLTRVYTDAGATGV-NMASMWNYNNAAPSFAEAAIRSP
              270     280     290     300     310     320
cry2ab2_820.  GARLNTFPNVGPGSTTTTHALLAARVNYSGGSSGDI GASPNFNCSTFLPPLLT
              320     330     340     350     360     370
C1BA_BACTK  HLLDFLEQLTIFSSASSNRMTYWRGHTIQSRPGGGLNTSGHATNTSINPVLRF
              330     340     350     360     370     380
cry2ab2_820.pcp
TXN5:U94191_1

Description: U94191 Bacillus thuringiensis Bacillus thuringiensis delta
endotoxin gene, compl
Accession/ID: U94191
LOCUS       U94191.1 [BTU94191]
DEFINITION  Bacillus thuringiensis delta endotoxin gene, complete cds. . . .
=====General comments=====
SCORES      Initl: 128      Initn: 168      Opt: 278      Z-score: 291.0 E(): 2.7e-10
>TXN5:U94191_1
initn: 168 initl: 128 opt: 278 Z-score: 291.0 expect(): 2.7e-10
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820.  FQKSLDITVQKEWTEWKNHSLYLDPIVGVASFLKLVKGVSLVGRILSELRLNLPFSG
              30      40      50      60      70      80
U94191_1      IPNCLSNPEVEVLGGERIETGYTIPIDISLSLTQFLISEF--VPGAGFVLGVLDIINGIF
              20      30      40      50      60

cry2ab2_820.  STNLMQDILRETEKFLNQLRLNTDLARVNAELTGL----QANVEEFNRQVNFNPNRNA
              90      100     110     120     130     140
U94191_1      GPSQWDAFLVOIEQLINQRIEEFARNQAISRLGLESLNLYQIYAESFREWEADPNP--A
              70      80      90      100     110     120
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cry2ab2_820.  VPSITSSVNTMQOLFLNELPQFMQGYQLLLPLFAQAANLHLSFIRDLVILNADWGIS
              150     160     170     180     190     200
U94191_1      LREEMRIQFNDMNSALITTAIFLFAVQNYQVPLLSVYQAQAANLHLSVLRLDSVFGQRMGPD
              130     140     150     160     170     180
cry2ab2_820.  AATLRTYRDYLNKYTRDYSNYCI--NTYQSAFKGINT-RLHDMLEFRTYMLNVEYV
              210     220     230     240     250
U94191_1      AATINSYNDLRLGNITDHAVRWYNTGLERVWGPDSR--DWIRYNQFRELTLVLDI
              190     200     210     220     230     240
cry2ab2_820.  VSIWSLFKYQSLVSSGANLYASGGPQQTQFTSQDMPFLYSLFQVNSYVNLNGFSGAR
              260     270     280     290     300     310
U94191_1      VSLFPNYSRTPYPIRTVSQ-----TREIYTN--PVLEN-FDGSFRGSAQGIEGSI
              250     260     270     280     290
cry2ab2_820.  LSNTFPNVGLPGSTTTTHALLAARVNYSGGSSGDI GASPNFNCSTFLPPL----
              320     330     340     350     360     370
U94191_1      RS---PHLMDILNSITITD-AHRGEYMW--SCHQIMASPVG--FSGPEFTFLYGTMGN
              300     310     320     330     340
cry2ab2_820.  -TPFVR--SWLDSGSDREGVATV--TNWQTESFETTLGLRSGAFTARGNSYVFPDYFTN
              380     390     400     410     420
U94191_1      AAPQORIVAQLGGVYRILSSILYRRPFGINNNQQLSVLDGTFAYGTSSNLPFSAYRK
              350     360     370     380     390     400
cry2ab2_820.  ISGVPLV--VRNEDLRLRHLHYNEIRNIASPGTGGARAYMVSVHKNKNIHAVHENGSM
              430     440     450     460     470     480
U94191_1      SGTVDLDEIPQNNNVPRQGFSHRLSHVSMFRSGFSNSSVSI-IRAPWFVHRSFAF
              410     420     430     440     450     460
cry2ab2_820.  IHLAPNDYGTFLSPI-HATOVNQTTFISEKFGNGSGSLRFQNNNTARYTLRGN---
              490     500     510     520     530     540
U94191_1      NNIIPS--SQITQIFLTKSTNLGSGTSVWKGPGFTG-GDILRRTSPQGIS--TLRVNITA
              470     480     490     500     510
cry2ab2_820.  --GNSYNLYRVSSISGNTSIRVTINGRVYTTATVNTTNNNDGVNDNGARESDINIGNVA
              550     560     570     580     590     600
U94191_1      PLSQRVVRIRVASTNLOPHSTIDGRPINQGNFSAFMSS--GSNMQSGSFRTVGFITPN
              520     530     540     550     560     570
cry2ab2_820.  SSNSDVELDINV-TLNSGTQFDLNMIMLVETNISPLY
              610     620     630
U94191_1      FNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQICL
              580     590     600     610     620     630
U94191_1      KTDVTDYHIDQVSNLVECLDESDFECLDEKSELSEKVKHAKRLSDERNLLODPNLRGINROL
              640     650     660     670     680     690
cry2ab2_820.pcp
TXN5:A09398_1

Description: A09398 Bacillus thuringiensis B.thuringiensis (var. Kurstaki HD1)
gene for delta
Accession/ID: A09398
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©01

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=====General Comments=====
LOCUS A09398_1 [A09398]
DEFINITION B.thuringiensis (var. kurstaki HD1) gene for delta-endotoxin.

SCORES Init1: 128 Init2: 128 Opt: 278 z-score: 291.0 E(): 2.7e-10
>>TXNS:A09398_1 Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FQKSLDVTQKEMTEWKNNHLYDPVIGVAVP... 30 40 50 60 70 80
A09398_1 IFYNCLSNPEVEVLGGRIETGVTPLDLSLSLTOFLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60 70 80

cry2ab2_820. STNLMQDILRETEKFLNORLNTDTLARNVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140
A09398_1 GPSQWDAFLVQIQEQLNRIEERFARNQAIISRLGLSNLYQVIAESFREWEADPTNP---A
70 80 90 100 110 120 130 140

cry2ab2_820. VPLSTTSVTNMQOLFNLRLPOFOMQGVOLLPLPFAQANLHLSELRNLIFPSSG
150 160 170 180 190 200
A09398_1 LAEEMRIQFNDMSALTTAIPFAVQNTQVPLSVVQANLHLSELRNLDVSVFGQRMGFD
130 140 150 160 170 180 190 200

cry2ab2_820. AATLTATYRDYLNKTRDYSNYCINTYQSAFK---GLNTRLHDM---EFTYVPLNVFEX
210 220 230 240 250
A09398_1 AATINSRYNDLTRIGNYTDHVRVWNTGLERVNGPDSR--DWIYNQFRELTLVLDI
190 200 210 220 230 240 250

cry2ab2_820. VSIWLFYQSLVSSGANLYASGSGPQQTQSFTSDWPFYLSLFQVNSNVLNFGSGAR
260 270 280 290 300 310
A09398_1 VSLFNFYDSRTYPIRTVSQL-----TREIYTN---PVLEN-FDGSFRGSAQGIEGSI
250 260 270 280 290 300 310

cry2ab2_820. LSGVPLV--VRNEDLRRLPHLYNEITNIAISPGTFCGARYVWVUNRKNHIAVHNGSM
430 440 450 460 470 480
A09398_1 SGTVDSLDEIPPNVNNVPPROGFSHRLSHVSMFPGFSNNSVSI--IRAPMFSIHRSAEF
410 420 430 440 450 460 470 480

cry2ab2_820. IHLAPNDYTGFTISPI--HATOVNQTFTFISEKFGNQDLSLRFQNNNTIARYLRN---
490 500 510 520 530 540
A09398_1 NNIIIPS--SQITQIELTKSTNLGSGTISVVKGPFTG--GDILRRISPGQIS--TLRVNITA
470 480 490 500 510 520 530 540
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cry2ab2_820. --GNSYGLYLRVSSIGNSTIRVTINGRVYATNVTNTTNDGNDGAPSDINIGNVVA
550 560 570 580 590 600
A09398_1 PLSORVYRIRVASTINLOFTISIDGRPINQGNFSAITMSS--GSNLQSGSFRVTGFTTFPN
520 530 540 550 560 570 580 590 600

cry2ab2_820. SSNSDVFLDINV--TLNSGTQFDLNMIMLVPTNISPLY
610 620 630
A09398_1 FSNCGSSVFTLSAHVNSGNEVYIDRIEFVPAETFEAEYDLERAKAVNELETSSNQIGL
580 590 600 610 620 630

A09398_1 KTDVTDYHDQVSNLVECLSDFCLEKSEKVKHAKRLSDERNLLODPNFRGINRQL
640 650 660 670 680 690 700

cry2ab2_820.psp
TXNS:CIAB_BACTK

Description: P06578 bacillus thuringiensis (subsp. kurstaki), bacillus
thuringiensis (subsp.
Accession/ID: P06578
=====General Comments=====
ID CIAB_BACTK STANDARD; PRT; 1155 AA.
AC P06578; P06577; P21257; P09663; P09666; P09667; . . .

SCORES Init1: 128 Init2: 128 Opt: 278 z-score: 291.0 E(): 2.7e-10
>>TXNS:CIAB_BACTK Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FQKSLDVTQKEMTEWKNNHLYDPVIGVAVP... 30 40 50 60 70 80
CIAB_BACTK IFYNCLSNPEVEVLGGRIETGVTPLDLSLSLTOFLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60 70 80

cry2ab2_820. STNLMQDILRETEKFLNORLNTDTLARNVNAELTGL---QANVEEFNRQVDNFLNPNRRA
90 100 110 120 130 140
CIAB_BACTK GPSQWDAFLVQIQEQLNRIEERFARNQAIISRLGLSNLYQVIAESFREWEADPTNP---A
70 80 90 100 110 120 130 140

cry2ab2_820. VPLSTTSVTNMQOLFNLRLPOFOMQGVOLLPLPFAQANLHLSELRNLIFPSSG
150 160 170 180 190 200
CIAB_BACTK LAEEMRIQFNDMSALTTAIPFAVQNTQVPLSVVQANLHLSELRNLDVSVFGQRMGFD
130 140 150 160 170 180 190 200

cry2ab2_820. AATLTATYRDYLNKTRDYSNYCINTYQSAFK---GLNTRLHDM---EFTYVPLNVFEX
210 220 230 240 250
CIAB_BACTK AATINSRYNDLTRIGNYTDHVRVWNTGLERVNGPDSR--DWIYNQFRELTLVLDI
190 200 210 220 230 240 250

cry2ab2_820. VSIWLFYQSLVSSGANLYASGSGPQQTQSFTSDWPFYLSLFQVNSNVLNFGSGAR
260 270 280 290 300 310
CIAB_BACTK VSLFNFYDSRTYPIRTVSQL-----TREIYTN---PVLEN-FDGSFRGSAQGIEGSI
250 260 270 280 290 300 310
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cry2ab2_820. 320 330 340 350 360 370
LSNTPFNVLGPGSTTHALLAARVNYSGGIGSGDGAAPFNQNCSTFLPPLL-----
C1AB_BACTK RS---PHMDLILNSITIID-AHGEYIW--SGHQIMASPVG--FSGPEFTFLYGTMGN
300 310 320 330 340
cry2ab2_820. 380 390 400 410 420
--TPFVR--SWLDGSDREGVATV--TNWQTESFETTLGRLSGAFTARGNSYFPDYFIRN
C1AB_BACTK AAPQORIVAQLGGGVYRTLSLTYRPFNIGINNQQLSVLGDTFAYGTSSNLPSAVRK
350 360 370 380 390 400
cry2ab2_820. 430 440 450 460 470 480
ISGVPLV--VRNEDLRRLPHYNEIRNIASPGIPGGARAYMVSVHNRKNNIHAVHENGSM
C1AB_BACTK SGTVDLSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNSSVSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460
cry2ab2_820. 490 500 510 520 530 540
IHLAPNDYTGFTISPI-HATOVNNOTRIFISEKFGNOGDSLPEQNNITARYTLRGN---
C1AB_BACTK NNIIIPS--SQITQIPLTSTNLGSGTSSVVKGGFTG-GDILRRTSPQGIS--TLRVNITA
470 480 490 500 510
cry2ab2_820. 550 560 570 580 590 600
--GNSYNLYLRVSSIGNSIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVVA
C1AB_BACTK PLSQRYRVIRYASTTNLOFHTSIDGRPINOGNFSATMSS--GSLNLSGSGFRTVGTTPFN
520 530 540 550 560 570
cry2ab2_820. 610 620 630
SNSNDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
C1AB_BACTK FNGSSVFTLSAHVFNSGNEVIDRIFVPAEVTFEAYDLERAQKAVNELFTSSNQIGL
580 590 600 610 620 630
C1AB_BACTK KTDVTDYHIDQVSNLVECLSDFCLEKSELSEKVKHAKRLSDERNLLQDPNFRGINRQL
640 650 660 670 680 690
cry2ab2_820.pep
TXN5:Q9F296
Description: Q9f296 bacillus thuringiensis. delta endotoxin. 6/2001
Accession/ID: Q9F296
=====General comments=====
ID Q9F296 PRELIMINARY;
AC Q9F296 PRT; 1155 AA.
DT 01-MAR-2001 (Tremblere). 16, Created)

SCORES Initl: 128 Initn: 168 Opt: 278 z-score: 291.0 E(): 2.7e-10
>TXN5:Q9F296
Initn: 168 Initl: 128 Opt: 278 z-score: 291.0 expect(): 2.7e-10
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. 30 40 50 60 70 80
FOHSLDTVQKEWTEWKNHSLYLDPIVGTASFLLKVGSLVGRILSELRLNIFPSG
Q9F296 IIPYCNLSPEVEVLGGERIETGVTPTIDISLSTQFDLLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60
90 100 110 120 130 140
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cry2ab2_820. STNMODILRETEKELNORLNTDILARVNAELTGL-----QANVEEFNRQVDNPLNPRNA
Q9F296 GPQWDAFLVOLEQLINORIEEFARQAISRLGLESLNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
cry2ab2_820. 150 160 170 180 190 200
VPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
Q9F296 LREEMRIQFNDMSALTATPLPAVQNYQVPLLSVYVQAANLHLSVLDRDVSFGORWGF
130 140 150 160 170 180
cry2ab2_820. 210 220 230 240 250
AAILRYRDYLNKYTRDYSNYCINTYQSAPK--GLNTRLHDML---EFTYMFNLNPFY
Q9F296 AATINSRYNDLTLRLIGNYTDHARWYNTGLERVMGPDNR--DWIRYNQFRRELTITVLDI
190 200 210 220 230 240
cry2ab2_820. 260 270 280 290 300 310
VSIWLFKYQSLVSSGANLYASGGPQQTQSFTSQDMPFLYSLFQVNSYVLNGFSGAR
Q9F296 VSLFPNYDSRTPIRTVSQL-----TREIYTN--PVLEN-FDGSFSGSQAQIESGI
250 260 270 280 290
cry2ab2_820. 320 330 340 350 360 370
LSNTPFNVLGPGSTTHALLAARVNYSGGIGSGDGAAPFNQNCSTFLPPLL-----
Q9F296 RS---PHMDLILNSITIID-AHGEYIW--SGHQIMASPVG--FSGPEFTFLYGTMGN
300 310 320 330 340
cry2ab2_820. 380 390 400 410 420
--TPFVR--SWLDGSDREGVATV--TNWQTESFETTLGRLSGAFTARGNSYFPDYFIRN
Q9F296 AAPQORIVAQLGGGVYRTLSLTYRPFNIGINNQQLSVLGDTFAYGTSSNLPSAVRK
350 360 370 380 390 400
cry2ab2_820. 430 440 450 460 470 480
ISGVPLV--VRNEDLRRLPHYNEIRNIASPGIPGGARAYMVSVHNRKNNIHAVHENGSM
Q9F296 SGTVDLSLDEIPQNNVPPROGFSHRLSHVSMFRSGFSNSSVSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460
cry2ab2_820. 490 500 510 520 530 540
IHLAPNDYTGFTISPI-HATOVNNOTRIFISEKFGNOGDSLPEQNNITARYTLRGN---
Q9F296 NNIIIPS--SQITQIPLTSTNLGSGTSSVVKGGFTG-GDILRRTSPQGIS--TLRVNITA
470 480 490 500 510
cry2ab2_820. 550 560 570 580 590 600
--GNSYNLYLRVSSIGNSIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVVA
Q9F296 PLSQRYRVIRYASTTNLOFHTSIDGRPINOGNFSATMSS--GSLNLSGSGFRTVGTTPFN
520 530 540 550 560 570
cry2ab2_820. 610 620 630
SNSNDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
Q9F296 FNGSSVFTLSAHVFNSGNEVIDRIFVPAEVTFEAYDLERAQKAVNELFTSSNQIGL
580 590 600 610 620 630
Q9F296 KTDVTDYHIDQVSNLVECLSDFCLEKSELSEKVKHAKRLSDERNLLQDPNFRGINRQL
640 650 660 670 680 690
cry2ab2_820.pep
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TXNS: M13898_1

Description: M13898 Bacillus thuringiensis B.thuringiensis (berliner)
crystalline entomocidal
Accession/ID: M13898

LOCUS M13898_1 (BACU1B)
DEFINITION B.thuringiensis (berliner) crystalline entomocidal protoxin g

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-----Genbank comments-----
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-----Genbank comments-----
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SCORES Initl: 128 Initn: 164 Opt: 174 z-score: 291.0 E(): 2.7e-10
>>TXNS: M13898_1
initn: 168 initl: 128 opt: 278 z-score: 261.0 E(): 2.7e-10
Smith-Waterman score: 284; 22.4% identity (60% aa overlap)
(60-634:41-610)

CRY2AB2_820. FOHKSLTVQKEWTEKKNNLSLYLDPIVGTAFSPFKNGSLGVGKRISELRNLPFSG
M13898_1 IPYNCLSNPEVEVLGGERTGYTPIDISLSLQFLSEFF--VFGANSLVLTLDIINGR
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

CRY2AB2_820. STNLMQDILRETEKFLINQRLNTDILARNALTLGL----QANVEEKNQDPLNPNKNS
M13898_1 GFSQWDAFLVQIBQLINQRIEFARNQAIISLEGLSNLYQIYAESFREMADNTP--A
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

CRY2AB2_820. VPLSITSSVNTMQOLFNLRFQFOMQGYQLLLPLFAQANLHLSFIRDVILNAEWGIS
M13898_1 LREEMRIQFNDNMNSALTITAIPLFAVQYQVPLLSVTVQAANLHLSVLVRDVFQGRWGDFD
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

CRY2AB2_820. AATIRYRDYLNKNTDYSNICYQSAFK--GLNTRLHDML---EFRTYMLNVEFY
M13898_1 AATINSRYNDLTRIGNYTDHAVRWYNTGLERVWVGDSR--DMIRYNQFRRELTITLVDI
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

CRY2AB2_820. VSINSLFKYGLSVSGANLHVSAGSGQQQFTSQDMPFLYSFQVNSNYVLNFGSAR
M13898_1 VSLFPNDSRTPIRTVSQL-----TREITYN---PVLLEN-PDGSFRGSAQOIEGSI
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

CRY2AB2_820. LSNTFPNIVGLPGSTTHALLAARVNVSGGSGDIGASPNQNFNCISFLPLPL----
M13898_1 RS---PHLMDLINSITITD-AHRGEYIW--SGHQIMASPVG--FGSPFTTFLITGWTGN
300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

CRY2AB2_820. -TPFVR--SWLDGSGDREGVAV--TNWQTESFTTLGLRGSAFTARGNSNYFPDPYFIRN
M13898_1 AAPQORIVAQLGGVYRTLSLTLYRRFPNIGINNQOLSVDLGTGTEFAGVTSSNLPASVARYK
350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500

CRY2AB2_820. ISGVPLV--VRNEDLRLPLHNETRINIAFSPTGPGARAYNVSVVHNRKXNIHAVHENGSM
M13898_1 SGTVDLSLDEIPFPNNNVPPRQGFSGHRLSHVMSFRSGSGNSVSVT--IRAPMFWSIHRSAEF
410 420 430 440 450 460 470 480 490 500

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X04698_1	IPYNCLSNPEVVLGGERIETGYTPIIDISLSTQFLLESEF--VPFGAGFVGLVDLIWGIF
	20 30 40 50 60
cry2ab2_820.	SINLMQDILRETEKFINLORNTDLTLARVAELTGL---QANVEEENRQVDFNLPNPNA
	90 100 110 120 130 140
X04698_1	GFSOWDAFLVOIQEOLNRIIEEFARNQAISRLEGLSNLYOIAESFREWEADPTNF--A
	70 80 90 100 110 120
cry2ab2_820.	VPLSITSVNTMOQLFNLRKFQOMQCYQLLLPLPAQAAHLHUSFTRVILINADEWGIS
	150 160 170 180 190 200
X04698_1	LREEHQRPNDMSALTATAPLFAVQNYQVPLLVSVOAANHLHLSVRDVSVFGRWGFD
	130 140 150 160 170 180
cry2ab2_820.	AATLTAYDYLVKNYTDYSNCINYOSAFAK--GLNTRLHDMU---ERTYMFNVNPEY
	210 220 230 240 250
X04698_1	AATINSRYNDLTBLIGNYTHNAVRYWTGLERVWGPDSR--DWIRYNQFRRLITVLUDI
	190 200 210 220 230 240
cry2ab2_820.	VSIWLFKYOSLLVSSGANLASGSGPQOTSFTSQDPFLYSLFQVNSNYVLNGFSGAR
	260 270 280 290 300 310
X04698_1	VSLFPVDSRTYDIRVSQI-----TREIYTN---PVLEN-FDCSPRGSAQIGIESI
	250 260 270 280 290
cry2ab2_820.	LSNTFPNIUGPGSTTHALLAARWNVSGISSGDIGASPFNQFNCSIFLPILI----
	320 330 340 350 360 370
X04698_1	RS---PHMILANSITIYTD-AHRGEYYW--SCHQIMASPGV--FCSGEFTFLXTGTWGN
	300 310 320 330 340
cry2ab2_820.	-TPFVR--SWLDGSDREGVATV-TTWQTESFTTILGRGAFTAGNSVNPDDFYURN
	380 390 400 410 420
X04698_1	APAQORIYAQLGGGVYRTLSLTVRRFPNIGINNOOLSVLOGTEFAVGTSSNLPASVARK
	350 360 370 380 390 400
cry2ab2_820.	ISGVFLV--VRNEDLRRPLHNEYRNIAISPSGPGGARAYMVSVHNRKNNIHAVHENGSM
	430 440 450 460 470 480
X04698_1	SGTVDSIDEIIPPQNWNPPROGFGRHLSHVSMFRSGSNSSVSI-IRAPMFWIHRSAEF
	410 420 430 440 450 460
cry2ab2_820.	IHLAPNDYTGTTSPT-HATQVNQOTRFISEAFKGNGDSIRFPQNNNTARTYLGRN---
	490 500 510 520 530 540
X04698_1	NNIIIPS--SQIOIPLTKSNLNGSGTSVVVGPGFTG-GDIILRTSPQGIS--TLRVNITA
	470 480 490 500 510
cry2ab2_820.	--GNSNYILRVSSGINSTRIVTGRTVYATVNTVNTDGVNDNGCARPSDINTGNVA
	550 560 570 580 590 600
X04698_1	PLSQRYRVRYASTTNLQFHTSIDGRPINOGNFSAWSS--GSNLQSGSFRTVTGTTFFN
	520 530 540 550 560 570
cry2ab2_820.	SNSNDVPLDINV-TLANSQTFQDLMIMLVTPTSPLY
	610 620 630
X04698_1	FNGSSVFTHSAHFVNSGNEVYIDRIEFVFAEYFEAEYDLERAQKAVNELFTSSNQIGL
	580 590 600 610 620 630

©01

X04698_1 KTDVTDYHIDOVSNLVECLSDFECLDEKKEKSEKVKHAKRLSDERNLLQDPNFRGINRQL
640 650 660 670 680 690

cry2ab2_820.pep
TXN5:M37263_1

Description: M37263 Bacillus thuringiensis B.thuringiensis 5.3 class
delta-endotoxin gene, co

Accession/ID: M37263

LOCUS M37263_1 [BACSTRD2]

DEFINITION B.thuringiensis 5.3 class delta-endotoxin gene, complete cds;

SCORES Initl: 128 Initn: 128 Opt: 277 Z-score: 289.9 E(1): 3.4e-10
>>TXN5:M37263_1

Initn: 128 Initl: 128 Opt: 277 Z-score: 289.9 E(1): 3.4e-10

Smith-Waterman score: 283; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHKS LDTVQKEWTEWKNHSLYLDPIVGVASFLKKVGLVGRILSLERNDLFFES
30 40 50 60 70 80

M37263_1 IPYNCLSNPEVEVLGGRIETGYTIDISLSLTQFLSFEF--VPGAGFVSNLVDLWINGIF
20 30 40 50 60

cry2ab2_820. STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNQVDNLPNRRNA
90 100 110 120 130 140

M37263_1 GPSQWDAFLVQIEQLINQRIEERFARNQAISRLGSLNLYQIYAESFREWEADPTNP--AA
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQFLNLPQFOMQGYQLLLPLFAQAANHLSPFIDVILNADEWGIS
150 160 170 180 190 200

M37263_1 LREEMRIQFNDMSALITAIPLFAVONQVPLLSVYVQAANHLHLVLRDVSVPQRMGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTRDYDKNTRDYSNYCINTYQSAFK--GLNTRLHDML---EFTYMLNVEFY
210 220 230 240 250

M37263_1 AATINSRYNDLTRELIGNYTDHVRWYNTGLERVYMGDSR--DWIRYQFRRELTLTVLDI
190 200 210 220 230 240

cry2ab2_820. VSINSLFKYQSLVSSGANLYASGGQOQSFTSQDWPFLYSLPQVNSYVNLGFSGAR
260 270 280 290 300 310

M37263_1 VSLFPNYDSRTYRTVTSQI-----TREIYTN---PVLEN--PDGFSFGSAQIEGSI
250 260 270 280 290

cry2ab2_820. LSNTFFNVLPGSTTHALLAARUNYSGGISGDIQASFPNFCNSTELPLLL-----
320 330 340 350 360 370

M37263_1 RS---PHLMILNSIIYTD-AHGEIYW--SGHQIMASVFG--FSGPEFTFFLYGTGMN
300 310 320 330 340

cry2ab2_820. --TPFVR--SWLDSGSDREGVATV--TNWOTESPETTLGLRSAGFTARNCSYPPDVFIN
380 390 400 410 420

M37263_1 AAPQRIVAQLGQGVYVTLSSTLVERPFNIGINNQQLSVLDGTEFAYCTSSNLFPSAVYRK
350 360 370 380 390 400

cry2ab2_820. AATLRTRDYDKNTRDYSNYCINTYQSAFK--GLNTRLHDML---EFTYMLNVEFY
430 440 450 460 470 480

cry2ab2_820. ISGVPLV--VRNEOLRRPLHNEIRNIASPSQPGARAYMVSVHNRKXNIIHAVHENGSM
410 420 430 440 450 460

M37263_1 SGTVDLDEIPQNNVPPRQGFSHLSHVSFMRSFGSSSVSI--IRAPMFWSIHRSANF
470 480 490 500 510

cry2ab2_820. IHLAPNDYTGFTISPI-HATQVNNQTRTFISEKFGNQDLSIRFEQNNTTARTYLRGN---
520 530 540 550 560 570

M37263_1 NNIIPS--SQITQIPLTKSNLQSGTSVVGKPGFTG-GDILRRISPGQIS--TLRVNITA
570 580 590 600 610 620

cry2ab2_820. --GNSYNLVRVSSISGNSTIRVINGRVYATNVNNTINNDGVNDNGARFSDINIGNVVA
630 640 650 660 670 680

M37263_1 PLSORVVRIRVASTTNLQPHSTIHGRPINOCNFSATMSS--GSLQSGSFRLHGTTFPN
690 700 710 720 730 740

cry2ab2_820. SSNSVDPLDINV-TLNGSTQFDMNIMLVPTNISPLY
750 760 770 780 790 800

M37263_1 FSNQSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAFYDLERAQKAVNELETSNQIGL
810 820 830 840 850 860

cry2ab2_820. KTDVTDYHIDOVSNLVECLSDFECLDEKKEKSEKVKHANGLSDERNLLQDPNFRGINRQL
870 880 890 900 910 920

cry2ab2_820.pep
TXN5:M37263_1

Description: Q9AM83 bacillus thuringiensis serovar kunthalarx24. insecticidal
protein

Accession/ID: Q9AM83

ID Q9AM83

AC Q9AM83

SCORES Initl: 128 Initn: 168 Opt: 276 Z-score: 289.1 E(1): 3.4e-10
>>TXN5:Q9AM83

Initn: 168 Initl: 128 Opt: 276 Z-score: 289.1 E(1): 3.4e-10

Smith-Waterman score: 284; 62% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHKS LDTVQKEWTEWKNHSLYLDPIVGVASFLKKVGLVGRILSLERNDLFFES
30 40 50 60 70 80

Q9AM83 IPYNCLSNPEVEVLGGRIETGYTIDISLSLTQFLSFEF--VPGAGFVSNLVDLWINGIF
20 30 40 50 60

cry2ab2_820. STNLMQDILRETEKFLNQLRNTDTLARVNAELTGL---QANVEEFNQVDNLPNRRNA
90 100 110 120 130 140

Q9AM83 GPSQWDAFLVQIEQLINQRIEERFARNQAISRLGSLNLYQIYAESFREWEADPTNP--AA
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQFLNLPQFOMQGYQLLLPLFAQAANHLSPFIDVILNADEWGIS
150 160 170 180 190 200

Q9AM83 LREEMRIQFNDMSALITAIPLFAVONQVPLLSVYVQAANHLHLVLRDVSVPQRMGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTRDYDKNTRDYSNYCINTYQSAFK--GLNTRLHDML---EFTYMLNVEFY
210 220 230 240 250

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Smith-Waterman score: 275; 23.4% identity in 286 aa overlap
(70-349:54-321)

cry2ab2_820_KIEWTEWKNHSLYLDPIVGTASFLKKVSGLVGKRILSELRLNLFPSGSTNLMODILR
 40 50 60 70 80 90
 |::||::|::|::|::|::|::|::|::|::|:
C1DB_BACTU DAERLETGNTVA DISLG LNF LYSNF VPGGG FIVG--LLELIWG FVGSPQ---WEIFLA
 30 40 50 60 70

cry2ab2_820_ETEKFLNQRLNTDTIARNAELTGLQANVEEFNRQVDNELNPNNRNVPUSITSSVNTMQ
 100 110 120 130 140 150
 |:::||::|::|::|::|::|::|::|::|::|:
C1DB_BACTU QIEQLISRIETEEFARNQAISRLEGLSNNYEITYTETFRAMEKDPGNPALREEMRTQFNVMN
 80 90 100 110 120 130

cry2ab2_820_QULFNRLPQMFGCHYOQLLLPLFAQAAHLHSFIIRDVLINADENGISAATLYRYRDYLN
 160 170 180 190 200 210
 |::|::|::|::|::|::|::|::|::|::|:
C1DB_BACTU SALTAATAIRLRVENVEALLSVYYOAAHLSLRDVSYGORMGFOPATVNSGRYSDLTR
 140 150 160 170 180 190

cry2ab2_820_YTRYDSNYVCINTYQS AFKGLN-TRLHDML--EFTMYELNVFEYVISLKFYQSLLVS
 220 230 240 250 260 270
 |::||::|::|::|::|::|::|::|::|::|:
C1DB_BACTU LIHVYTDCVDTYNDSLKNLESRLSDVVVNFRRLRTISVLDIIAFFNFYIDIEAVPIQ
 200 210 220 230 240 250

cry2ab2_820_SGANLASGSGPOQTOSTSQDWPFSLFYQNSTVLNGFSGARLSNTP-PNIVLGPQS
 280 290 300 310 320 330
 |::||::|::|::|::|::|::|::|::|::|:
C1DB_BACTU TAS-----QLTREYVLDLPFVNETLSPPASPYPT-FSAAESAIRSHPLVDPLNS
 260 270 280 290 300 310

cry2ab2_820_TTHHALAARVNSGISGSDDIGASPQQNPNFCSTFLPLLTFPVRSWLDSGDREGVAT
 340 350 360 370 380 390
 |::||::|::|::|::|::|::|::|::|::|:
C1DB_BACTU FTIYDLSLAYWGMGHVLSNPRTGTTTNIRSPLYGREGNTERTPVITASPSVPIFRTL
 310 320 330 340 350 360

cry2ab2_820_pep
TXMS:AAK48937

Description: Aak48937 bacillus thuringiensis, insecticidal crystal protein.
6/2001

Accession/ID: 000000

ID AAK48937 PRELIMINARY;
AC AAK48937;

SCORES Initl: 152 Inith: 176 Opt: 275 z-score: 287.8 E(): 4e-10
>>TXMS:AAK48937
Initl: 176 Inith: 152 opt: 275 Z-score: 287.8 expect(): 4e-10
Smith-Waterman score: 275; 23.4% identity in 286 aa overlap
(70-349:54-321)

cry2ab2_820_KIEWTEWKNHSLYLDPIVGTASFLKKVSGLVGKRILSELRLNLFPSGSTNLMODILR
 40 50 60 70 80 90
 |::||::|::|::|::|::|::|::|::|::|:
AAK48937 DAERLETGNTVA DISLG LNF LYSNF VPGGG FIVG--LLELIWG FVGSPQ---WEIFLA
 30 40 50 60 70

100 110 120 130 140 150

©07

```

cxy2ab2_820. EWGISAATLTYRDYLYKNYTRDYSNCINTYQSAFKGINTLRHLDMLEFPTYNFLNVEFYV
      :|:::  :  :|:::  :|:::  :|:::  :|:::  :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
L32019_1     RWGLTTKNDYINRQREITHEYSNCDVTYTELRGR--SIAQWRIY---NQFRRE
      180   190   200   210   220   230   240   250   260

```

[illegible]

cry2ab2_820. SIWSLFKYOSLLVSSGANLYASGSGPQQTQS- TSQWPFLYSLFQVSNVYVNGFSGAR
L32019_1 LTTVLIDIVALFPNVDLSLYPIOTFSQLTREIVTSPEFYGV-- INSGNIIGTLTREQQ
240 250 260 270 280 290 320 330 340 350 360 370

```

cry2ab2_820.LSNFTFNIVGLPGSTTTTHALLAARVNVGGIS-----SGDIGAS-----360      370
I---:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--:::--
IRR--PMLMDFNFSIMVTSNDNRREHYWGSGLBMTAYFTGFAGAQVFPLVLVTRGESA--P

```

CRY2AB2_820. LSNTFNIVGLPGSTTHALLARVNYSGGIS-----SCDIGAS---PQNQPNFCSTELF
:
: : : : :
L32019_1 IRR--PHLMDFFNSIMVTSDNRREHYWSGLEMTAYFTFGAQGVGFPLAVLTGRGESA--P
:
: : : : :
300 310 320 330 340
380 390 400 410 420 430

```

      300      310      320      330      340
crv2ab2_820.  PLPTPVRSWLDSGDRGAVTNQTESFETTLIGRSAGFTAGNSVFPDYIRNIS
                ||| ||| ||| : : : : : : : : : : : : : : :
PLT---VRSWND-----GYRIL---SAPFYSAPFLGTIVLGSRGEK---F-DFAANNIS
L32019_1

```

cy2ab2_820. PLTPTFRSMLDSSGDRGVATVNNQTESPETTLGLRSAGFTARGNSVFPDYPFIRNI
L32019_1 PLT---VRSVND-----GYRIL---SAPFYSAPFLGTIVLGSRGEK--F-DFALNIS
350 360 370 380 390

350 360 370 380 390
GVF-LVVRNEDRLRLHYNEIRNTASPTGGARAYVSVHNRKNIIHAVHENGSMIH-
CRY2262_820
PPSTYRHPGVDSLVISIPQDQSVPPHRRGSHLSHVTWRASSPIFWHTHRSATTNT
L12039_1

cy2002_020. GVP-LVVRNEDLRRLPHYNETRNTASPSCTPGGARAYMVSVHNRKNNIHAVHENGSMITH
L32099_1 PPSTYRHPGTVDLSVSIIPQNSVPPHRGSSHLSHVTWRASSPFHWTHTSSATTTT

~~L32019-1~~

7

CA02ab2_B20 LAPNDYGGTATGSPPIHATOVNNQTRTFISKFKNGDSSLRFFQNNTA--RYTLRG-NGN-
L32019_1 INPNAI--TOTPLVSNFNLASGATVVGSGFTGG-GDLIRRTNGTGTTADRVNVITGLSQSR
550 560 570 580 590 600
... ..
... ..
... ..

cry2ab2_820. INLH RVSSIGNSTVINGNYITNNVTIINDGVNDGAFSDIINGNVASSNSD
 550 560 570 580 590 600
 460 470 480 490 500 510
 YRVRLVNASTDLQPSFVITTSVUNQNGFQTMNR - GNLESGNFRTAGTSFPFSFNAQ
 550 560 570 580 590 600

cr2ab2_820_ L32019_1

YVVRINAVASTDLOQFSTGTSVQNGVQFQWNR-GNLESNGRTAGCFSTPFPSNAQ

610 620 630 640 650 540 550 560

VPLDITVITINISCTQENAKNMLVETLSSV

rv2ab2_820

~~SECRET~~

CRY2AB2_820_VPDIINTVLTSGTQFDLNNMLYPLNLSPEY
L32019_1 STFTLGTOAFSNOEQYVIDRIVEFVEITEASD JERACKAWALNTSTNOLGLKTDVTD

```

CRYZGDZ_620_VFGUINVUNSGQFDBNNSQLPFWSSD
      :   :   :   :   :   :   :   :   :
L32019_1_STFTLGTOAFSQQEVYIDRIEVPVETFEASDIERACKAWALNTSNGLKLTDTVD
      570    580    590    590    600    610    620

CRY2AB2_820_BSD

```

crv2ab2_820.pep
TXN5:ClJA_BACTU

cry2ab2_020.pep
 TXN5:ClJA_BACTU
 Description: Q45738 bacillus thuringiensis. pesticidal crystal protein
 (insecticidal)
 Accession/ID: Q45738
 General comments=====

Accession/ID: Q45738
(insecticidal)
=====General comments=====

ID	C1JA_BACTU	STANDARD;	PRT; 1167 AA.
AC	Q45738;		

ID	C1JA_BACTU	STANDARD;	PRT;	1167 AA.
AC	Q45738; . . .			

SCORES	Initl: 150	Initn: 203	Opt: 275	z-score: 287.7 E(1: 4.le-18)
>TXNS:C1JA_BACTU				(1167 aa)

```
SCORES Initl: 150      Initn: 203      Opt: 275      z-score: 287.7 E(): 4.1e-18
>TXNS:C1JA.BACTU      (1167 aa)
initn: 203 initl: 150 opt: 275 z-score: 287.7 expect(): 4.1e-10
```

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Product Characterization Center

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Smith-Waterman score: 337; 21.3% identity in 598 aa overlap
(54-634:32-597)

```
cry2ab2_820. AHDPFSQHKSLDTQKWTWKNNHSLYLDP--IVGVASFLIKKVGSLVKRILSEL      80
CLJA_BACTU  BINNQKQCIYPNCLSNPEVLLDGERILDPIDPLEVLSLLQLFNNF--VPGGGFISGL      70
              10 20 30 40 50 60 70
cry2ab2_820. ENLFPSSGSLNMODILRETEKFLNQLNTDTLARIYNAELTGLQANVEEFNRQVDNFLN    140
CLJA_BACTU  VDKIWGALRPESEWDLFLAQIERLDQRIEATVRAKAIIELEGGRNTQIYAEAFKEWESD    130
              70 80 90 100 110
cry2ab2_820. PNRNAVPLSITSSVNTMQOLFNLRFQFMQGYQLLLPLFAQANLHLSFIRDVLNAD      180
CLJA_BACTU  PDNEAAKSRVIDRFRILDGLTEANIPSFRIIGFEVPLLSVYQAANLHLLRDSVIFGE      170
              120 130 140 150 160
cry2ab2_820. EWGISAAILRTYDYKNTYRDYNSYNCINTYQSAFKGLNTRLHDMLEFRYMFNLVFEV      260
CLJA_BACTU  RWGLTTKNVNDIYNQRIEIRHEYSNCHVDITTELERLGR--SIAGWRIY--NQFRRE      250
              180 190 200 210 220 230
cry2ab2_820. SIMSLFRYQSLVSSGANLYASGSGPOQTOSF--TSQDWPFLYSLFQVNSVYLVNGFSGAR    310
CLJA_BACTU  LTLVLQIVLAFPNYDSRLYPIQTFSLTRIVTSPVSEFYGV--INSNGIITGLITEQ      300
              240 250 260 270 280 290
cry2ab2_820. LSNTFPNVLPGSITTHALLAARVNSGGIS-----SGDIGAS----PFNQNFNCSTFLP      370
CLJA_BACTU  IRR--PHLMDPFNSIMYTSNRRHEVWSGLEMTAVFTGFAGAQVSPPLVGTGRGESA--P      360
              300 310 320 330 340
cry2ab2_820. PLLTFPVRSLDGSREGVATVNWQTESFETTLGRSGAFTARGNSYFPDYFIRNIS      430
CLJA_BACTU  PLT---VRSVND-----GIYRIL---SAPFYSAPELGTIVLGRGEEK--F-DPALNNIS      420
              350 360 370 380 390
cry2ab2_820. GVP--LVVRNEDLRRLPHYNEIRNIASPSGTPGAGARVYVSNRKNHIAHVHNGSMIH-      480
CLJA_BACTU  PPTPTIYRHGPGTVDSLSVSPQDNVSPHGRSGHRLSHVTRASPIFHVTHRSATITNT      470
              400 410 420 430 440 450
cry2ab2_820. LAPNDYTGFTISPIHATQVNRQTRIFISEKFGNQGDSLRFEQNNNTA--RYTLRGN-GNS      540
CLJA_BACTU  INPNAI--IQIPLVKAFNLHSGATVVRGPGFTG-GDILRRNTGTGTFADMRVNIITGPLSOR      530
              460 470 480 490 500 510
cry2ab2_820. YNLXLRVSSIGNSTIRVINGRVYATNNTTNDGVNDNGARFSPDINIGNVASSNSD      600
CLJA_BACTU  YRVRIYASVTTDLQFFRTINGTSVNOGNFQRTMNR--GNLSEGNFRTAGSTPFPFSNAQ      590
              520 530 540 550 560
              610 620 630
```

```
cry2ab2_820. VPLDINVTLNSGTQFDLMNIMLVPTNISPLY
CLJA_BACTU  SFTLGTQAFNQSVYIDRIEFVPAEVTPEASLERAQKAVNALFTSTNQGLKXTDVT      620
              570 580 590 600 610
cry2ab2_820.pep
TXN5:CJAA_BACTJ
Description: O32307 bacillus thuringiensis (subsp. jegathesan). pesticidal
crystal protein c
Accession/ID: O32307
=====General comments=====
ID CJAA_BACTJ STANDARD; PRT; 648 AA.
AC O32307; .
SCORES Init1: 135 Initn: 135 Opt: 270 z-score: 287.1 E(): 4.4e-10
>>TXN5:CJAA_BACTJ (648 aa)
initn: 135 init1: 135 opt: 270 z-score: 287.1 expect(): 4.4e-10
Smith-Waterman score: 282; 21.3% identity in 610 aa overlap
(57-632:74-648)
cry2ab2_820. PFSFQHKSLDTQKWTWKNNHSLYLDPIVGVASFLIKKVGSLVKRRI--LSELFNL      80
CJAA_BACTJ  YKDWLNVCVGYHIENPREASVRAGLKGIGIVSTIVGFFG--GSIILDTIGLFYQISEL      70
              50 60 70 80 90
cry2ab2_820. IFFSGSTNLM--QILRETEKFLNQNLNLTDLARVNA--ELTGLQANVEEFNRQVDNFLN    140
CJAA_BACTJ  LWPEDDTQYQWQIMHVEDLIDKRI--TEVI--RGNAIRTLADLQGVDDVNNMLKKWKD      130
              110 120 130 140 150
cry2ab2_820. PNRNAVPLS--ITSSVNTMQOLFNLRFQFMQ--GYQLLLPLFAQANLHLSFIRDVI      190
CJAA_BACTJ  DPKSTGNSTLTVTFTALDSDDFNGAIRTVNNQSGFGEHLLLPVYQAANLHLLLRDAQ      180
              160 170 180 190 200 210
cry2ab2_820. LNADEMGISAATLR--TYRDYLNKNTYRDYNSYNCINTYQSAFKGLNT--RLHDMLEFRYMF      250
CJAA_BACTJ  IYGDKWKWSARANARDNYQIQLEKTEYECINWKNKGLNDFRTAGQWVNFNRVREMT      240
              200 210 220 230 240 250 260 270
cry2ab2_820. LNVFEVSIWLSLFK---YQSLVSSGANLYASGSGPOQTOSFTSQDWPF--LYSLFQVNS      300
CJAA_BACTJ  LTVLDIISMFPIYDARLYPTEVATELREIYSDVINGEIIYGLMTPYFSFEKASLY--TRA      290
              260 270 280 290 300 310 320 330
cry2ab2_820. NVYLVNGFSGARL--SNTFPNIVGLPGSITTHALLAARVNSVSGI--SSGDIGASFPNQNF      360
CJAA_BACTJ  PHLFTWLKGFPRVTSISYVTFLSGGQNKYSYTNSSINSGSPRGQDTDYGTGSTINIP      350
              310 320 330 340 350 360 370 380 390
cry2ab2_820. CSTFPPPLLTLP---FVRSWLDGSREGVATVNWQTESFETTLGL--RSGAFTARGNSY      420
CJAA_BACTJ  SNSEYVNLWTEYEVYIPWGDVPNIITKNFVSVD--NNSSKELIYGAAHRTKPVVTRTDFD-      410
              370 380 390 400 410 420 430 440 450
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00707603_1      220      230      240      250      260      270
IYCDKWSARANARDNYIQLEKTEYTEYCYINWYKGLNDFRTAQGVNFRVREMI

00707603_1      260      270      280      290      300
LNVFEXVSIWSLFK---YQSLVSSGANLYASGSGPQOTQSTFSQDWPFF--LYSLFQVNS
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
LTVLDDISMFPLIDARLYPTEVKTJELTRREIYSDVINGEIVGLMTPFYSPKEASLY-TRA
280      290      300      310      320      330

00707603_1      310      320      330      340      350      360
NYVLNGFSGARL-SNTFNTVIGLPGSTTHALLAARVNYSGGI--SSGDIGASPFNQNFN
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PHLFTWLGKFRFVNISISYWTFLSGQNKYKSYTNNSNINEGSRFGQDQTYDGTSTINIP
340      350      360      370      380      390

00707603_1      370      380      390      400      410      420
CSIFLPLPLTP---FVRSWLDSGSDREGVATVNNQWTESPETILGL-RSGAFTARGNSNY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
SNSVYNLNWTENYEYTFWGDVNNITKMMFVTD--NNSKELIYGAHRTNKKPVVTRDFD-
400      410      420      430      440      450

00707603_1      430      440      450      460      470      480
FDPDYFRINISGVPLVVRNEDLRPLHYNEIRNIASPGTTCGGAAYWVSVHNRKNNIHAV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
----FLTNKEGTELAKYND-----YNHLSYMLINGEITGQKHGYSFATHSS--V-
460      470      480      490      500      510

00707603_1      490      500      510      520      530      540
HENGSMIHLAPNDYTGTFISPIHATQVNNQTRTFSEKFGNQSGSLRFEQNN--TTARYTL
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
BPNMTI---AANKITQIPV--VKASSINGSISIEKGPQGTG-GDLVKMRADSLGTLWRFKA
510      520      530      540      550

00707603_1      560      570      580      590
ELDDKKYKRYRYKQVSSKLIILRWKKGEGYIQQQIHNIISPTGA-----FSYLESETI
560      570      580      590      600

00707603_1      600      610      620      630
VASSASDPLDNLVLTASQF--DANNIM-----VPTNISPLY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
TITENI-FDNKNTVETPYGQFEDPISDLINKIKISLEFTN
610      620      630      640

00707603_1      640      650      660      670      680      690
Description: Q45744 bacillus thuringiensis (subsp. kurstaki), pesticidia
crystal protein cry
Accession/ID: Q45744
ID C3CA_BACTK
AC Q45744; .
General comments=====
PRTI; 649 AA.
=====
SCOPES Init1: 118 Initn: 146 Opt: 270 z-score: 287.1 E(0): 4.4e-10
Initn: 146 Init1: 118 Opt: 270 z-score: 287.1 expect(): 4.4e-10
Smith-Waterman score: 271; 23.4% identity in 304 aa overlap
(70-361:84-355)

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```
cry2ab2_820. KWTWKNNHNSLYLDPIVGTVASFLKKVSLVGRKILSELNLIIPSSSTNLMODILR
C3CA_BACTK ALDSSTTKDAIQIGISIIIGDLGVVGFPGYGGALVS--FYTNLLNTINFG--EPLKAFMQ
100 110 120 130 140 150 160
cry2ab2_820. ETEKFLNORLNTDTLARVNAELTGLQANVEEFNRQVDNFPNRRNAVPLSITSSVNTMOQ
C3CA_BACTK OVEALIDOKIADYAKDKATAELQGLKNVFKDYVSALDSW--DKTPLTLRDSGSGRIE
110 120 130 140 150 160
cry2ab2_820. LNR-LPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWGMGISAATLRTY
C3CA_BACTK LFSQAESHFRSRMPSFAVSGVEVLFPTYQAANTHLLLLKDAQIYGTDMGYSTDLNLF
170 180 190 200 210 220
cry2ab2_820. RDYLNKNTDRSYNYCINTYQSAFKGL-NTRLHDMLEFRTY---MFLNVFEVSIWLSFKY
C3CA_BACTK HTKQKDLTIETTHCAKWKYAGLGRGTYEAWKFNRYRREMTLTVDLITLFLPYDV
230 240 250 260 270 280
cry2ab2_820. QSLLVSSGANLYASGSGPOQTOSTQDWPFLYSLFQVNSNVLVNFGSGARLSNTFPNTIV
C3CA_BACTK RT-----YTKGVKTELTDVLTD--PIV-----AVNN---MNGY-GTFESN-IENVI
270 280 290 300 310 320
cry2ab2_820. GLPGSTT-THALLAARVNYSGISGIDGASFPNQPNPCSTLPLLPFFVRSLWDSGSD
C3CA_BACTK RKPHLFDYLHA-----IQFHSRLQPGVFGDPSFNYSNGVYSTRSIGSDIIRSPFYGN
330 340 350 360 370 380
cry2ab2_820. REGVATVNNQTESFETTLGLRSGAFTARGNSYFPDPIRNSGVPLVVRNEDLRPLH
C3CA_BACTK KSTLDVQNLFNENGEKVFRAVANGNLAVWPGTGTKIHSGVTKVQFSQYNDKDEVRTQT
390 400 410 420 430 440
cry2ab2_820.pcp
TXN5:C3BB_BACTU
Description: Q06117 bacillus thuringiensis. pesticidal crystal protein cry3bb
Accession/ID: Q06117
ID C3BB_BACTU STANDARD; PRT; 652 AA.
AC Q06117; Q45717;
=====General comments=====
SCORES Initl: 154 Initn: 192 Opt: 270 z-score: 287.1 E(): 4.4e-10
>>TXN5:C3BB_BACTU
Initn: 192 Initl: 154 Opt: 270 Z-score: 287.1 expect(): 4.4e-10
Smith-Waterman score: 286; 20.8% identity in 534 aa overlap
(83-582:97-601)
cry2ab2_820. YLDPIVGTVASFLKKVSLVGRKILSELNLIIPSSSTNLMODILRTEKFLNORLNTD
C3BB_BACTU GTGISVVGQILGVVGFPGYGGALVS--FYTNLLNTINFG--EPLKAFMQ
60 70 80 90 100 110 120
```

```
cry2ab2_820. TLARVNAELTGLQANVEEFNRQVDNFPNRRNAVPLSITSSVNTMOQLFL-----N
C3BB_BACTU AKSKALAEQLQONNFEDYV---NALNSWKKT-PLSLRSKRQSDRIELFSQAESHFRN
130 140 150 160 170 180
cry2ab2_820. RLQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWGMGISAATLRTYRDLKNTYRDI
C3BB_BACTU SMPFAVSGFEVLFPTYQAANTHLLLLKDAQVFGWEGYSSSEDVAEFYHRLQLKLTQCY
170 180 190 200 210 220 230 240
cry2ab2_820. SNYCINTYQSAFKGLNTRLHDML---EFTYMFNLNVFEVSIWLSFKYQSLVSSGANL
C3BB_BACTU TDHCNVNWNVGLNGLRGSTDYDAWVKENREREMTLTVDLIVLFPFYDIR--LYSKGVKT
230 240 250 260 270 280 290
cry2ab2_820. YASG---SGPOQTOSTQDWPFLYSLFQ-VNSNYVLNFGSGARLSNTF-PNIVGLPGS-
C3BB_BACTU ELTRDIFTDPIPSLNTLQYCGPTFLSIENSIRKPHLFDYQLQIEFHTRLQPGYFGKDSFN
300 310 320 330 340 350
cry2ab2_820. --TTHALLAARVNYSGISS---GDIGASFPNQ-NFNCSTFLPLLPFFVRSLWDSGSD
C3BB_BACTU YWSGNTVETRPSIGSSKTTITSPFYGDKSTEPVQKLSFDGQKVRTTANTDVAAM-PNGKV
360 370 380 390 400 410
cry2ab2_820. REGVATV-TNMQTESFETTLGLRSGAFTARGNSYFPDPIRNSGVPLVVRNEDLRPP
C3BB_BACTU YLGVTKVDSQYDDQKNETS---TOTYDSKENNGHVSQAQ--DSIDLPEPTTDEPLEKA
390 400 410 420 430 440 450 460 470
cry2ab2_820. LHYNEIRNTASPSGTPGGAAYMVSVHNNKNNI-HAVHENGSMIHLAPNDYTGFTISPIH
C3BB_BACTU --YSHOLNYA-----ECFLM--QDRRGTPFFTWTRSVDFNTIDAEEKITQLPVP
450 460 470 480 490 500 510
cry2ab2_820. ATOVNNQTESFETTLGLRSGAFTARGNSYFPDPIRNSGVPLVVRNEDLRPP
C3BB_BACTU KAYALSSGASIT-EGPGFTGGLNLLFLKSSNSIAKFKVTTLNSAALLQRYRVRIRYASTTN
510 520 530 540 550 560 570
cry2ab2_820. STIRVTINGRVYTAIVNTTNDGVNDNGARFSDINIGNVASSNDVPLDINVLNSG
C3BB_BACTU LRLFVQNSNDPLVIYIKTMKNKDDLLTYQTFDLATNSNMFGSGDKNELIIGAESFVSN
560 570 580 590 600 610 620 630
cry2ab2_820.pcp
TXN5:Q45745
Description: Q45745 bacillus thuringiensis. delta-endotoxin. 6/2001
Accession/ID: Q45745
ID Q45745 PRELIMINARY; PRT; 1144 AA.
AC Q45745;
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DT 01-NOV-1996 (MEMEL:01, Created)

SCORES Initl: 85 Initn: 216 Opt: 273 z-score: 285.7 E(): 5.2e-10
>TXNS:Q45745
Initn: 216 Initl: 85 Opt: 273 z-score: 285.7 expect(): 5.2e-10
Smith-Waterman score: 314; 22.7% identity in 532 aa overlap
(57-563:51-549)

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
Q45745 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. NGSNLYLVRVSSIGN--STIRVTINGRVVYATNVNTITNDGVNDGARFSDINIGNVVA
Q45745 PGFTGDIILRRGTGTRVTRITAPLQRYVRIRFRFASTINLFIGIRVGQVQVYDF
530 540 550 560 570 580

cry2ab2_820.pcp
TXNS:X75019_1

Description: X75019 Bacillus thuringiensis B.thuringiensis cryIX gene for
delta-endotoxin. 4/
Accession/ID: X75019
=====General comments=====

LOCUS X75019_1 [BTRCRIX]
DEFINITION B.thuringiensis cryIX gene for delta-endotoxin.
SCORES Initl: 85 Initn: 216 Opt: 273 z-score: 285.7 E(): 5.2e-10
>TXNS:X75019_1
Initn: 216 Initl: 85 Opt: 273 z-score: 285.7 expect(): 5.2e-10
Smith-Waterman score: 314; 22.7% identity in 532 aa overlap
(57-563:51-549)

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PFSQHSKSLDVTQKWEKNNHSLDIPVIGTVASFLLKVGSLVGRKILSELNLI
X75019_1 KYLKMSEGDIYDSYINPGNVRTGLQTDIDIVAVVVGALGPGVGGILTG--FLSTLFGFL
30 40 50 60 70 80

cry2ab2_820. PDYFIRNLSGVPLVWNEEDLRPLHYNEIRNIASPSGTFPGGARAYWVSHNRKNNIHAVH 430 440 450 460 470 480
X75019_1 P-----GGYSVTORNALTCEQINSIDELPSLODFEIRSRSHLSHITSYLRHLV 430 440 450 460 470
cry2ab2_820. ENGSMIHLAPNDYTGFTISPIHATQVNNQTRFISEKFGNQGSRLRFQNNNTIARYTLRG 490 500 510 520 530 540
X75019_1 TIDGI-----NIYSGNLPTVYVWTHRDVLTNTITADRTITQLPLVKSFEIPAGTI--VVRG 480 490 500 510 520
cry2ab2_820. NGNSNLYLRVSSIGN-STIRVTINGRVYTATNVNTINNDGVNDNGARFSDINIGNVA 550 560 570 580 590 600
X75019_1 PGFTGGDLRTAGVGTFGTIRVTITAPLTQRYIRFRFASITNLFIFIGIRVGDQVNFDF 530 540 550 560 570 580
cry2ab2_820.pcp
TXN5:U31633_1
Description: U31633 Bacillus thuringiensis Bacillus thuringiensis
coelepteran-toxic protein (cry3Bb2) gene, . . .
Accession/ID: U31633
LOCUS U31633.1 (BTU31633)
DEFINITION Bacillus thuringiensis coleopteran-toxic protein (cry3Bb2) gene, . . .
SCORES Init1: 154 Initn: 154 Opt: 268 Z-score: 285.0 E(): 5.8e-10
>>TXN5:U31633_1
Initn: 154 Init1: 154 Opt: 268 Z-score: 285.0 expect(): 5.8e-10
Smith-Waterman score: 276; 23.1% identity in 295 aa overlap
(83-360:97-381)
cry2ab2_820. YLDPVIGTVASFLKKVGLVGRILSELNLIFFPSGSTNLMDQILRETEKFLNRLNTD 60 70 80 90 100 110
U31633_1 GTGISVQCILGVGVFPFAGALTSPYQSFLDTIWPDSA-DPWKAFMAQVEVLIDKXIEY 70 80 90 100 110
cry2ab2_820. TLARVNAELTGLQANVEEFNRQVDFNPNFNAVPLSITS--SVNTMQQLF-----N 120 130 140 150 160
U31633_1 AKSKALAELOQLNNFEDVY---NALNSWKT-PLSLRSKSQDRIRLFSQAESHFRN 130 140 150 160 170 180
cry2ab2_820. RLDPQFMQGVQLLLFLFAQAANLHLSFIRVILNADWGISAAATLRTYRLKNTDY 170 180 190 200 210 220
U31633_1 SMPSPAVSKFEVLFLPTFYAQAANTHLLLDKDAQVFGGEWGYSSDVAEFYHRQLKLTQY 190 200 210 220 230 240
cry2ab2_820. SNYCINTYQSAFKGLNRLHDM-----EFRTYMLNVEFVSWLSFKYQSLVSSGANL 230 240 250 260 270
U31633_1 TDHCVNWNVGLNGLRGSGTYDAWVFNFRFEMTLTLDVLVILFFYDVR--LYSKGVKT 250 260 270 280 290
cry2ab2_820. YASG---SGPQQTQSFTSQDWPFLYSLFQ-VNSNYLVNGFSGARLSTFPNIVGLPGSTT 280 290 300 310 320 330

U31633_1 ELTRDIFTPIFSLNTLQEXGPTFLSGIENSIRKPHLPDYLGQIEFHTRLP--GYSGKDS 300 310 320 330 340 350
cry2ab2_820. THALLAARVNYSGGSSGDICAGFPNQFNCSITFLPLLPFFVRSWLDGSDREGVAIVT 340 350 360 370 380 390
U31633_1 FNYWSGNYVETRPSIGSKSITITSPFYGDKSTPEPVQKLSFGDGKYRTIANTDVAAMPNGK 360 370 380 390 400 410
cry2ab2_820.pcp
TXN5:U04366_1
Description: U04366 Bacillus thuringiensis Bacillus thuringiensis japonensis
Buibui CryIII de
Accession/ID: U04366
LOCUS U04366.1 (BTU04366)
DEFINITION Bacillus thuringiensis japonensis Buibui CryIII delta-endotoxin . . .
SCORES Init1: 152 Initn: 152 Opt: 263 Z-score: 275.0 E(): 2.1e-09
>>TXN5:U04366_1
Initn: 152 Init1: 152 Opt: 263 Z-score: 275.0 expect(): 2.1e-09
Smith-Waterman score: 277; 22.7% identity in 613 aa overlap
(56-632:87-659)
cry2ab2_820. DPFSFQHKSLDVTQKEMTKNNHSLYLDPIVGTVASFLKKVGLVGRILSELNLI 30 40 50 60 70 80
U04366_1 SRNPGTFISAQDAVGTGIDIVSYIISGLGIPVIGEVFSIL-----GSLIG-----LL 60 70 80 90 100
cry2ab2_820. FPGSGTNLMQDILRETEKFLNRLNTDILARVNAELTGLQANVEEFNRQVDFNPL-NPNRN 90 100 110 120 130 140
U04366_1 WPSNNENVMQIFMNRVEELIDQKILDSVRSRAIALANSRIAIVEYIYQNALDWRKNPHST 110 120 130 140 150 160
cry2ab2_820. AVPLSITSSVNTMQQLFNRLPQFMQGVQLLLFLFAQAANLHLSFIRVILNADWGI 150 160 170 180 190 200
U04366_1 RSAALVKERFGNAEAILRTNMGFSFSQNTYETPLPFTYAQAASLHLVMDRVDIYKGEWY 170 180 190 200 210 220
cry2ab2_820. SAATLRTYRLKNTDYRNSYCNITYQSFA---KGLNTRLH-DMLEFRTYMLNVEFYV 210 220 230 240 250 260
U04366_1 PQNDILDFYKEQVSTIARYSDHCVQWYNAGLNKLRGTGAKOWDYNRFRFNMNVWLDLV 230 240 250 260 270 280
cry2ab2_820. SIMSLEFKYQSLVSSGANL-----YASGSGPQQT-QSFTSQDWPFLYSLFQVNSNYLVNGF 270 280 290 300 310
U04366_1 ALPPNYDARIYPLETNAELTREIFTDPVGSYVYGOSSTLISW---YDMIPA---ALPSF 290 300 310 320 330
cry2ab2_820. SGARLNTF--PNIVGLPGSTTHALL-----AARVNYSGG--ISSGDIAGFPNQFNFC 320 330 340 350 360
U04366_1 S--TLNELLRKDPDFLLQELRIEYFRQNTIEYNTWYWGQRLTSLYIYVGSFNNKYSV 340 350 360 370 380 390
370 380 390 400 410 420

CRY2ab2_820. STFLRLTLPTKVRSLDSDREGVATVNMOTSPETTLGLRSGAFTARGNSNYF--P
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. DVF--PNI-SCGELVVRN-EDLRRLPRLNRIEIRNIASPSGTGGGARAAMVSVHN--RK
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. NNIHAVHENGSMIHLAPNDVNTGNTISPIKATQVNMOTRIFCEKNGQSDSLRPEQNNT
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. NFIYATKISQIPINKASRT--SGGAVNMFQGLYAGGATMKLSGS--GQVNLRLVATDA--
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. ARYLTRNGNSNLYLRVSS--IGNSTI--RVTLNGRVVATVNTTITNDGVNDNDRF
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. SDINIGNV-VASSNSDVLDTNLSGT--QFDLMNMLVPTNISPLY
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. AVAESGPNLIGSGSRTFDISITKEAGANLYIDRIEFIPVWTLFEAEEDLDVAKKAN
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. GLFTNEKDALOTSVTDYQVNOAANLIECLSDLEYNEKRMMLDVAKEAKRLVQARNLQD
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. pep
TXNS:C8CA_BACTP
Description: Q45706 bacillus thuringiensis (subsp. japonensis). pesticidal
crystal protein c
Accession/ID: Q45706
ID C8CA_BACTP STANDARD; PRT: 1160 AA.
AC Q45706; . . .
=====General comments=====

CRY2ab2_820. DPFPSFOHKSLLDTQKWEKTKNNLSLYLDPIVGTVAFLKKVGVSGVKRILSELRLNI
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. PFGSGTNLMQDILRETEKFLNQLNTDLARVNAELTGLQANVEEENROVDNFL-NPNRN
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. WPNENNVMQIPFMRVVELIDQKILDSVRSRAIADLANSRIAYEYQNALEDWRKNPHST
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. AVPLSTSSVNTMQQLFNRLPQFMQGYQLLLFLFAQAANLHLSFIRDVLNDEWI
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

C8CA_BACTP RSAALVKEKREAGNAEAILRTNMGFSQTNVETPLLETYAQAASLHLLVMRDVQIYKREWG
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. SAAATLRYDYLKNTROYSNVCINTYOSAF--KGLATRLH-DWLEERTYMEINUYEVV
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. PONDIDLYEKEQVSYIARYSDHCQVWYNAGLNKRGTKAKOWVDYNNFRREMNMVLDLV
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. SIMSLFKYQSLLVSSGANL---VASSGSGPQOT--QSFTSQDMPELYSLFQVNSNYVNLGF
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. ALFPNDARYPLETNAELTREIFTPDVGSYVTGOSSTLSW---YDMIPA---ALPSF
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. SGARLSNTF--PNIVGLPGSTTTTHALL-----AARVNYSGG--ISSGDIGASPFNFNFC
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. S--TLENLKRKDPFLLQEIEMTYTSFRQNGIIEYNYWGGORLTLIYIGSSFNYSYGV
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. STEFLPPLLTFFVRSMIDSDREGVATVNTWOTESPETTLGLRSGAFTARGNSNYF--P
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. LAGREDII-P-----VGQNDIYRVVWYIIGRYTNSL---LGVNPTVYFSNNTQKYSKP
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. DVF---IRNT--SGVPLVVRN--EDLRFLHYNEIRNIASPSGTGGGARAAMVSVHN---RK
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. KQAGSKTKTIDSGEELTYENQSYSHRVSYITSEIKSTGGTGLGVVPIFGWTHSSASRN
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. ARYLTRNGNSNLYLRVSS--IGNSTI--RVTLNGRVVATVNTTITNDGVNDNDRF
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. WFIYAKISQIPINKASRT--SGGAVNMFQGLYAGGATMKLSGS--GQVNLRLVATDA--
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. AVAESGPNLIGSGSRTFDISITKEAGANLYIDRIEFIPVWTLFEAEEDLDVAKKAN
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. GLFTNEKDALOTSVTDYQVNOAANLIECLSDLEYNEKRMMLDVAKEAKRLVQARNLQD
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. pep
TXNS:AF056933_1
Description: AF056933 Bacillus thuringiensis strain c
crystal protei
Accession/ID: AF056933
=====General comments=====

CRY2ab2_820. PFGSGTNLMQDILRETEKFLNQLNTDLARVNAELTGLQANVEEENROVDNFL-NPNRN
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. WPNENNVMQIPFMRVVELIDQKILDSVRSRAIADLANSRIAYEYQNALEDWRKNPHST
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
CRY2ab2_820. AVPLSTSSVNTMQQLFNRLPQFMQGYQLLLFLFAQAANLHLSFIRDVLNDEWI
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

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cry2ab2_820. TARTYLRGN---GNSWNLVLRVSIGNSIRTVINGRVYTAIVNTTTNDGNDGNGARF
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
AF056933_1 FGHVRVNIINPPFAQRYRVRMSYASTDLPQHTSINGKAINQGNFSATMNR-GEDLDYKTF
550 560 570 580 590 600

cry2ab2_820. SDINIGNVVASNSDVPDLDINV---TLNSGTDFLMLNTLPTNISPLY
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
AF056933_1 R-TVGFTTFPSFSDVQSFTTIGAWNFSNGNEVIGRTEFPVFTVEAYEYDFEKAQEKV
610 620 630 640 650 660

AF056933_1 TALFTSTNPRGLKTDVKQYHDQDVSNLVESSLDELVDLDEKRELFYKYAKQAHIERNM
670 680 690 700 710

cry2ab2_820.pgp
TXNS:CLIC_BACTU

Description: O87404 bacillus thuringiensis. pesticidal crystal protein cryIc
(insecticidal)
Accession/ID: O87404
=====General comments=====
ID CLIC_BACTU STANDARD; PRT; 719 AA.
AC O87404; . . .

SCORES Initl: 185 Initn: 247 Opt: 259 z-score: 274.6 E(): 2.2e-09
>>TXNS:CLIC_BACTU
Initn: 247 Initl: 185 opt: 259 Z-score: 274.6 expect(): 2.2e-09
Smith-Waterman score: 273; 21.3% identity in 616 aa overlap
(57-634:70-646)

cry2ab2_820. PPSQHKSLDTVQKEWTEKMKNNHSLYLDPIVGTVASFLKKVYSGKRLSFLNRLIF
30 40 50 60 70 80
CLIC_BACTU EDYLRMSEHSIDPFSVASTTGTGTGAGIKLGTGVFPFGQASLYS-FILGEL---W
40 50 60 70 80 90

cry2ab2_820. PSGSTNLMMQILRETEKFLNQRNTDTLARVNAELTGLQANVFEFNQVDNFINRNNAV
90 100 110 120 130 140
CLIC_BACTU PKGKSO-WEIFMEHVEALINRKISTYARNKALTDLKGDLALAVVHESLSSWGNNNTR
100 110 120 130 140 150

cry2ab2_820. PLSIT-SSVNTMQQLFNRLPQFMQMGYQLLLPLFAQANLHLSFTIRDVILNADWEGIS
150 160 170 180 190 200
CLIC_BACTU ARSVVKNQYIALELMPVQKLPSPAVSGEEVPLLPPIYAQANLHLLLRDASIFEKNGGLS
160 170 180 190 200 210

cry2ab2_820. RAATLRTYRDVLYKNYEDSYNYCI---NTYQSAPKGNTR-LHDMLEPRTYMLNVEPYS
210 220 230 240 250 260
CLIC_BACTU ASESTFYNRQVERTRDYSYHCVKWNNTGLNNLRATNGOSWVRVYQPKDIEMLVDLVR
220 230 240 250 260 270

cry2ab2_820. TWSLIFYKQSLVSSGANL---YASGSGP-QQTSQFSDQMPFLYSLFQVNSVNLNGFS
270 280 290 300 310
CLIC_BACTU VFPSPVDILVPIKTTSQLTRVYTDALGTVDPPQALRSITW---YN---NNAPSFAIE
280 290 300 310 320

cry2ab2_820. GARLSTNFFNIVGLPGSTTTALLA-----ARVNYSGG---TSSGDIG-APFPNQNFNCST
320 330 340 350 360

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Description: L32020 Bacillus thuringiensis Bacillus thuringiensis crystal protein (cryI Ets)
Accession/ID: L32020
LOCUS L32020.1 [BACCRYIE]
DEFINITION Bacillus thuringiensis crystal protein (cryI Ets) gene, complete . . .
=====
General comments=====

SCORES Initl: 140 Initn: 140 Opt: 263 Z-score: 274.5 E(): 2.2e-09
initn: 140 initl: 140 opt: 263 Z-score: 274.5 expect(): 2.2e-09
Smith-Waterman score: 287; 21.1% identity in 611 aa overlap
(56-634;73-643)

cry2ab2_820. DPFSQHKSLDTVQKEMTKNNHSLYLDPIVGTVASFLKKVGLGKRISELRLNI
L32020_1 EVNIDPFVASTVQTGINIAGRIILGLVGPAGQASFY----SFLVGE-----L
30 40 50 60 70 80

cry2ab2_820. FPGSTNLMODILRETEKFLNRLNTDTLARVNAELTGLQANVEEFNRQVDNLPNRNA
L32020_1 WPSGR-DPWEIFLHVQLRQVQVNTNTAIALRGLGRGYSYQQALDTLNRDA
90 100 110 120 130 140

cry2ab2_820. VPLSITSSVNTMOQL-FLNLPQFQMOGYQLLLPLFAQANLHLSFIRDVILNADWGI
L32020_1 RRSIILERYVALEDITTAIPLRIRNEEVPLMVYAQAANLHLLRLDASLFGSEGM
150 160 170 180 190 200

cry2ab2_820. SAATLRDYRLKNYTRDYSNYCINTYQSAFKGL-NTRLHDML---EFTYMFANVFEYV
L32020_1 ASSDVNOYQEQIRYITEYSNHCQVYNTGLNLRGTNAESWLRYNQFRDITLGVLDLV
210 220 230 240 250 260

cry2ab2_820. SIWSLFKYQSLVSSGANL-----YASGGPQQTQS-FTSQDWPFLLYSFLQVNSYVLNGF
L32020_1 ALFFSYDTRTYPIINTSAQLTREIYTDPIGRNAPSGFASIN-----FNNNAP-----SF
270 280 290 300 310

cry2ab2_820. SGARLSNTF--PNTVGLPGSTTTHALLA-----ARVNSGG--ISSGDIGAS--PFQCNF
L32020_1 SALE-AAIFRPHLLDPFEOGLTIYSASSEWSSTOHMYWVGHRLNFRPIGLGINTSTQGL
320 330 340 350 360 370

cry2ab2_820. NCSTFLPFLTPFV-----RSLDGSREGVATVN--WQTESFETTLGRSGAFTARG
L32020_1 TWTISNPVTIQTFRDVRVATESNAGTILFTTPVNGVPWAFNF-----INPQNIYERG
370 380 390 400 410 420 430

cry2ab2_820. NSNYFDYFIRNISGVLVVRNEDLRPLHNEYIRNIAISPGTGGARAYMVSVNRNN
L32020_1 ATTYQPY-----QGVGIQFDSFETELPPTETPRNYESYSHLSHI--GLIIGNTLRAPV
440 450 460 470 480

cry2ab2_820. IHAVHNGSMIH-LAPNDYTGFTISPIHATQNNQTRTFISERKFNQGSLLRFEQNNTTA
480 490 500 510 520 530

L32020_1 YSWHRSADTNTIGNRIITQPL--VKALNLSGVTVVGGPFTG-GDILRTRNTGTG
490 500 510 520 530 540

cry2ab2_820. RYTLRGN--GNSYNLYLRVSSIGNSRIVRTINGRTATVNTTINNDGVNDGNGARFSD
540 550 560 570 580 590

L32020_1 DIRLNINPLSQRYRIRYASTTDLOFFTRINGRTVIGNFSRTMNR-GDNLEYRSFRT
550 560 570 580 590 600

cry2ab2_820. INIGNVASSNSDPLDINVLNLSGTQFDLMNIMLVPTNISPLY
600 610 620 630

L32020_1 AGFSTPFNLAQSTFTLGAQSFNSQEVYIDRVFVPAEVIPEAEYDLERAQKAVNALFT
610 620 630 640 650 660

L32020_1 STNPRRLKTDVTDYHIDOVSNWVACLDEFCLDEKHELFEKVKYAKSLSDERNLLQDPNF
670 680 690 700 710 720

cry2ab2_820.pap
TXNS:C1BD_BACTZ
Description: Q9Zaz5 bacillus thuringiensis (subsp. wuhanensis). pesticidal
crystal protein c
Accession/ID: Q9ZAZ5
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General comments=====

ID C1BD_BACTZ STANDARD; PRT; 1231 AA.
AC Q9ZAZ5; . . .

SCORES Initl: 140 Initn: 164 Opt: 263 Z-score: 274.5 E(): 2.2e-09
>TXNS:C1BD_BACTZ
initn: 164 initl: 140 opt: 263 Z-score: 274.5 expect(): 2.2e-09
Smith-Waterman score: 318; 23.5% identity in 622 aa overlap
(56-623;73-652)

cry2ab2_820. DPFSQHKSLDTVQKEMTKNNHSLYLDPIVGTVASFLKKVGLGKRISELRLNI
C1BD_BACTZ EGNINPLVASTVQTGINIAGRIILGLVGPAGQASFY----SFLVGE-----L
50 60 70 80

cry2ab2_820. FPGSTNLMODILRETEKFLNRLNTDTLARVNAELTGLQANVEEFNRQVDNLPNRNA
C1BD_BACTZ WPSGR-DPWEIFLHVQLRQVQVNTNTAIALRGLGRGYSYQQALDTLNRDA
90 100 110 120 130 140

cry2ab2_820. VPLSITSSVNTMOQL-FLNLPQFQMOGYQLLLPLFAQANLHLSFIRDVILNADWGI
C1BD_BACTZ RRSIILERYVALEDITTAIPLRIRNEEVPLMVYAQAANLHLLRLDASLFGSEGM
150 160 170 180 190 200

cry2ab2_820. SAATLRDYRLKNYTRDYSNYCINTYQSAFKGL-NTRLHDML---EFTYMFANVFEYV
C1BD_BACTZ ASSDVNOYQEQIRYITEYSNHCQVYNTGLNLRGTNAESWLRYNQFRDITLGVLDLV
210 220 230 240 250 260

cry2ab2_820. SIWSLFKYQSLVSSGANL-----YASGGPQQTQS-FTSQDW-----
270 280 290

CRY2ab2_820. ALPFDNDTRVNTSAQLTREIYTDPIGRNAPSGFAGSTNFWNNAPSFSAIEAIFRP
CIBC_BACTM 270 280 290 300 310 320
cry2ab2_820. PLPLGLDQNSNVV---NGFSGARLSNTFPNIVGLPGSTTHALLA-ARVN-
CIBC_BACTM 310 320 330 340
CRY2ab2_820. PHLDLFFQTLTIYASRWSSSTOHNVVSHRL-NFRP--IGTUNTSTQGLNNTSINP
CIBC_BACTM 330 340 350 360 370 380
CRY2ab2_820. YSGGSSGDIAGSPENONFCSTFPLALVDFVR-SALDSGSDREGVATVNMOTESFET
CIBC_BACTM 350 360 370 380 390 400
CRY2ab2_820. VTLOFTSRDVRRTESNAGNLTNTVNSUPWAFNFINPONLYRGATTYSQPYQG--V
CIBC_BACTM 390 400 410 420 430 440
CRY2ab2_820. TLGRLSGAFTAGNSYFPDY--FIRNISVPLDVYRNEDLAPLHYNEIRNARSGTPG
CIBC_BACTM 410 420 430 440 450 460
CRY2ab2_820. GIQLPDSFETLPPETTERPNYESYSHRLSHIGLIGNT-LRAPV-YSYTHRSADRINTIG
CIBC_BACTM 450 460 470 480 490 500
CRY2ab2_820. GARAYWV-SVHNKNNIHAVHENGSMIHLAPNDYTGFTSPIHARQVNMOTETNSKFG
CIBC_BACTM 470 480 490 500 510 520
CRY2ab2_820. PNRITQIPAVAGR-----FLFNGVIS-GPG-FIGGDVRLNRNNGNINRGKIEVP-
CIBC_BACTM 510 520 530 540 550
CRY2ab2_820. NOGDSLRFQEQNTIARYTLRGNGNSY-NLYLRVSSIGNSTIRVTINGRVYATVNTVITIN
CIBC_BACTM 530 540 550 560 570 580
CRY2ab2_820. ----IQP--TSSTAYRVVRVYASVTSIELNVN-LGNSSIFT--NLPATAASLDNLQS
CIBC_BACTM 560 570 580 590 600
CRY2ab2_820. ND-GVNDNGARFSDINIGVVA-----SSNSDVPLD----INVTLSNGTQFOLMMIMLVPT
CIBC_BACTM 590 600 610 620 630
CRY2ab2_820. GDFGVETNNAFTSAT-GNIVGARNFSAEVIIDREFEIPVTATFEAYDLERAQKAVN
CIBC_BACTM 610 620 630 640 650 660
CRY2ab2_820. NISPLY
CIBC_BACTM 670 680 690 700 710 720
CRY2ab2_820. ALFTSTNPRRLKTDVTDYHIDQVSNWVACLDFCLDEKRELFEKVYAKRLSDERNLLQ
CIBC_BACTM 670 680 690 700 710 720
CRY2ab2_820. pep
TXNS: CIBC_BACTM
Description: Q45774 bacillus thuringiensis (subsp. morrisoni). pesticidal
crystal protein cr
Accession/ID: Q45774
ID CIBC_BACTM STANDARD; PRT: 1233 AA.
AC Q45774; ..
=====General comments=====

SCORES Init1: 140 Initn: 140 Opt: 263 Z-score: 274.5 E(): 2.2e-09
>TXNS: CIBC_BACTM (1233 aa)
Initn: 140 Init1: 140 Opt: 263 Z-score: 274.5 expect(): 2.2e-09
Smith-Waterman score: 287; 21.1% identity in 611 aa overlap
(56-634:73-643)

CRY2ab2_820. DPFSQHKSLDQVQKWEWKNNHSLYLDPIVGTVASFLKKVGLVGLKRLSELNLI
CIBC_BACTM 50 60 70 80
CRY2ab2_820. EVNNIDPFVSASTVQTGINIAGRIILGVLPFAGOLASFY----SPLVGE-----L
CIBC_BACTM 90 100 110 120 130 140
CRY2ab2_820. FPGSNTLMQDLIRETEKFNQRLNQLTDTLVARVNAELTGLQANVEEFNRQVDNLPNRNA
CIBC_BACTM 140 150 160 170 180 190
CRY2ab2_820. WPSGR-DPWEIFLEHVQLRQVQVNTENTTAIRLEGLRGVRSYQQALETWLDNRDA
CIBC_BACTM 190 200 210 220 230 240
CRY2ab2_820. VPLSITSSVNTMQQL-FLNRLPOFOMQGYQLLLPLPAQANLHLSFIRDVILNADWGI
CIBC_BACTM 210 220 230 240 250 260
CRY2ab2_820. RSRSIILERYVALELDITTAIPLFRINNEVEVPLLVYAAQANLHLLLRDASLFGSEWGM
CIBC_BACTM 260 270 280 290 300 310
CRY2ab2_820. SAATLRTYDLYKNYTRDYSNYCINTYQSAFKGL-NTRLHDML---EFRTYMLNVFEYV
CIBC_BACTM 310 320 330 340 350 360
CRY2ab2_820. ASSDVNQYVQEOIRYTEYSNHCVQWYNTGLANLRGTNAESWLRYNQFRDLTLGLVLDLV
CIBC_BACTM 360 370 380 390 400 410
CRY2ab2_820. SIMSLFKYQSLLVSSGANL-----YASGSGPQIQS-FTSQDWPFYLSLQVNSNVUNLGF
CIBC_BACTM 410 420 430 440 450 460
CRY2ab2_820. ALFPYSYDTRTYPINTSAQLTREIYTDPIGRNAPSGFAGSTN-----FNNAP----SF
CIBC_BACTM 460 470 480 490 500 510
CRY2ab2_820. AGGALNTF--PNIVGLPGSTTHALLA-----ARVNYSGG--ISSGDIGAS--PNNQNF
CIBC_BACTM 510 520 530 540 550 560
CRY2ab2_820. NCSTFFLPLTLPFV---SSWLDGSDREGVATVNT--MQTESFETTLGLRSGAFTARG
CIBC_BACTM 560 570 580 590 600 610
CRY2ab2_820. TNNISNPVTLQFIRRDYKRESNAGNLTFTTPVNGVPMARFNF-----INPQNIYERG
CIBC_BACTM 610 620 630 640 650 660
CRY2ab2_820. NSNFFPDYTRNRCVPLVAKNDLRRPHRDEINIASPSGTPGCGARAYMVSVNRRKN
CIBC_BACTM 660 670 680 690 700 710
CRY2ab2_820. IHAHVHENGSMIH-LAPNDYTGFTSPIHARQVNMOTETNSKFGQGLRFEQNTTIA
CIBC_BACTM 710 720 730 740 750 760
CRY2ab2_820. RYTLRGN---GNSYNLYLRVSSIGNSTIRVTINGRVYATVNTVNTNNDLAPARFSD
CIBC_BACTM 760 770 780 790 800 810
CRY2ab2_820. DIRLNINVLPSQRYVRIRYASTTDLQFFTRINGTIVNIGNFSRNNR-CDNLEYVSEFT
CIBC_BACTM 810 820 830 840 850 860
CRY2ab2_820. INGNVVASNSDVLDDINVTLSNGTQFOLMMIMLVPTNISPLY
CIBC_BACTM 860 870 880 890 900 910
CRY2ab2_820. AGFSTFPNLAQGSFNSQEVNIDRVFVPEAVTFEAEYDLERAQKAVNALFI
CIBC_BACTM 910 920 930 940 950 960

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CIBC_BACTM STNPRRLKTDVTDYHIDQVSNMVACLSDFCLDEKRELFEKVYKAKLSDERNLQDPNF
670 680 690 700 710 720

cry2ab2_820.ppep
TXN5:Z46442_1
Description: Z46442 Bacillus thuringiensis B.thuringiensis cryIbC gene for
delta-endotoxin. 1
Accession/ID: Z46442
LOCUS Z46442.1 [BTMCRYIBC]
DEFINITION B.thuringiensis cryIbC gene for delta-endotoxin.
=====
General comments=====
SCORES Initl: 140 Initn: 140 Opt: 263 Z-score: 274.5 E(): 2.2e-09
>TXN5:Z46442_1
Initn: 140 Initl: 140 opt: 263 Z-score: 274.5 expect(): 2.2e-09
Smith-Waterman score: 287; 21.1% identity in 611 aa overlap
(56-634:73-643)

cry2ab2_820. DPFSQHKSLDVTQKTEWKNNHSLYLDPIVGTVASFLPKKVGSLVGRKILSELNLI
30 40 50 60 70 80
Z46442_1 EVNNIDFVSASTVQTGINIAGRILGLVGLVFPFAGQASFY----SFLVGE-----L
50 60 70 80

cry2ab2_820. PFSGSTNLMDILRETEKFLNQRNLDTTLARVNAELTGLQANVEEFNRQVDFLNPNRVA
90 100 110 120 130 140
Z46442_1 WPSGR-DPWEIFLEHVEQLIRQOVNTNTARLEGIGRYSYQALETWLDNRDA
100 110 120 130 140

cry2ab2_820. VPLSITSSVNTMOQL-FLNRLPQFMQGYQLLLPLFAQAAHLHLSFIRDVILLNADEWGI
150 160 170 180 190 200
Z46442_1 RSRGILIERIVALELDITTAIFLFRINEEVPLMVYAQAANLHLLLRDASLFGSEWG
150 160 170 180 190 200

cry2ab2_820. SAATLRTYRDYLNKYTRDYSNYCINTYQSAFKGL-NTRLHML---EPTYMFLNVFEYV
210 220 230 240 250 260
Z46442_1 ASSDVNQYQEQIRYTEEYNSHCWQYNTGLNLRGTNAESLRYNQPRDLTLGLVLDLV
210 220 230 240 250 260

cry2ab2_820. SIWLSFYQLSLVSSGANL-----YASGSGQQIQTS-FTSQDPFFLYSLFQVNSYVINGF
270 280 290 300 310
Z46442_1 ALFFSYDRTYPTINTSAQLTREIYTDPIGRTPNAPSGFASFNW-----FNNAP-----SF
270 280 290 300 310

cry2ab2_820. SGARLSNTF--PNIVGLPGSTTHALLA-----ARVNSGG--ISSGDIGAS--PNQNF
320 330 340 350 360
Z46442_1 SAIE-AAIFRPHLLDFPEQLTIYSASSRWSSTQHNNYVWGHRLNFRFIGTLNTSQGL
320 330 340 350 360 370

cry2ab2_820. NCSTFLPLLPFPV-----RSLWDSGSDRGVATVTN--WQTESPTTLGRSAGTARG
370 380 390 400 410
Z46442_1 TNNISINPVLQTSRDVYRTESNAGTNILFTTPVNGVPWAEFNF-----INPQNIYERG
380 390 400 410 420 430
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cry2ab2_820. NNNYFDPYFINISGVLVVRNEDLRRLHYNERNIRNIASPSGTPGAGAYVYVNRKNN
420 430 440 450 460 470
Z46442_1 ATTSQPY-----QGVGIQFQSETELPETTERPNYESYSHLSHI-GLIGNTLRAPV
440 450 460 470 480

cry2ab2_820. IHAHVENGSMIH-LAPNDYTGFTSPFIHATOVNNOTRIFISEKFGNQGDSLRFFQNNITTA
480 490 500 510 520 530
Z46442_1 YSWTHRSADRNTIGPNRITQPL--VKALNLHSGVTIVGGPGFTG-GDILLRNTGTGFG
490 500 510 520 530 540

cry2ab2_820. RYTLRGN---GNSYNLYRVSSIGNSTIRVTINGRVYATNVTNTTNNNDGNGARFSD
540 550 560 570 580 590
Z46442_1 DTRLNINPLSQRYVRIRYASTTDLQPFTRINGTIVNIGNFSRTNMR-GONLEYRSFRT
550 560 570 580 590 600

cry2ab2_820. INIGNVASSNSDVLINVTNLNSGTQFDLNMILVPTNISPLY
600 610 620 630
Z46442_1 AGSTPFNPLNAQSTFTLGAQSFNQEVYIDRVFVFAEVTFEAYEDLERAQAKVNAFLT
610 620 630 640 650 660

Z46442_1 STNPRRLKTDVTDYHIDQVSNMVACLSDFCLDEKRELFEKVYKAKLSDERNLQDPNF
670 680 690 700 710 720

cry2ab2_820.ppep
TXN5:C1HA_BACTU
Description: Q45748 bacillus thuringiensis. pesticidal crystal protein cryIha
(insecticidal)
Accession/ID: Q45748
ID C1HA_BACTU STANDARD; PRT; 1172 AA.
AC Q45748;

=====
General comments=====
SCORES Initl: 224 Initn: 255 Opt: 262 Z-score: 273.9 E(): 2.4e-09
>TXN5:C1HA_BACTU
Initn: 255 Initl: 224 opt: 262 Z-score: 273.9 expect(): 2.4e-09
Smith-Waterman score: 262; 23.9% identity in 222 aa overlap
(64-279:47-261)

cry2ab2_820. SLDTQKTEWKNNHSLYLDPIVGTVASFLPKKV--GSLVGKRLSELRLNLPFSGST
40 50 60 70 80 90
C1HA_BACTU SPNEILDIELSRSREQVAISLGLTRFLLESLLFGASFGALFDIINGVIGFD-QW
20 30 40 50 60 70

cry2ab2_820. NLMDILRETEKFLNQRNLDTTLARVNAELTGLQANVEEFNRQVDFN-LNPNRNVPLSI
100 110 120 130 140 150
C1HA_BACTU NLF---LAQIEQLIDQIEAHVRNQAISLEGLGDSVEVYIESLIREWEASPNNEALQODV
80 90 100 110 120 130

cry2ab2_820. TSSVNTMOQLFLNRLPQFMQGYQLLLPLFAQAAHLHLSFIRDVILLNADEWGISAAFLR
160 170 180 190 200 210
C1HA_BACTU RNRFSNTDNALITAPILRQGFPEIPLLSVYQAANLHLSLLRDVAVFQQRWGLDVTVN
140 150 160 170 180 190

220 230 240 250 260
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130      140      150      160      170      180
cry2ab2_820.  TGLQANTVEENRQVDNF-LNENRNAVPLSITSSVNTMQQLFNLRFPQOMOGYQLLILPL
100      110      120      130      140      150
M73254_1      RGLADSEYIIEALREWEANPNNAOLREDVIRFANTDDALITANNFTLTSFEIPLSV
100      110      120      130      140      150

190      200      210      220      230
cry2ab2_820.  FAQAANHLHGFIRDIVLNADWEGISAATRTYRDYLNKNTDRYSNYVCINTYQSAF---KG
200      210      220      230      240
M73254_1      VYQANLHLSLLRDVAVSFGQGWGLDIATVNNHYNRLNLHRYTKHCLDTYQGLENLRG
160      170      180      190      200      210

240      250      260      270      280      290
cry2ab2_820.  LNTRLHMDL-EFRYTMFLNVFVYSIMSLFKYQSLVSSGANLYASGSGPQOQSFTSQD
200      210      220      230      240      250
M73254_1      TNTRQWAFNQFRDLTLVLDIVALFPNYDVRTYPIQTSSQL---TREIYTSVVI-ED
220      230      240      250      260      270

300      310      320      330      340      350
cry2ab2_820.  WPFLYSLFOVNSVNLNGESGARLSNTFPNIVGLPGSTTHALLAARVNYSGG---ISSGD
300      310      320      330      340      350
M73254_1      SP-----VSAN-IPNGFNRAEFGVRPPLHMDFMNLSFVTAETVRSQTVMGWGLSSRN
280      290      300      310      320      330

360      370      380      390      400
cry2ab2_820.  IGAS-----PFNQFNCSITFL-----PPLLTFFVRSMLDGSREGVAT---VTNMQTESF
330      340      350      360      370      380
M73254_1      TAGNINFPYGVNFGGAIWIADEDP--RPFYRTLSDPVVRGFGFPHVVLGLRGVAF
330      340      350      360      370      380

410      420      430      440      450      460
cry2ab2_820.  ETTGLRSGAFTARGNSYFPDYFIRNISGVPVLRNEDLRPL-HYNEIRNIASPSGTP
410      420      430      440      450      460
M73254_1      CQTGNHTRFRNSGTIDSLDEIPQDNGSGAPW---NDYSHVLRNHFVVRWPGGEISGD
390      400      410      420      430      440

470      480      490      500      510      520
cry2ab2_820.  GGRAYVWSVHNKNIHVAHENGSMIHLANDYTGFTISPHATQVNNQTRTFISEKFG
470      480      490      500      510      520
M73254_1      SW-RAPMFSWTHRS---AIPNT-----IDPERITQIPLVKAHTLQ--SGTIVVRGPGFT
440      450      460      470      480      490

530      540      550      560      570
cry2ab2_820.  NOGSLRFEQNNITARYTLRNGN---SYNLXLRVSSIGNSTRIRVTING-RVYATVWNT
530      540      550      560      570
M73254_1      G-GDLRRTSGGFATVINGQLPQRYRARIYASTNLRIYVYVAGEIIPAGQENKT
490      500      510      520      530      540

580      590      600      610      620      630
cry2ab2_820.  ITNNDGVNDGAPSDINIGNVVASSNDVPLDINVLNLSGTQFDLMIMILVPTNISPLY
580      590      600      610      620      630
M73254_1      MDTGDPLTFQSFYATINTAFTFPMSSQSSFTVGAD-TFSSGNEVYIDRFELIPATFEA
550      560      570      580      590      600

610      620      630      640      650      660
M73254_1      EYDLERAQKAVNALFTSINQIGIKTDVTDVHIDQVNLVDCLSDEFCLDKRELSEKVKH
610      620      630      640      650      660

cry2ab2_820.pep
TXN5:Q9S5V8

Description: Q9s5v8 bacillus thuringiensis. btt84a1 crystal protein. 6/2001
Accession/ID: Q9S5V8
=====General comments=====
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ID      Q9S5V8      PRELIMINARY;      PRT;      1180      AA.
AC      Q9S5V8;
DT      01-MAY-2000 (Tremblrel.13, Created)

SCORES      Init1: 128      Initn: 168      Opt: 261      z-score: 272.7      E(): 2.8e-09
>>TXN5:Q9S5V8
initn: 168      init1: 128      opt: 261      z-score: 272.7      expect(): 2.8e-09
Smith-Waterman score: 292;      22.2% identity in 600 aa overlap
(60-634:41-609)

30      40      50      60      70      80
cry2ab2_820.  FQKSLDTVKREWTEWKKNNHSYLDPIVGTVASFLKKYKSLVGRKILSELRLNIPFSG
30      40      50      60      70      80
Q9S5V8      IPYNCLSNPEVEVLGGERIETGVTPTIDISLSTQFLSEF--VEGAGFVLGLVDIIMGIF
20      30      40      50      60      70

90      100      110      120      130      140
cry2ab2_820.  STNLMODILIRETEKELNORLNTDLARVNAELTGL---QANVEEFNRQVDNFLNPNNA
90      100      110      120      130      140
Q9S5V8      GPSQWDAFLVQTEQLINRIEERFARNOAISRLGSLNLYQIYAESFREWEADPTNP---A
70      80      90      100      110      120

150      160      170      180      190      200
cry2ab2_820.  VPLSITSSVNTMQQLFNLRFPQOMOGYQLLPLFAQANLHLSFIRDIVLNADWEGIS
150      160      170      180      190      200
Q9S5V8      LREEMRIQFNDMNSALTATPLFAVQYQVPLLSYVQANLHLSVLRDVSVFGQWGF
130      140      150      160      170      180

210      220      230      240      250
cry2ab2_820.  AALRTYRDYLNKNTDRYSNYVCINTYQSAF---GLNTRLHMDL---EFTYTMFLNVFEY
210      220      230      240      250
Q9S5V8      AATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSR--DWRYNQFRRELTITVLDI
190      200      210      220      230      240

260      270      280      290      300      310
cry2ab2_820.  VSIWSLF---KYQSLLYSS--GANLYASGSGPQOQSFTSQDWPFYLSLFQVNSNYLVNGF
260      270      280      290      300      310
Q9S5V8      VALFSNYDSRRYPRTVSQTRTYTNVPLENFDGSGFRGMAQRIEQNIROPHLMDILN--
250      260      270      280      290      300

320      330      340      350      360
cry2ab2_820.  SGARLNTFPNIVGLPGSTTHALLAARVNSYSGISS---GDIG--ASFPNQNFCSTF
320      330      340      350      360
Q9S5V8      ---RII-IYTDVHRGFNYWGHQITASPGFSGPPEFAPPLFGNAGNAAPPVLYSLIGLGI
310      320      330      340      350      360

370      380      390      400      410      420
cry2ab2_820.  LPPLLTFFVRSW-LDGSDDREGVATVNNQTESFET-TLGLRSGAFTARGNSYFPDYFI
370      380      390      400      410      420
Q9S5V8      FRTLSSPLRYRRIILGSGPNQOEL-FVLDTGTEFSFASLTNLPSTIYRQRTVDSL-DVIP
360      370      380      390      400      410

430      440      450      460      470      480
cry2ab2_820.  RNTSGVPLVRNEDLRPLHYNIRNIASPSGTGCGARAYNVSVHNRKNIHVAHENGSM
430      440      450      460      470      480
Q9S5V8      PQDQSVF--PRAGFSHRLSH---VTMLSQAGAVTTLRAFTFSWQHSRAEFNNIIPSSQI
420      430      440      450      460      470

490      500      510      520      530      540
cry2ab2_820.  --IHLAPNDYTGFTISPHATQVNNQTRTFISEKFGNODSLRFEQNNITARYTLRNGN
490      500      510      520      530      540
Q9S5V8      TQIPLTKSNLSGTSVVKGPGTGGD--ILRRTSPGQISTLRV---NITAPLSQR----
480      490      500      510      520      530
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CICB_BACTG      RTHPLEFDVLLNLTITFDWFSVGRRFWGHVRVISNRIG-GONITSPIYGREANQCPFRPSR
              300    310    320    330    340    350

cry2ab2_820..   NFNCSTFLP---PLLTPFVSRLDSDSGREGVATVMNQTESFTTLRGASGAFTARGNS
              370    380    390    400    410

C1CB_BACTG      TFNGCFVRTLSNPTRERLPQQWPAPPENLRGV-----EGVEFTSLNSTFYVEGRGTV
              360    370    380    390    400    410

              420    430    440    450    460    470

cry2ab2_820..   NYFPDYFIIRNISGLPVVRNEDEURRPLHYNEIRNIASPSTPGARAYMVSVHNKNNIH
              :     :     :     :     :     :
C1CB_BACTG      DSUTELPPEDNSVP--REGYSHRLECHATFQRSGTGPLTTGPVFESWTHRSAIDRNIIY
              410    420    430    440    450    460

              470    480    490    500    510    520

cry2ab2_820..   AVHENGSMIHLAPNDYTGFILSPIHAQTQNNTRTFISEKFQGQSRLFEQWNTRYARTY
              :     :     :     :     :     :
C1CB_BACTG      PDVINQLPKAFNLTSISVTVRGGPTGGDIIRNVNGSVLSM--SLNF-SNTTLQRYR
              470    480    490    500    510    520

              530    540    550    560    570    580    590

cry2ab2_820..   LRGNGSYNLYLRVSSIGNSTRIVTINGRVYATVNVTINNDSG-VNDGARFSDINIG
              :     :     :     :     :     :
C1CB_BACTG      VR-----VRYYAASOTWMVSVTWGSGTGCGFSTWSANGALTSOSFRPAEPFG-
              530    540    550    560    570    580    590

              600    610    620    630

cry2ab2_820..   WVASSNDVPLDNVLNMSGTO-FDLNMIMLVPTNISPLY
              :     :     :     :
C1CB_BACTG      TSAGSOGA--SISISNNVGRQMFHLDRTEFLPVTSTFESEYDLERAQAENVALLTSTNO
              580    590    600    610    620

              630    640    650    660    670    680

C1CB_BACTG      LGLAKTDVVYADQVSNLVCLSDPELCDELSEKKUAKKLSDLERNLLODRNIFRSIN
              630    640    650    660    670    680

cry2ab2_820..   PDP
TXNS:Q45720

Description: Q45720 Bacillus Euringiensis cry(a) (fragment).. 6/2001
Accession/ID: Q45720
ID            PRELIMITARY, (PRJNA: 620 AA).
AC            Q45720
DT            01-NOV-1996 (Tremblrel. 01, created)

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SCORES       Initl: 128   Inithn: 168   Opt: 255   Zscore: 271.5 EBL: 3.2e-09
               >>TXNS:Q45720
             inithn: 168 ini1: 128 opt: 255 z-score: 271.5 expect( ): 3.2e-09
             Smith-Waterman score: 286;   21.8% identity in 840 aa overlap
             (60-634:41-609)

cry2ab2_820.. FOHKSLDITVOKEWTWKNNHSILYLDPIVTGWASFLLKKVKVSGNGRIUSEHEAVIPSG
              90    100    110    120    130    140
Q45720         IPNYCLSNEPVEVLGGERIETGYTFIDISLSITOFFLSEF--VPGAAGVULSNVAITNGK
              20    30    40    50

cry2ab2_820.. STNLMDQILRETKFLQRNLINTDLARVNAELTG----QANYEENRFQVDFLNPNRNA
              :     :     :     :     :     :
Q45720         GPSQWDAFVIQIEOLIKORTEEFARNOAISLEGLSNLYOIVAESGFREWAEPTNP---A
              :     :     :     :     :     :
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LOCUS U43605_1 [BTU43605]
DEFINITION Bacillus thuringiensis cryIA(a) gene, partial cds; . . .

SCORES Init1: 128 Initn: 168 Opt: 255 Z-score: 271.5 E(): 3.2e-09
>>TXN5:U43605_1
initn: 168 init1: 128 opt: 255 Z-score: 271.5 expect(): 3.2e-09
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)

cry2ab2_820. FOHKSLSDTQVKEWTEKKNNHSLYLDPIVTSFVASFLLKKVSLVGRKILSELRLNIPFSG
30 40 50 60 70 80
U43605_1 IPYNCLSNPEVEVLGGERIETGYTPIDISLSTQLLSEF--VPGAGFVLGLAVDIWGIF
20 30 40 50 60
cry2ab2_820. STNLMQDILRETEKFLINQRLNTDITLARVNAELTGL----QANVEFNQRQVDNPLNPNRA
90 100 110 120 130 140
U43605_1 GFSQWDAPLVQIEQLINQRIEEFARNQATSRLEGLSNLYQVAFSPREWEADFTNP---A
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVTMQQLFLNRLPQFOMQGYQLLLPLPAQAANLHLSPIRVILNADWEGIS
150 160 170 180 190 200
U43605_1 LPEEMRIQFNDNNSALTATPILAVQNYQVPLISVVVQAANLHLSVLRVDSVFGQGWGFD
130 140 150 160 170 180
cry2ab2_820. AATIRYRDYLNKRYRDYSNYCINTQSAFK--GLNTRLHDML---EFRTYFMYLNFVEY
210 220 230 240 250
U43605_1 AATINSYNDLTRELIGNYTDYAVRWYNTGLERVWGFDSR--DWRYNQFRRELITLTVIDI
190 200 210 220 230 240
cry2ab2_820. VSIMSLF---KYQSLVSGS-GANLYASGSGPQQTOSTSQDWPLLSLFQVNSVNLVNGP
260 270 280 290 300 310
U43605_1 VALFSNVDSSRYPIRTVSQLTRELYTNFVLENFDSGFRGMAQRINQIRPHLMDLINSI
250 260 270 280 290 300
cry2ab2_820. SCARLSNTFFNIWGLPGSTTTTHALLAARVNYSGISS---GDIG--ASFPNQNFNCSTF
320 330 340 350 360
U43605_1 T-----IYTDVHRGFNVMWSGHQITASPVGFSGPEFAPPLFGNAGNAAPVLVLSLTGLGI
310 320 330 340 350
cry2ab2_820. LPPLLTFFPSW-LDSGDRGVAIVTNWQTESFT-TLIGURSGATFARGNSYPPDYFI
370 380 390 400 410 420
U43605_1 FRTUSSPLXYRRIILGGFNGNQL-FVLDDGTFSFASLTINLPSTIYRQGRTVDSL--DVIP
360 370 380 390 400 410
cry2ab2_820. RNISGFLPVNREDRLRPLHNEYNRTNATPSGTPGGGARVYWSVHNRKNNIHAVHENGSM
430 440 450 460 470 480
U43605_1 PQDMSVP--FRAGFSHRLSH---VTMLSOAAGAVTYLRPTFSQWHSRAEFNIIPSSQI
420 430 440 450 460 470
cry2ab2_820. --IHLPNDYVTGFTSPIHATQVNNQTRTFISEKFGNGQDSLRAFEQNNTIARYLRNGN
490 500 510 520 530 540
U43605_1 TQIPLTKSTNLWASGTSVVKGPGFTGSD--ILRATSPGQISTLRV---NITAPLSR----
480 490 500 510 520

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=====
Accession/ ID: 043003
=====
General comments=====
```

cry2ab2_820. SYNTLVSSIGSTIRVTINGRVVATNTVNTINNDGVNDGARFSDINGNVVASSNS
U43605_1 -YRVRLASTTNLQPHSLDORPINOGNESATMSS- GSNLQSGSFRVGTFTPPNFSNG

cry2ab2_820. DVPLDINV-INSSTQDFLMNIMVPTNISPLY

U43605_1 SSVFTLSAHVPSGNGVVIDRSEFVFAVTFEAWDLSRAQ

cry2ab2_820.pdp
TXNS:CLIFB_BACTM

Description: O66377 bacillus thuringiensis (subsp. morrisoni), pesticidal
crystal protein cr
Accession/ID: O66377
ID CLIFB_BACTM STANDARD; PRT; 1169 AA.
AC O66377; Q9RC19;

SCORES Init1: 189 Initn: 216 Opt: 259 z-score: 270.7 EN: 3.6e-09
>TXNS:CLIFB_BACTM
Initn: 216 Init1: 189 opt: 259 z-score: 270.7 expect(): 3.6e-09
Smith-Waterman score: 330; 22.1% identity in 611 aa overlap
(46-634:26-602)

cry2ab2_820. ICDAYNVAADHPFQHKSLDVTQKEMTKNNHSLYLDPTVGVASFLLKXVGLVGK
CLIFB_BACTM MKNQIQOCVPYCNLSNPEVEILSEERSIGRLPLD-LSLSLRLFLSLSEFVGVG-

cry2ab2_820. RILSELRLIFFSGSTNLMQDILRETEKFNQRLNLTDLARVNAELTGLQANVEEFNRQV
CLIFB_BACTM -VAFGLDLIWGFTTPSEWSFLQLQIEQRIETLERNRAITTLRLGLADSYEVYLEAL

cry2ab2_820. DNFLNPNRVAVPLSTSSVNTMQQLFLNRLPQFMQGYQLLLLELFAQANLHLSFIRD
CLIFB_BACTM REWENPNNAQLREDVIRFANTDDALITANNFTLTSFEIPLSVVYQAAHLHLSLRD

cry2ab2_820. VILNADWGISAAITLRYDKNVTRDYSNICYQSASF--KGLNTRLHML-EPRT
CLIFB_BACTM AVSFGCGWGLDIAVNNHYNLNLHRYTEHCLDYNGLENLRCNTNQWRSRFPQPR

cry2ab2_820. YNFINVPEYYSINSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDMPFLYSLFQVNSNY
CLIFB_BACTM ELTLVLIDIVALFPNDYARAPIQTSSQL---TREIYTSVI-EDSP-----VSAN-

cry2ab2_820. VLNFGSARLNTFFNIVGLPGSTITHALLAARVNVSGG--TSSGDIGASFPNQFNCSIT
CLIFB_BACTM IPNGFNRAEFGRPPHLMDFMNSLFTVTAETVRSQTVMGHVLVSSRNTAGNPFPPIY-GV

cry2ab2_820. FLPLPLT-----PVRSMWLSGSDREGVAT---VTNQTESFETTLGLRSGAFTARG
CLIFB_BACTM FNPQGAIWIADEDPFRPYRLSDPFRVGGGPNPHYVLGRGVGFOQTGTNTRIFRNSG

cry2ab2_820. NSNYFPDYFIRNISGVFLVVRNEDLRPL-HYNEIRNIASPGTGGARAYVSVVNRKN
CLIFB_BACTM TIDSLEIPPODNGSAPW---NDYSHVLNHVTVFRWPEGIAGSDSW-RAPMFSWTHRSA

cry2ab2_820. NIHAVHENGSMHLAPNDYTGFTISPIHATQNNQTRTFISEKFGNQSDSLRFEQNNTTA
CLIFB_BACTM DRINI-----INPNIIIT--QIPAVKAHNLHSGSTVVRGPGFTG-GDLLRRTNTGTFA

cry2ab2_820. --RYTLRGN-GNSYNLXLYRVSSIGNSTIRVTINGRVVATNTVNTINNDGVNDGARFSD
CLIFB_BACTM DIRVNITGLSORVVRIRVASTDLOPFTIRINGTSVNOGNFORTWNRGNLESN-FRT

cry2ab2_820. INIGNVASSNDVPLDINLTNLSGTFQFLMIMLVPTNISPLY
CLIFB_BACTM ASFTSPFSGNAQSTFTLGTQAFSGNOEVYIDRIEFAEVTFEAEESDLERAQKAVNALFT

cry2ab2_820. STSQDEKKNVGTGHIDQVSNLVACLSDDEFCLDEKRELSKVHAKRLSDKKNLLQDPNF
TXNS:Q45749

Description: Q45749 bacillus thuringiensis, crystal protein. 6/2001

Accession/ID: Q45749

ID Q45749

DT 01-NOV-1996 (Trembl et al., 1996)

SCORES Init1: 189 Initn: 216 Opt: 259 z-score: 270.6 E: 3.6e-09

>TXNS:Q45749

Initn: 216 Init1: 189 opt: 259 z-score: 270.6 expect(): 3.6e-09

Smith-Waterman score: 331; 22.1% identity in 612 aa overlap

(46-634:26-602)

cry2ab2_820. ICDAYNVAADHPFQHKSLDVTQKEMTKNNHSLYLDPTVGVASFLLKXVGLVGK

Q45749 MKNQIQOCVPYCNLSNPEVEILSEERSIGRLPLD-LSLSLRLFLSLSEFVGVG-

cry2ab2_820. RILSELRLIFFSGSTNLMQDILRETEKFNQRLNLTDLARVNAELTGLQANVEEFNRQV

Q45749 -VAFGLDLIWGFTTPSEWSFLQLQIEQRIETLERNRAITTLRLGLADSYEVYLEAL

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Accession/ID: Q45718
=====General comments=====
ID C1HB_BACTM STANDARD; PRT; 1155 AA.
AC Q45718;

SCORES Initl: 222 Initn: 247 Opt: 256 z-score: 267.6 E(): 5.4e-09
>>TXN5:C1HB_BACTM
Initn: 247 Initl: 222 opt: 256 Z-score: 267.6 expect(): 5.4e-09
Smith-Waterman score: 256; 21.2% identity in 217 aa overlap
(64-279:46-260)

cry2ab2_820. SLDTVQKEWTEWKNKHSLYLDPIVGTAVSFLLKKVSGSLVKRIILSELNLIFFSGSTNL
40 50 60 70 80
CRY2AB2_820 SLDTVQKEWTEWKNKHSLYLDPIVGTAVSFLLKKVSGSLVKRIILSELNLIFFSGSTNL
C1HB_BACTM KNPKIEMLDIEGISSRSREQVAEISLGLTRFLLESLLPGASFGFGLFDIIMGVIGPD
20 30 40 50 60 70
C1HB_BACTM KNPKIEMLDIEGISSRSREQVAEISLGLTRFLLESLLPGASFGFGLFDIIMGVIGPD

cry2ab2_820. MODILRETEKFLNORLNTDLARVNAELTGLQANVEFNRQDNF-LNPNRNAVPLSITS
100 110 120 130 140 150
CRY2AB2_820 MODILRETEKFLNORLNTDLARVNAELTGLQANVEFNRQDNF-LNPNRNAVPLSITS
C1HB_BACTM WSLFLTQIBQLIDQRIQAHVRNOAISRLGLESDSYVEVIESLREWEASPNNESLQQDVNRN
80 90 100 110 120 130
C1HB_BACTM WSLFLTQIBQLIDQRIQAHVRNOAISRLGLESDSYVEVIESLREWEASPNNESLQQDVNRN

cry2ab2_820. SVNTMQQLFNLNLPQFMQGVQVQLLLPLFAQANLHLSFTRDVLINADRWGISASITRTY
160 170 180 190 200 210
CRY2AB2_820 SVNTMQQLFNLNLPQFMQGVQVQLLLPLFAQANLHLSFTRDVLINADRWGISASITRTY
C1HB_BACTM RFSNTNALITAIPIRLREQGFELPLTVVYQANLHLSLRDVAVYQGRWGLDTATVNNH
140 150 160 170 180 190
C1HB_BACTM RFSNTNALITAIPIRLREQGFELPLTVVYQANLHLSLRDVAVYQGRWGLDTATVNNH

cry2ab2_820. RDYLKAVTRDYSNYCINTYQSAFKGNLRLHDMLEFRTYMLFNVEFVSIWLSFKYQSL
220 230 240 250 260 270
CRY2AB2_820 RDYLKAVTRDYSNYCINTYQSAFKGNLRLHDMLEFRTYMLFNVEFVSIWLSFKYQSL
C1HB_BACTM YNRLINLINITYSDHCAQWFRNGDNGFVGTARYDLDFQREVTISVLDIVALFPNVDIRIYP
200 210 220 230 240 250
C1HB_BACTM YNRLINLINITYSDHCAQWFRNGDNGFVGTARYDLDFQREVTISVLDIVALFPNVDIRIYP

cry2ab2_820. VSSGAILYAGSGPOQTSFTSQDWPLFLYLPQVNSVYLVNGFSGARLSNFTPNPNIIVGLPG
280 290 300 310 320 330
CRY2AB2_820 VSSGAILYAGSGPOQTSFTSQDWPLFLYLPQVNSVYLVNGFSGARLSNFTPNPNIIVGLPG
C1HB_BACTM IQLTSQLTREIYVTSVPAEPGASLNVDLRNLREPHLMDFLTRLVIVITGVQGGIYHWAGHE
260 270 280 290 300 310
C1HB_BACTM IQLTSQLTREIYVTSVPAEPGASLNVDLRNLREPHLMDFLTRLVIVITGVQGGIYHWAGHE

cry2ab2_820.pep
TXN5:U35780_1
Description: U35780 Bacillus thuringiensis Bacillus thuringiensis crystal
toxin gene, complete cds.
Accession/ID: U35780
=====General comments=====
LOCUS U35780_1 [BTU35780]
DEFINITION Bacillus thuringiensis crystal toxin gene, complete cds.

SCORES Initl: 222 Initn: 247 Opt: 256 z-score: 267.6 E(): 5.4e-09
>>TXN5:U35780_1
Initn: 247 Initl: 222 opt: 256 Z-score: 267.6 expect(): 5.4e-09
Smith-Waterman score: 256; 21.2% identity in 217 aa overlap
(64-279:46-260)

cry2ab2_820. SLDTVQKEWTEWKNKHSLYLDPIVGTAVSFLLKKVSGSLVKRIILSELNLIFFSGSTNL
40 50 60 70 80
CRY2AB2_820 SLDTVQKEWTEWKNKHSLYLDPIVGTAVSFLLKKVSGSLVKRIILSELNLIFFSGSTNL
C1HB_BACTM KNPKIEMLDIEGISSRSREQVAEISLGLTRFLLESLLPGASFGFGLFDIIMGVIGPD
20 30 40 50 60 70
C1HB_BACTM KNPKIEMLDIEGISSRSREQVAEISLGLTRFLLESLLPGASFGFGLFDIIMGVIGPD

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Description: Q45718 bacillus thuringiensis (subsp. morrisoni). pesticial crystal protein cr

©01 Prioritization Information

```
cry2ab2_820_1 100 110 120 130 140 150
WSFLQVLEQLDQFQAAHVRNQAISRLQGLGDSYEVIESLREWEASPNNSLQDDVRN
160 170 180 190 200 210
SVNTMQQLFLNRPQVQNGYVQLLPLFAQAANHLSTIRVDVILNADEWGISAAFLRTY
120 130 140 150 160 170 180 190 200 210
RFNTDNALITAIPILRQGFPLPLVYVQANHLSLDADAVFGQRWGLDTATVNNH
140 150 160 170 180 190
cry2ab2_820_1 160 170 180 190 200 210
RDYLKNYTRDYSNYCINTYQSAFKGLNLTLMLEFRKYMFLANVFYVWSKRYQSL
120 130 140 150 160 170 180 190 200 210
YNELINLINTYSDHCAQFNRGDNGVVTARDFSEVTSIVLDIVAEPNYDRTFP
200 210 220 230 240 250
cry2ab2_820_1 280 290 300 310 320 330
VSSGANLYASGSGPQQTQSFTSQDWPFLYSFQVNSNYLVNGSGCANSTFENLGLPG
260 270 280 290 300 310
IQTLQTLREITYTSPVAEPGASLNVDLRLNLRPHLMDFLTRLVITGQGGVYHQAUP
260 270 280 290 300 310
cry2ab2_820.pep
TXNS:Q45736
Description: Q45736 bacillus thuringiensis. insecticidal crystal protein.
6/2001
Accession/ID: Q45736
ID Q45736 PRELIMINARY;
AC Q45736;

SCORES Initl: 128 Initn: 168 Opt: 255 z-score: 266.4 E(): 6.3e-09
>TXNS:Q45736
Initn: 168 Initl: 128 Opt: 255 z-score: 266.4 expect(): 6.3e-09
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)

cry2ab2_820_1 30 40 50 60 70 80
FOHKSLDIVQEWETWKKNNHSLYLDPIVGVASFLLKVGSLVGRKILSELRLIPFSG
100 110 120 130 140
IPYNCLSNPEVLGSGRIETGYTIPDISLSLTQFLLEP--VPGAGFVLGLVDIINGIF
20 30 40 50 60
Q45736

cry2ab2_820_1 90 100 110 120 130 140
STNLMDILRETEKFLNQLRNTDILARVNAELTGL-----QANVEFNQVDFNPNRNA
150 160 170 180 190 200
VPLSITSSVNTMQQLFLNRPQVQNGYVQLLPLFAQAANHLSTIRVDVILNADEWGIS
120 130 140 150 160 170 180 190 200
LREWRIQFNDMNSALTITAILLAVQNYQVPLLSVYQAAHLSLVLDVDSVFGQWGF
130 140 150 160 170 180
cry2ab2_820_1 210 220 230 240 250
AAILRTYDYLKNYTRDYSNYCINTYQSAFK---GLNLRHMDL----EFTYMFANVFY
```

```
Q45736 190 200 210 220 230 240
AATINSRYNDLTRLIGNYTDYAVRWNTGLERVWGPDNR--DWVRYNQFRELTLTLDI
260 270 280 290 300 310
cry2ab2_820_1 VSIWSLF---KYQSLLVSS--GANYASGSGPQQTQSFTSQDWPFLYSFQVNSNYLVNGF
250 260 270 280 290 300
VALFSNYSRRYPRTYVTSQTLREIYTFVLENFDFGFRGMAQRIEQNIQPHLMDILNSI
250 260 270 280 290 300
cry2ab2_820_1 SGARLSNTEFNIVGLPGSTTTTHALLAARVNSGSISS-----GDIG--ASFPNQFNCSFT
320 330 340 350 360
T-----IYDVRHGTFYWSGHQITAGSPGFSGPEFAFPFGNAGNAAPPVVLVSLTGLGI
310 320 330 340 350
cry2ab2_820_1 LPPLLTFFVRSM--LDSGSDREGVATVNMQTESFET--TLGLRSGAFTARGNSNYFPDYFI
370 380 390 400 410 420
FRTLSPLRYRRILGSGPNNOEL--FVLDTGTFEFSASLTNLPSTIYQRTGVDSL--DVIP
360 370 380 390 400 410
cry2ab2_820_1 KNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGAGRAYMVSVHNRKNNIHAVHENGSM
430 440 450 460 470 480
PDNSVP--FRAGFSRLSH---VTMLSQAAGAVYTLRAPTFSMQHRSAEFNNIIPSSOI
420 430 440 450 460 470
Q45736 480 490 500 510 520
TQIPLTSTNLGSGTSVVGKPGFTGGD--LLRRTSPQISILRV---NITAPLSQR----
480 490 500 510 520
cry2ab2_820_1 SYNYFIVSVAGNSRTIRNGRVYTAIVNTINNVDGNDNGARFSDINIGNVASSNS
560 570 580 590 600
LRVRIKASITNLQFHTSLDGRPIINGNPFSAITMSS--GSNLOSGETVGTFTPFNFSG
530 540 550 560 570
cry2ab2_820_1 DVPLDIN--TLASGTQFADAPVPTNLSPLI
610 620 630
Q45736 640 650 660 670 680 690
SSVFILSAHVFNSSNENVIDRIKVFQVITFEAEYDLRPAQKAVNELFTSSNGIGLKTIV
580 590 600 610 620 630
cry2ab2_820.pep
TXNS:Y05663_1
Description: Y05663 Bacillus thuringiensis delta-endotoxin.
Accession/ID: Y05663
LOCUS Y05663.1 [BTRCVBNS3]
DEFINITION B.thuringiensis mRNA for delta-endotoxin.
SCORES Initl: 128 Initn: 168 Opt: 255 z-score: 266.4 E(): 6.3e-09
>TXNS:Y05663_1
Initn: 168 Initl: 128 Opt: 255 z-score: 266.4 expect(): 6.3e-09
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)
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cry2ab2_820_pep
TXN5:Q9RC30

Description: Q9rc30 bacillus thuringiensis (subsp. kurstaki). 135 kda
insecticidal protein. 6
Accession/ID: Q9RC30
=====General comments=====
ID Q9RC30 PRELIMINARY; PRT: 1176 AA.
AC Q9RC30: .

SCORES Init1: 128 Initn: 168 Opt: 255 Z-score: 266.4 E(): 6.3e-09
>>TXN5:Q9RC30
Initn: 168 init1: 128 opt: 255 Z-score: 266.4 expect(): 6.3e-09
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)

cry2ab2_820. FQHSKSLDTQKEMTWKKNHSLYLDPIGVTVASFLKKVGLVGRKILSELRLNIPFSG
30 40 50 60 70 80
Q9RC30 IPYNCLSNPEVEVLGGRTGTGYPIDISLSLTQLLSEF--VFGAGFVLGLVDIIWGIF
20 30 40 50 60

cry2ab2_820. STNLMDQILRETEKFLNQKLNLTDTIARVNAETGL----QANVEEFNRQVDFLNPNRNA
90 100 110 120 130 140
Q9RC30 GPSQMDTFLVQIEQLINQRIEFAFNQASRLGLESLNLYQIYABSPREWEADPTNP--A-
70 80 90 100 110 120

cry2ab2_820. VPLSTSSVTNQQLFLNKLQFQMOQYQLLLLPQAQANLHLSPFIRVDILNADENGIS
150 160 170 180 190 200
Q9RC30 LREENRQFNDMNSALTTPAILLAVQNYQVPLSLVYQAAHLSLVLRDVSFVGQRWGFD
130 140 150 160 170 180

cry2ab2_820. AATLTFRYDYLKNYTRDYSNICYTQSAFK--GLNTRLHML--EPTMYELNVEFY
210 220 230 240 250
Q9RC30 AATINSRYNDLTFLIGNYTDVAVRWYNTGLERWGPDSR--DWRYNQFRRELTITVDI
190 200 210 220 230 240

cry2ab2_820. VSIWMLSF--KYOSLLVSS-GANLYASGSPQQTQSTSDWPLFSLFQVNSVNLVNGF
260 270 280 290 300 310
Q9RC30 VALFSNYSRRYPRTVYSQLTRREIYTPVLENFNFDGSGFGMAQRTEQINRQPHLMDILNSI
250 260 270 280 290 300

cry2ab2_820. SGARLSNFTFNVLGPGSTTTHALAARVNYSGGSS----GDIG--ASGPFQNNNCSTF
320 330 340 350 360
Q9RC30 T-----IYTDVHRGNYWSGQHITASPVFGSGPEFAPFLPGNAGNAAPPAVSLTGLGI
310 320 330 340 350

cry2ab2_820. LPPLLTFFVRSM-LDGSGRDREGVATVNTMQTESFET-TLGRSCAFTARGNSYPPDYFI
370 380 390 400 410 420
Q9RC30 FRTISSPLYPRIILGSGPNQEL-FVLDTGTFESFASLTINLPSTIYHQRTQVDSL-DVIP
360 370 380 390 400 410

cry2ab2_820. RNISGFLVAVNRNEDLRPLFLHYNEIRNTASPSGTGGAAYVYVHNRKNHIAVHENGSM
430 440 450 460 470 480

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cr2ab2_820. VSIWLFYQSLVSSGANL----YAGSGPQQTQSTSDWPFLYSLFQVNSNYVLNGF

Q9AW82 VALFPNYSRTYPIRTVSQLTREIYTNPNVLENFDSFRGSAQGTSSIRSPHLMDLNSI
250 260 270 280 290 300

cry2ab2_820. SGARLSNTFPNIVCLPGSTTTTHAL--LAARVNYSGGISSGDIGASP---FNQNFNCSTF

Q9AM82
TIYRMH--IEDIIIGQGIKKRLLEFGFQQNSLFLYLGKGMQLHPNRLLLNKKVRCIEH
310 320 330 340 350 360

cr2ab2_820. LPPLLTPFVRSWLDGSDREGVATVNWQTESFETILGLRSGAFTARGSNVFPDYFIRN

Q9AW82	370	380	390	400	410
YRPL--YIEDLFKEGINNQQL-SVLDGTGFAYGTSNLPSSAVVRKSGTVDLSLDEIPPQN					

ccry2ab2_820.. 430 440 450 460 470 480
ISGVPLVRNEDLRPLHYNEINIASPSTGGARAYMVSVHNRKNNIHAVHENGSMIH

Q9AM82
 -NNVP--PQGFCHRLSHVSMFRSGFSNSV-SIIRAPMFSW-----IHRSAEFNN
 420 430 440 450 460

490 500 510 520 530 540
LAPNDVTGFTISPI - HATOVNNOTRTFISEKEFGNOGSLRFEONNTARYTLRGN-----
CS2282 820.

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000

~~SQRVRVIRVASNTNLFHTSIDGRPINQGNFSATWSS-GSNLQSGSFRTVGFTTFPNFS~~

~~CRYZADZ 826 NDUVPELVN-ILNSGTQFOLMLMLVPINISPLY
NGSSVFSLSAHVREISAEVEYIDRTEFFVAEVTFEAEYDLERAQKAWNELFTSSNQIGLKT~~

Q9AM82 :
DVTDYHIDVSNLWFLCSDZCCLDEKOEISENKKHKKRLSDERNILQDPNFRGINRQLDR

640 650 660 670 680 690

cry2ab2_820.pep
TXN5:CHAA_CLOBI

Description: 005102 clostridium bifermentans pesticial crystal-like pr
cry17a (insec
Accession/ID: 005102

```
=====General comments=====
IID CHAA CLOBI STANDARD; PRT; 618 AA.
AC 005102.
```

[illegible]

```
>>>TXN5:CHAA_CLOBI
scores      initl: 69      initn: 102      opt: 248      Z-score: 264.1      expect(): 8.4e-09
              (618 aa)
```

Smith-waterman score: 248;
25.8% identity in 229 aa overlap
(56-269:43-259)

Age Group	Percentage of Respondents
30	35
40	45
50	55
60	65
70	70
80	75

Monsanto Company

Final Report

Product Characterization Center

cry2ab2_820. DPFSQHKSLDTQKWEWKNNHSLYLDPIVGTVASFLKKVGLKVKRILSELNLNI
CHAA_CLOBI EYNSNLDIQPRELNTLGLVFTGATVSIILPLIGITA--VVPVGGVIG--IIAALLPVI
cry2ab2_820. FPGSGT---NLMQDILRETEKFLNQLRNTDTLARVNAELTGLQA--NVVEFNQVDNFLN
CHAA_CLOBI WPAGTSSNDNLDFAVMKDTIMDEKISEYV--VNDAMTRLESNLNLDYRLSKDFWE
cry2ab2_820. PNRNAVPLSITS---SVNTMQQLFLNRLPQFOMQGYQLLLPLFAQAANLHLSFIRD-VI
CHAA_CLOBI KNKDD-PLAIAELKERFSLKHSQFIESMAYFKRANYEVLLPAYANAANLHLLREGLL
cry2ab2_820. LN--ADEWGISAATLRTYRDYLNKYTRDYSNYCINTYQSAFKGLNLTLDH--MLEFRTY
CHAA_CLOBI LNKVIDNF-----ITEGLHYEEFKTKRSTYIAHCSTWKNKGLNKKRDNFKNKYDAY
cry2ab2_820. MFLNVFEYVSIW-SLFKYQSLVSSGANLYASGSGPQQTQSFQSDMPFLYSLFQVNSNY
CHAA_CLOBI MNLVLDLIISLFLSDPYQYDKATKLQTLTRTVFSDPLQRAPRDLVISPKEETLFLKNLKG
cry2ab2_820. pep
TXNS:X99478_1
Description: X99478 Clostridium bifermentans C.bifermentans cbm72 gene. 7/1998
Accession/ID: X99478
LOCUS X99478.1 [CBM72]
DEFINITION C.bifermentans cbm72 gene.
DATE 17-JUL-1998
SCORES Initl: 69 Initn: 102 Opt: 248 z-score: 264.1 E(): 8.4e-09
>TXNS:X99478_1
initn: 102 initl: 69 opt: 248 z-score: 264.1 expect(): 8.4e-09
Smith-Waterman score: 248; 25.8% identity in 229 aa overlap
(56-269:43-259)
cry2ab2_820. DPFSQHKSLDTQKWEWKNNHSLYLDPIVGTVASFLKKVGLKVKRILSELNLNI
X99478_1 EYNSNLDIQPRELNTLGLVFTGATVSIILPLIGITA--VVPVGGVIG--IIAALLPVI
cry2ab2_820. FPGSGT---NLMQDILRETEKFLNQLRNTDTLARVNAELTGLQA--NVVEFNQVDNFLN
X99478_1 WPAGTSSNDNLDFAVMKDTIMDEKISEYV--VNDAMTRLESNLNLDYRLSKDFWE
cry2ab2_820. PNRNAVPLSITS---SVNTMQQLFLNRLPQFOMQGYQLLLPLFAQAANLHLSFIRD-VI
X99478_1 KNKDD-PLAIAELKERFSLKHSQFIESMAYFKRANYEVLLPAYANAANLHLLREGLL

U28801_1 DFLNLTIVTSSNGT--IMNLWAGHRI--TFNRIOG--GSTSEMYGAI-----TNPVS
330 340 350 360 370

cry2ab2_820. SDOIGASFFACFNCSTFLPPLPFFVRSWLDSDGREGVATVNMQTESFETTLGLRS
360 370 380 390 400 410

U28801_1 VSDI-----YFVNRDIAVRYVSLAGGLSL--SGIRYGLTRVDFDMI-----FRNHDPDVT
380 390 400 410 420

cry2ab2_820. GATFAGNSNYFPFNNISGVFPRNVDLRRPDMNINRNIASPGTGGARAYMVS
420 430 440 450 460 470

U28801_1 GLF-----YHPGH-----AGATOVKASDTEPPETTEQNTAFSHLLS-----HIS
430 440 450 460 470

cry2ab2_820. VHNKKNHIAVHENGSMIHIAFNIDYGFISPHATOV-----NNQTRFISEKFG-NQ
480 490 500 510 520

U28801_1 MGPTTQDVPPVY--SWTHOSA-DRTN--TNSDRITDTPPLVKAHTLOAGTIVVKGPGFTG
480 490 500 510 520

cry2ab2_820. GDSLRFEQNNITARYTLRGNGN---SYNLYLRVSSIGNSTIRVTSNGRYVATVNMVTTN
530 540 550 560 570 580

U28801_1 GDILRRTSGGPFAPFNSVNLDFNLISQRYRIRYASTTNLRIYTVAGERFAGQDKTMR
530 540 550 560 570 580

cry2ab2_820. NDGVNDGAFSDINIGNVVASSNSDVPLOINV-TLNSGTG-----FDLNMIMLVPTNIS
590 600 610 620 630

U28801_1 A-GAPLTQSFYSATINTAFTFPERSSSLTIGADTFSSGNEVYVDFELIQVTAFEAS
590 600 610 620 630 640

cry2ab2_820. PLY

U28801_1 DLERARKAVNALFTSTNPRGLKTDVTDYHIDQVSNLVECLSDSEFCCLKKRELEEVKYAK
650 660 670 680 690 700

cry2ab2_820.pep
TXN5:CIKA_BACTM

Description: Q45715 bacillus thuringiensis (subsp. morrisoni). pesticidal
crystal protein cr
Accession/ID: Q45715
=====General comments=====

ID CIKA_BACTM STANDARD; PRT: 1215 AA.
AC Q45715;

SCORES Initl: 148 Initn: 177 Opt: 252 z-score: 262.9 E(): 9.7e-09
>>TXN5:CIKA_BACTM
initn: 177 initl: 148 opt: 252 z-score: 262.9 expect(): 9.7e-09
Smith-Waterman score: 257; 23.3% identity in 622 aa overlap
(56-626:73-636)

cry2ab2_820. DPFSDHKSLOTQKWEWKNNHSLYLDPIVGVASFLKKVKGSLGVKRLSELANLI
30 40 50 60 70 80

CIKA_BACTM EGNIDIPFVSASTVQTGISIAGRIGLVGVPPFAGQLASFY-----SFLVGE-----L
50 60 70 80

cry2ab2_820. FPGSTNMODILRETEKEFLNRLNLTDLARVN-AELTGLQANVEEFNRQVDNFLNRRN
90 100 110 120 130 140

CIKA_BACTM WPSGR-DPEWFEHVEHQVROQQTDSVRDTAIGRLGGRYSYQQALETWLDNRND
90 100 110 120 130 140

cry2ab2_820. AVPLSITSSVNTMQOL-FLNRLPQFMQOGYQLLLPLFAQANLHLSFIRVILNADENG
150 160 170 180 190 200

CIKA_BACTM ASRSITIRERYIALEDDITTAIPFSIHNEEVPLLMVYACAAHLHLLLRDASLFGSEWG
150 160 170 180 190 200

cry2ab2_820. ISAAATLRTYRDYLNKYTRDYSNYCINTYQSAFGLNLRHDML---EFRTYMLFNVEFY
210 220 230 240 250

CIKA_BACTM MGSADVNCYQEOIRYTEYSNHCQWNTGLNRLRGTTAETWRYNQFRDRLTLGVLDL
210 220 230 240 250 260

cry2ab2_820. VSIWSLFYKYSLLVSSGANL---YA--SG--SGPOQTQ-----SFTSQD-----WPFYLY
260 270 280 290 300 310 320 330 340 350

CIKA_BACTM VALFSPDYDTRTPIPTTAOLTRREVYDPNGVWAGPNNWFRNGASFSIAENAIIRQPHLY
270 280 290 300 310 320

cry2ab2_820. SLF-----OVNSNVYLVNGSGARLSNTFPNIVGLPGSTITTHALLAARVNYSGGIS
310 320 330 340 350 360 370

CIKA_BACTM DFLNLTIVTSSNGT--IMNLWAGHRI--TFNRIOG--GSTSEMYGAI-----TNPVS
330 340 350 360 370

cry2ab2_820. GCDGASPP-NQNFNCSTFLPPLTPFVRSWLDSDGREGVATVNMQTESFETTLGLRS
360 370 380 390 400 410

CIKA_BACTM VSDI--PNSNRDVTYVSLAGGLSL--SGIRYGLTRVDFDMI-----FRNHDPDVT
380 390 400 410 420

cry2ab2_820. GAPFARNSNYFPFNNISGVFPRNVDLRRPDMNINRNIASPGTGGARAYMVS
420 430 440 450 460 470

CIKA_BACTM GLF-----YHPGH-----AGATOVKASDTEPPETTEQNTAFSHLLS-----HIS
430 440 450 460 470

cry2ab2_820. VHNKKNHIAVHENGSMIHIAFNIDYGFISPHATOV-----NNQTRFISEKFG-NQ
480 490 500 510 520

CIKA_BACTM MGPTTQDVPPVY--SWTHOSA-DRTN--TNSDRITDTPPLVKAHTLOAGTIVVKGPGFTG
480 490 500 510 520

cry2ab2_820. GDSLRFEQNNITARYTLRGNGN---SYNLYLRVSSIGNSTIRVTSNGRYVATVNMVTTN
530 540 550 560 570 580

CIKA_BACTM GDILRRTSGGPFAPFNSVNLDFNLISQRYRIRYASTTNLRIYTVAGERFAGQDKTMR
530 540 550 560 570 580

cry2ab2_820. NDGVNDGAFSDINIGNVVASSNSDVPLOINV-TLNSGTG-----FDLNMIMLVPTNIS
590 600 610 620 630 640

CIKA_BACTM A-GAPLTQSFYSATINTAFTFPERSSSLTIGADTFSSGNEVYVDFELIQVTAFEAS
590 600 610 620 630 640

cry2ab2_820. PLY

CIKA_BACTM DLERARKAVNALFTSTNPRGLKTDVTDYHIDQVSNLVECLSDSEFCCLKKRELEEVKYAK
650 660 670 680 690 700

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X13535_1      TFSQWHRSAEFNNIIPSSQITQIPLTKSNLGSVTSVKPGPFTGGD---ILRRTSPGGQII
              460      470      480      490      500
cry2ab2_820.  SLRFEQNNITARTYLRNGNSYLYLRVSSGNSITRVINGRVYATATVNTTTNDGQVN
              530      540      550      560      570      580
X13535_1      TLRV--NITAPLSQR-----YRVIRYASTINLQFHTSIDGRPIQGNFASATSS--GSN
              510      520      530      540      550
cry2ab2_820.  DNGARFSDINGNVASSNDVPIDINV-TLMSGTQFDLMNMLVPTNISPLY
              590      600      610      620      630
X13535_1      LQSGSFRTVGFPTPFNFSGSVFTLSAHVFNSGNEVIDRIFVPAEYTFEAEYDLERA
              560      570      580      590      600      610
X13535_1      QKANVELFTSSNGIGLKTDYTDYHIDOVSNLVECLSDFCFLDEKQELSKSVKRAKLSDE
              620      630      640      650      660      670
cry2ab2_820.pep
TXNS:C1AA_BACTK
=====General comments=====
ID   C1AA_BACTK   STANDARD;   PRT; 1176 AA.
AC   P02965; P16478; P09664; Q0965; P09665; .
Description: P02965 bacillus thuringiensis (subsp. kurstaki), bacillus
thuringiensis (subsp.
Accession/ID: P02965
>>TXNS:C1AA_BACTK
initn: 168 initl: 128 opt: 251 Z-score: 262.1 expect(): 1.1e-08
Smith-Waterman score: 282; 22.1% identity in 560 aa overlap
(100-634:79-609)
SCORES Initl: 128 Initn: 168 Opt: 251 Z-score: 262.1 E(): 1.1e-08
>>TXNS:C1AA_BACTK
cry2ab2_820.  GSLVGKRIKSELNLIFFPGSGTNLMQDILRETEKFLNRLNTDTRVNAELTGL---Q
              70      80      90      100      110      120
C1AA_BACTK   EFVFGAGVLGVLDIWIIGFGPSQWDAPFVQLEQLINQRIEERFARVQASLRLEGLSNLYQ
              50      60      70      80      90      100
cry2ab2_820.  ANVFEFNKQVDNPLNPNNAVPSITSSVNTWQQLFLNRLFPQMGGYQLLLPLFAQAA
              130      140      150      160      170      180
C1AA_BACTK   IYAESFREWADPTNP--ALREEMRIQFNDMNSALTATAPLAVQNYQVPLLSVYVQAA
              110      120      130      140      150      160
cry2ab2_820.  NLHSFSDRIVLNADQEWGISATRIYRDYLNKYTRDYNSYCNITQSAFK---GLNTRL
              190      200      210      220      230      240
C1AA_BACTK   NLHLSVLRDVSVPQGRWGFDAATINSRYNDLTGLTNTDYAVRVWNTGLERVWGFDSR
              170      180      190      200      210      220
cry2ab2_820.  HDML---EFTTYMFLNVEYYSIWSLF--KYQSLVSS--GANLYASGGSPQQTOSTFSQ
              250      260      270      280      290
C1AA_BACTK   -DWRYNQFRELITLVDI VALFSYNDSSRRPIETBSQLTREIYNFVLENFDSFRGM
              230      240      250      260      270      280
cry2ab2_820.  DMPLYSLFQWNSYVNLGFGSGLRSLNTFNFIYGLFTGTTTHALLAARYNYSIGSS---
              300      310      320      330      340      350
C1AA_BACTK   AORIEONIROPHLMDILNSIT-----IYDVHRGNFNWNSHOITASPVGFSGPEFAFPL
              300      310      320      330      340      350

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cry2ab2_820. GDIG--SPTNQNFCSTPPLTPFVRSM--LDSSDREGVATVNNQTESPET-ILG
340 350 360 370 380 390 400
CIAA_BACTK FSNAGNAPPPVMS--TGIFRTLSPPRRRIILGSGPNQEL--FVLDGTESFASLTTN
340 350 360 370 380 390
cry2ab2_820. LRSGAFTARGNSVFPYFIRNAGVAVVNEEDRRPHYNIRNIASPSGTGGARAY
410 420 430 440 450 460
CIAA_BACTK LPSITYRGVDSL--DWPSPNSVFP--PASFHRLSH--VTMLSOAGAVVTLRAP
400 410 420 430 440 450
cry2ab2_820. MYSVNRKNNIHAVHENG--SMIHLAPRYTFTIS--HATVNNQTRP--SEAFNGQD
470 480 490 500 510 520
CIAA_BACTK TFSQWHRSAEENIIPSSQITQPLTKSTNLGSETSVKKGFTGGD--LRRRTSRGGS
460 470 480 490 500 510
cry2ab2_820. SURFQNNNTARYTLRNGNSVNLVRSVSSIGNSTIRVTNGKTYATVNTVNNQSVN
530 540 550 560 570 580
CIAA_BACTK TLRV---NITAPLSQR-----YRVIRYASTINLQFHTSIDGRFINQGHFSAWSS--GSN
510 520 530 540 550 560
cry2ab2_820. DNGARFSDINGNVVASSNSDVPDLINV--TLNSGTQFDLNMVLTNISPLY
590 600 610 620 630
CIAA_BACTK LOGSFRVGTTFPFNSGNSVFLISAHVNSGNEVYIDRIEFVPAEVEAYDLERA
560 570 580 590 600 610
CIAA_BACTK OKAVNELTSSNIGLKIDVDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDE
620 630 640 650 660 670
cry2ab2_820.pcp
TXN5:CIAD_BACTA

Description: Q03744 bacillus thuringiensis (subsp. aizawai). pesticidal
crystal protein cry1
Accession/ID: Q03744
ID CIAD_BACTA STANDARD; PRT; 1179 AA.
AC Q03744;

SCORES Initl: 151 Initn: 192 Opt: 251 Z-score: 262.1 E(): 1.1e-08
>TXN5:CIAD_BACTA (1179 aa)
initn: 192 initl: 151 opt: 251 Z-score: 262.1 expect(): 1.1e-08
Smith-Waterman score: 295; 23.2% identity in 608 aa overlap
(60-634:41-609)

cry2ab2_820. FOHKSLDTVQKEMTEWKNKNSLYLDPVIGTVASFILKVGSLVGRKILSELNLIIPSG
30 40 50 60 70 80
CIAA_BACTA VPYCNLDPTTIELEGERIETGYTIDISLSLTFLSEF--VPGAGVFLGIDLINGFV
20 30 40 50 60
cry2ab2_820. STNLMQDILRETEKFLNQLRNTDILARVNAELTGL----QANVEFNRQVNFNLPNRNA
90 100 110 120 130 140
CIAA_BACTA GPSQWDAFLVQIEQLINQRIEFARNOAISLEGLSNLYQIVAEAFREWEADPTNP--A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTWQOFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGIS
150 160 170 180 190 200
CIAA_BACTA LTEMRIQFNDMNSALITTAIFLVQYQVPLLSVVOAANLHLSVLDRVSVFGQWGED
130 140 150 160 170 180
cry2ab2_820. AATLRTYRDVLYKNYTRDYSNYCINTYOSAFK--GLNTRLHDML---EFRTYMLNFVEY
210 220 230 240 250
CIAA_BACTA VATTINRYNDLRLTIGTYTDVAVRWYNTGLRVMGPDSCR--DWRYNQFRRELTLTVDI
190 200 210 220 230 240
cry2ab2_820. VSIWLSFKYQSLVSGANL---YAS-----GSGPOQTSFTSO--DWPFYLSLFOVN
260 270 280 290 300
CIAA_BACTA VSLFPNYDSRTYPIRTVSQLTRELYTNVPLENFDSFRGMAQRIEQNIQPHLMOLLNSI
250 260 270 280 290 300
cry2ab2_820. SNY--VLNGF---SGARLNTFPNVGLPGSTITHALLAARVNYSGSISSDGIGASPFNQ
310 320 330 340 350 360
CIAA_BACTA TIYDVRHGFNVMSGHQITAS--P--VGFAPEFTFPRTYGTMGNAAPVPLISITGLGIFR-
310 320 330 340 350
cry2ab2_820. NFNCSTFLPLTPFVRSWLDSDREGVATVNNQTESPET--TLGRSGAFTARGNSY
370 380 390 400 410 420
CIAA_BACTA ---TLSSPL---YRRILGSGNNQNL--FVLDTGTEFSFASLTADLPSTIYRQRTVDS
360 370 380 390 400 410
cry2ab2_820. PPDYFINIS--GVPLVVRNEDLRRLHVNEIRNIASPSGTGGARAYVSVHNEKNNIHAV
430 440 450 460 470 480
CIAA_BACTA L-DVIRPOONSVP--RAGFSHRLSH--VTMLSOAGAVVTLAAPTFSWR-----
420 430 440 450
cry2ab2_820. HENGSMIHLAPNDYFTTISTPHATVNNQTRTFISEKFG--NOGDSLRFEQNN--TTARY
490 500 510 520 530
CIAA_BACTA HRSAE--SNLSPS--SQV--LTKS--NLGSGTSVVKVGFTGDIILRITSPQISTLRV
460 470 480 490 500 510
cry2ab2_820. TLRCN--GNSVNYLVRWSSNSSTLNTVNNQYTTATVNTTNDGVDNDGA--RPSDINI
540 550 560 570 580 590
CIAA_BACTA TITAPUSQRRVRIYASTINQPHSIDGKPMQ--SNSATWSSGNSLOSFSRPTAGFTT
520 530 540 550 560 570
cry2ab2_820. GNVVASSNSDVPDLINVTLNSGTQFDLNMVLTNISPLY
600 610 620 630
CIAA_BACTA PFNFSNGSSIFTLSAHV--FNSGNEVIERIEFVPLENTF--EYEDLEACQAVNALPNSN
580 590 600 610 620 630
CIAA_BACTA QLGLKINVTYDHYDQVSNLVECLSGDFCLDEKRESEKVKHANNISDRNLLOSSTPFI
640 650 660 670 680 690
cry2ab2_820.pcp
TXN5:M73250_1

Description: M73250 Bacillus thuringiensis Bacillus thuringiensis (cryIA(a))
Gene, complete C

Accession/ID: M73250
-----General comments-----
LOCUS M73250_1 [BACCRYAD]
DEFINITION Bacillus thuringiensis (cryIA(d)) gene, complete CDS.

SCORES Initl: 151 Initn: 192 Opt: 251 z-score: 262.1 E(): 1.1e-08
>>TXN5:M73250_1 (1179 aa)
initn: 192 initl: 151 opt: 251 z-score: 262.1 expect(): 1.1e-08
Smith-Waterman score: 295; 23.2% identity in 608 aa overlap
(60-634:41-609)

cry2ab2_820. FQHKSLDTQKEWTEWKKNNHSLYLDPIVGTAVSFLLKKVGLVGRILSELRLIPPSG
M73250_1 VPYNCLNDPIETIELEGRIETGYTPIDISLSLTQFLLSF--VPGAGFVLGLDLWGTV
20 30 40 50 60
30 40 50 60 70 80

cry2ab2_820. STNLMQDILRETEKFLNQLNTDILARVNAELTGL-----QANVEEFNQVDNFLNPNRHA
M73250_1 GFSQMDAPLVQISLQINRIEFAFNQAISLEGLSNLYQIYAEAFREWEADFTNP---A
70 80 90 100 110 120
130 140 150 160 170 180

cry2ab2_820. VFLSITSSVNTMOQLFNLRFQOMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGIS
M73250_1 LTEMRIQFNDMSALTITAIPLFTVQNYQVPLLSVYVQAANLHLSVLRDVSVEGQWGF
130 140 150 160 170 180
190 200 210 220 230 240

cry2ab2_820. AATLRTYRDYKNTYRDYNYCINTYQSAFK--GNLRLHML---EFRTYMLPNVFEY
M73250_1 VATINSRYNDLRLIGITYDYAVRWYNTGLERVWGPDNR--DWRYNQFRRLTLVLDI
190 200 210 220 230 240

cry2ab2_820. VSIMSLFKYQSLVSSGANL---VAS-----GSGPQQTQSTQ-DMPFLYSLFQVN
M73250_1 VSLFENYDSRTYIIRTYSQITREITVNTPLENFDGSGFRGWAQRIEQNTQRPHMLDLNLSI
250 260 270 280 290 300

cry2ab2_820. SNY--VLNGF---SGARLSNTFPNIVLPGSTTHALLAARVNYSGGSSGDIGASFPNQ
M73250_1 TIYDVRHGFYVWSGHQITAS-P--VGFAGPEFTFPYGTMGNAAPPVLISITGLGIFR-
310 320 330 340 350

cry2ab2_820. NFNCSTFLPLLPFFVRSMWDSGDRGVATVNMQTESFET-TGLRSGAFTARGNSNY
M73250_1 -----TLSSPL---YRRIILGSGPNQNL-FVLDGTFESFASLTADLPSTIYRQRTVDS
360 370 380 390 400 410

cry2ab2_820. PPDYFIRNIGSVPLVVRNEDLRPLHYNEIRNIASPSGTPGCGARVYVHNRKNIHAV
M73250_1 L-DVIPQDMSVP--ARAGFSHRUSH---VTMLSQAGAVYTLRAPTFSMR-----
420 430 440 450

cry2ab2_820. HENGSMHLPANDYTGTITSPHATOVNNOTRTFISEKFG-NOGDSLRFQNN--TTARY
M73250_1 HSAEFSNLIPS--SQITQIPLTKS-INLGSITSVVKGFGFTGGDILRIITSPGQISLAV
490 500 510 520 530

460 470 480 490 500 510
540 550 560 570 580 590
cry2ab2_820. TLRGN-GSNYNLYRVSIGNSTIRVTINGRVYATNNTITNDGVNDNGA-RFSDINI
M73250_1 TITAPISQRYRVIRYASITNLQFHTSIDGRPIINGQNFSAITMSSGGNLQSGSFRTAGFTT
520 530 540 550 560 570
580 590 600 610 620 630
cry2ab2_820. GNVVASSNDVPLDINVTILNSGQFDLMMIMLVPIINISPLY
M73250_1 PFFNSGSIFTLSAHV-FNSGNEVYIERIEFVPAETFAEYDLERAQAVNALFTSSN
580 590 600 610 620 630
640 650 660 670 680 690
M73250_1 QLGLKTNVTDYHIDQVNLVECLSGEFCDEKRELSEKVKHANRLSDERNLLQDNPFRGI
640 650 660 670 680 690

cry2ab2_820.pcp
TXN5:X99103_1
Description: X99103 synthetic construct Artificial sequences mRNA for
delta-endotoxin. 1/1997
Accession/ID: X99103
LOCUS X99103_1 [ASCYRIC]
DEFINITION Artificial sequences mRNA for delta-endotoxin.

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 260.8 E(): 1.3e-08
>>TXN5:X99103_1 (630 aa)
initn: 206 initl: 206 opt: 245 z-score: 260.8 expect(): 1.3e-08
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KENTWKKNNHSLYLDPIVGTAVSFLLKKVGLVGRILSELNLIFFPSGSLNMQDILR
X99103_1 DGERISTGNSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVVGIVGPSOWDAFLVQI--
30 40 50 60 70
100 110 120 130 140 150
cry2ab2_820. ETEKFLNQLNTDILARVNAELTGLQANVEEFNQVDNFL---NPNRNVFLSITSSVN
X99103_1 --EQLNERIAB--PAR-NAAIANLEGLGNFNFIYVEAFKEWEEDNPNPATRVIDRFR
80 90 100 110 120 130

cry2ab2_820. TMOQLFNLRFQOMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGISAATLRTYRDY
X99103_1 ILDGLLERDIPFRISGFEVPLLSVYVQAANLHLSFIRDVILNADEWGISAATLRTYRDY
140 150 160 170 180 190
200 210 220 230 240 250
cry2ab2_820. LKNYTRDYSCINTYQSAFKG-NTRLHDMLEF---RTYMFNLNVFEYVSWLSFKYQSL
X99103_1 LTRHIDEYADHCANTYRANGLNLPKSTYQDQWITTYNRURDLTLTVLDIAAFAFPFNDRRY
200 210 220 230 240 250
260 270 280 290 300 310
cry2ab2_820. LVSSGANLYASGSGPQQTQSTQDWPFLYLFQVNSNYVLNGFSGARLSNTFPNIVGLP
X99103_1 PLOPVSQLTREYVYTDPLINFPNPOQSVAQLPFTFNVMESSAIRNPPLHFDILNLTIFTDMF
260 270 280 290 300 310

Smith-Waterman score: 257; 21.4% identity in 611 aa overlap
(60-634:41-611)

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cry2ab2_820. FOHKSLLTVQKEWTEKKNNHSLYLDPIVTSASEFLVKKVSGSLVGRKILSELNRNLIPFSSG
30      40      50      60      70      80
MI2661_1  IPYNCLSNPEVEVLGGERIETGYTPIDISLITQFLSEF---VPGAGFVLGVGDVIWGIF
20      30      40      50      60
cry2ab2_820. STNLMODILRETEKELFNORLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA
:      :      :      :      :      :
MI2661_1  GPSOWDAFLVQIEQLINQRIEFAARQAISRLIEGLSNLYQTYAESFREWEADPTNP---A
70      80      90      100     110     120     130     140
cry2ab2_820. VPLSITSSVNTWQQQLFLNRLPQFMQMGYQLLLPLPFAQAANLHLSTFROVILNADGWGIS
150     160     170     180     190     200
MI2661_1  LREEMRIQFNDWNSALITAPLFAVONYQVPLSVYQAANLHLVSLRDLVSFVGFGWGMFSD
130     140     150     160     170     180
cry2ab2_820. AATLRITRDYLNKYTRDYSNYCINTQSAFK---GLNTRLHDML---EPTMYFNLNVPEY
210     220     230     240     250
MI2661_1  AATINSRYNDLRLGNYTDHRYRWYNTGLERVWGPDSR---DMIRYNQFRRELITLVIDI
190     200     210     220     230     240
cry2ab2_820. VSIWLSFKYQSLVSSGANLYVASGSPQOFTSQDMPFLYSLFQVNSYVNLINGFSGAR
260     270     280     290     300     310
MI2661_1  VGLPFPNVDSKRTYPIRTVSOL-----TRRIYTN---PVLEN-FDGSFRGSAQGIIEGI
250     260     270     280     290
cry2ab2_820. LSWERNIVGLNGSSSTHALLAARVNSGGISGDIASPPNQNFNCSTFLPPLTPPVR
320     330     340     350     360     370
MI2661_1  RS---PRLADILNSITVYTR-AHRGEYYW---SGHQIMASPVG---FSG-----PEFTFPLYG
300     310     320     330
cry2ab2_820. SWLSDSSDAEGVATVAPQVETETLGLNGSAFTARGNSNYFD-----YPIRNSGV
380     390     400     410     420     430
MI2661_1  TMGNAAPQQRVYAGVGGGVATKTSLSLYLRPNPNTLNQQQLSGDGGGRICLNLNLKLPFGQP
340     350     360     370     380     390
cry2ab2_820. PLVVRNEDLRRLPHLYNEIRNRKASLGGTETCARVNVSVHKKNNHVAHENGSMIHLP
440     450     460     470     480     490
MI2661_1  PYTEKAEPVDSPEIPPPONNNVPPRGGFVHRCLEAVSNVNGGFSNSV---SVIR-AP
400     410     420     430     440     450
cry2ab2_820. NDYV-----GFTISPIHATQVNNQTRTASEFGNQSLSPEFQNNITTPRYT
500     510     520     530
MI2661_1  NDSSWTYCSAEFGDVFSSQITQIPITKLQSLMNSVVKVGGTFSGDILLESFSS--T
460     470     480     490     500
cry2ab2_820. LRGN-----GNSYNLVLRVSGISNSTRIVTNGRYVYATNVITINDGVNNGAFSFDI
540     550     560     570     580     590
MI2661_1  LRVNITAPLUSQRYRVRYRYASTNLNQLQFTSIDGREINGNFSATMSS--GSNT-QSGSSTT
520     530     540     550     560     570

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cry2ab2_820. NIGNVASSNSDVLPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
M12661_1 GPTTFPNSGSSVFTLSAHVNSGNEVYIDRIEFPAEYFPAEYDLERAQKAVNELFT
M12661_1 SSNQIGLKTVDYDHYDQVSNLVECLSEDFCLDEKSELSEKVKHAKRLSDERNLLQDPNF
cry2ab2_820.pep
TXN5:Q9S514

Description: Q9S514 bacillus thuringiensis. insecticidal crystal protein.
Accession/ID: Q9S514
ID Q9S514 PRELIMINARY;
AC Q9S514; . . .

=====General comments=====
PRT; 1176 AA.

SCORES Init1: 128 Initn: 160 Opt: 248 Z-score: 258.9 E(): 1.6e-08
>>TXN5:Q9S514
Initn: 160 Init1: 128 opt: 248 Z-score: 258.9 expect(): 1.6e-08
Smith-Waterman score: 288; 22.5% identity in 609 aa overlap
(60-634:41-609)

cry2ab2_820. FQKSLDTQKWEKTEWKKNNHSLYLDPIVGTVASFLKKVGLVGRILSELRLNLIFFSG
Q9S514 IPYCLSNPEVEVLGGERIETGYTIDISLSLQFLSEF--VPGAGVGLGLVDLIWGIF
cry2ab2_820. STNLMOQLIRETEKFLNQRLNTDTLARNVAELTGL---QANVEEFNQVDNFIENRRA
Q9S514 GPSQWDAFLVQIEQLINQRIEFAFNQAIKSLRLEGLSNLYQIVAESFREWEADPTNP--A
cry2ab2_820. VPLSITSSVNTMQQLFNLPLQFQMGVQYQLLLPLFAQANLHLSFIRDVLNADENGIS
Q9S514 LREEMRIQFNDMNSALTITAPLLAVQNYQVPLLSVYVQAAANLHLSVLRYDSVFGQRMGFD
cry2ab2_820. AATLRTYRDVLYKNYTRDYSNYCINTYQSAFK--GLNTRLHDML--EFRTYFLNVEFY
Q9S514 AATNSRYNDLTGLIGNYTDVAVRWYNTGLERVWGDSR--DWVRYNGFRRELTLIVLDI
cry2ab2_820. VSIWSLF--KYQSLIVSS--GANLYAS-----GSGPOQTQSFTSQ--DWPFYLSFQVN
Q9S514 VALFSNYDSRRYPIRTVSQLTREIYTNFVLENFDGSRFGMAQRIEPEYRQPHLMDILNSI
cry2ab2_820. SNY--VLNGF--SGARLSNTFPNIVLPGSGTTHALLARNVYSGGSSGDGASFPNQ
Q9S514 TIYTDVHRGFNYWSGHQITTS-P--VGFSGPEFAFFLFGNAGNAAPVLYSLTGLGIFR-
cry2ab2_820. NFNCSTLPLLLTPFVRWLDSSDREGVATVNWQTESFET-TLGLRSAGFTAGNSNY
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Q9S514 -----TLSSPL---YRRILGSGPNQDEL-FVLDGTESFASLTNTNLPSTIYRQGTVD
cry2ab2_820. PPDYFIRNISGVPLVVRNEDLRPLHNEIRNIASPSGTGCGARAYVSVHNRKNNIHAV
Q9S514 L-DVIIPQDQNSVP-----PRAGFSHLSHVPMLSQAAGAVVTLRASLFLR-----L
cry2ab2_820. HENGSMIHLAPNDYTGFTTSPHATQVNNQTRIFISEKFGNQSDSRFQNNNTIARYTLR
Q9S514 DPSAEFNNIIPS-FTNYQIPLTKSTNLGSGTGVWKGPGFTG-GDILRRTPGLIS--TLR
cry2ab2_820. GN-----GNSYNLYLRVSSIGNSTIRVTINGRYTATVNTTNDGVDNGARFSDINI
Q9S514 VNITAPLSORYRVRIRYASTTNLQFHTSIDGRPINQGNFYATMSS-GSNLQSGSFRTVGF
cry2ab2_820. GNVVASSNSDVLPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
Q9S514 TTPNFNSGSSVFTLSAHVNSGNEVYIDRIEFPAEYFPAEYDLERAQKAVNQVLTSS
cry2ab2_820. NQIGLKTQDTHYDQVSNLVECLSEDFCLDEKSELSEKVKHAKRLSDERNLLQDPNFRG
TXN5:Q9S514
Description: X13620 Bacillus thuringiensis Bacillus thuringiensis aizawai
delta-endotoxin gen
Accession/ID: X13620
=====General comments=====
LOCUS X13620_1 [BITOXDA]
DEFINITION Bacillus thuringiensis aizawai delta-endotoxin gene 5'-region;
SCORES Init1: 206 Initn: 206 Opt: 245 Z-score: 258.6 E(): 1.7e-08
>>TXN5:X13620_1
Initn: 206 Init1: 206 opt: 245 Z-score: 258.6 expect(): 1.7e-08
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KEWTEWKKNNHSLYLDPIVGTVASFLKKVGLVGRILSELRLNLIFFSGSTNLMOQLIR
X13620_1 DGERISTGNSIDISLSLQVFLVSNFVPGGGLVG--LIDFVWGIVGSPQWDAFLVQI--
cry2ab2_820. ETEKFLNQRLNTDTLARNVAELTGLQANVEEFNQVDNFIENRNVAVELSTSSVN
X13620_1 --EQLINERIAE--FAR-NAAIANLEGLGNFNFIYVFAKWEEDPNPATRVIDRFR
cry2ab2_820. TMQQLFNLPLQFQMGVQYQLLLPLFAQANLHLSFIRDVLNADENGISAAITLRYDY
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X13620_1 ILDGLNRPDIPSRISGFEVPLLSVYAQAANHLAILRDSVIFGERWGLTITNVNENYR
140 150 160 170 180 190
cry2ab2_820. LKNTYRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMLNVEFYVSIWLSFKYQSL
220 230 240 250 260 270
X13620_1 LIRHIDEVADHCANTYNGNLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNVDNRY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQOTQSFSDQMPFLYKGFQVNSNYVNGFSGARLSNTFFNIVGLP
280 290 300 310 320 330
X13620_1 PIQVQGLTREVTDPDLINFPQLQSVAFQTFNVMESSAIRNPHLDLNNLTIFTDMF
260 270 280 290 300 310
cry2ab2_820.pcp
TXN5:Q9L877
Description: Q9L877 bacillus thuringiensis. toxin cry2ab2. (20307)
Accession/ID: Q9L877
ID Q9L877 PRELIMINARY; PRT: 1189 AA.
DT 01-OCT-2000 (Tremblrel. 15, Created)
SCORES Initl: 208 Initn: 208 Opt: 247 z-score: 257.8 E(): 1.9e-08
>>TXN5:Q9L877
initn: 208 initl: 208 opt: 247 z-score: 257.8 expect(): 1.9e-08
Smith-Waterman score: 247; 25.2% identity in 202 aa overlap
(70-263:54-246)
cry2ab2_820. KEWTEWKNHSLYLDPIVGTIVASFLKKVGLSVKRLSELNLIFFPGSGTNLMODILR
40 50 60 70 80 90
Q9L877 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGPGQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNRLNTDILARVNAELTGLQANVEEFNRQVDFL---NPNRNAVPLSITSSVN
100 110 120 130 140 150
Q9L877 --EQLINERIAE--FAR-NAATANLEGLGNFNFIYVEAFKEWEEDPNPATRTRVIDRFR
80 90 100 110 120 130
cry2ab2_820. LKNTYRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMLNVEFYVSIWLSFKYQSL
160 170 180 190 200 210
Q9L877 LIRHIDEVADHCANTYNGNLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNVDNRY
140 150 160 170 180 190
cry2ab2_820. LKNTYRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMLNVEFYVSIWLSFKYQSL
220 230 240 250 260 270
Q9L877 LIRHIDEVADHCANTYNGNLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNVDNRY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQOTQSFSDQMPFLYKGFQVNSNYVNGFSGARLSNTFFNIVGLP
280 290 300 310 320 330
Q9L877 PIQVQGLTREVTDPDLINFPQLQSVAFQTFNVMESSAIRNPHLDLNNLTIFTDMF
260 270 280 290 300 310
```

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cry2ab2_820.pcp
TXN5:AF215647_1
Description: AF215647 Bacillus thuringiensis Bacillus thuringiensis toxin
Cry1Ca6 (cry1Ca6) g
Accession/ID: AF215647
====General comments=====
LOCUS AF215647_1 [AF215647]
DEFINITION Bacillus thuringiensis toxin Cry1Ca6 (cry1Ca6) gene, complete cds;
SCORES Initl: 208 Initn: 208 Opt: 247 z-score: 257.8 E(): 1.9e-08
>>TXN5:AF215647_1
initn: 208 initl: 208 opt: 247 z-score: 257.8 expect(): 1.9e-08
Smith-Waterman score: 247; 25.2% identity in 202 aa overlap
(70-263:54-246)
cry2ab2_820. KEWTEWKNHSLYLDPIVGTIVASFLKKVGLSVKRLSELNLIFFPGSGTNLMODILR
40 50 60 70 80 90
AF215647_1 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGPGQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNRLNTDILARVNAELTGLQANVEEFNRQVDFL---NPNRNAVPLSITSSVN
100 110 120 130 140 150
AF215647_1 --EQLINERIAE--FAR-NAATANLEGLGNFNFIYVEAFKEWEEDPNPATRTRVIDRFR
80 90 100 110 120 130
cry2ab2_820. LKNTYRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMLNVEFYVSIWLSFKYQSL
160 170 180 190 200 210
AF215647_1 LIRHIDEVADHCANTYNGNLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNVDNRY
140 150 160 170 180 190
cry2ab2_820. LVSSGANLYASGSGPQOTQSFSDQMPFLYKGFQVNSNYVNGFSGARLSNTFFNIVGLP
260 270 280 290 300 310
AF215647_1 PIQVQGLTREVTDPDLINFPQLQSVAFQTFNVMESSAIRNPHLDLNNLTIFTDMF
260 270 280 290 300 310
cry2ab2_820.pcp
TXN5:A27531_1
Description: A27531 Bacillus thuringiensis B. thuringiensis PS41RRI endotoxin
gene 9/1995
Accession/ID: A27531
====General comments=====
LOCUS A27531_1 [A27531]
DEFINITION B.thuringiensis PS41RRI endotoxin gene.
SCORES Initl: 151 Initn: 192 Opt: 246 z-score: 256.8 E(): 2.1e-08
>>TXN5:A27531_1
initn: 192 initl: 151 opt: 246 z-score: 256.8 expect(): 2.1e-08
Smith-Waterman score: 290; 23.2% identity in 608 aa overlap
(60-634:41-609)
```

cry2ab2_820. FQHSKSLDVQKTEWEMKNNHSLYLDPIVGTVASFLKKVGLSVGKRIILSELRNLIFPSG
A27531_1 VPIVCLNDPTTEILLEGRIETGTPIDISLITQELLSEF--VFGAGFVLGIDILNGFV
cry2ab2_820. STNLMDILRETERFLNQLRNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNENA
A27531_1 GPQSDAFVLQLEQLINQRIEFAFNQALSRLEGLSNLYOYIAEAAREWEADPNP--A
cry2ab2_820. 30 40 50 60 70 80 90 100 110 120 130 140
A27531_1 20 30 40 50 60 70 80 90 100 110 120 130 140
cry2ab2_820. 150 160 170 180 190 200
A27531_1 130 140 150 160 170 180 190 200
cry2ab2_820. 210 220 230 240 250
A27531_1 190 200 210 220 230 240 250
cry2ab2_820. 260 270 280 290 300
A27531_1 250 260 270 280 290 300
cry2ab2_820. 310 320 330 340 350 360
A27531_1 310 320 330 340 350 360
cry2ab2_820. 370 380 390 400 410 420
A27531_1 360 370 380 390 400 410 420
cry2ab2_820. 430 440 450 460 470 480
A27531_1 420 430 440 450 460 470 480
cry2ab2_820. 490 500 510 520 530
A27531_1 480 490 500 510 520 530
cry2ab2_820. 540 550 560 570 580 590
A27531_1 530 540 550 560 570 580 590
cry2ab2_820. 600 610 620 630
A27531_1 590 600 610 620 630

A27531_1 PFNFSNGSIFTLSAHV-FNSGNEVYIDRIEFYPAEVTFEAYDLERAQAVNALFTSSN
A27531_1 QLGKTNVTYHDQVSNVNEVCELSGECLEKSEKVKHAKRLSDERNLLQDPNFRGI
cry2ab2_820.pgp
TXN5:C1CA_BACTE
Description: P05518 bacillus thuringiensis (subsp. entomocidus), and bacillus
thuringiensis (
Accession/ID: P05518
ID C1CA_BACTE STANDARD; PRT: 1189 AA.
AC P05518; F10327; Q03742; Q45725;
=====General comments=====

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 255.7 E(): 2.5e-08
>TXN5:C1CA_BACTE
Initn: 206 Initl: 206 Opt: 245 z-score: 255.7 expect(): 2.5e-08
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KEWTEWKNNHSLYLDPIVGTVASFLKKVGLSVGKRIILSELRNLIFPSGSTNLMDILR
C1CA_BACTE DGERISTGNSSIDISLSLVQFLVSNFVPGGFLVG--LIDFWGIVGFSQWDAFLVQI--
cry2ab2_820. 40 50 60 70 80 90
A27531_1 30 40 50 60 70 80 90
cry2ab2_820. 100 110 120 130 140 150
A27531_1 90 100 110 120 130 140 150
cry2ab2_820. 160 170 180 190 200 210
A27531_1 140 150 160 170 180 190 200 210
cry2ab2_820. 220 230 240 250 260 270
A27531_1 200 210 220 230 240 250 260 270
cry2ab2_820. 280 290 300 310 320 330
A27531_1 260 270 280 290 300 310 320 330
cry2ab2_820.pgp
TXN5:M73251_1
Description: M73251 Bacillus thuringiensis Bacillus thuringiensis (cryIC(b))
gene, complete C
Accession/ID: M73251
=====General comments=====

LOCUS M73251_1 [BACCRYICB]
DEFINITION Bacillus thuringiensis (cryIC(b)) gene, complete CDS. . . .

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SCORES Initl: 128 Inltn: 206 Opt: 245 z-score: 255.7 E(): 2.5e-08
>TXNS:M73251_1
Initn: 206 Inltn: 206 Opt: 245 z-score: 255.7 expect(): 2.5e-08
Smith-Waterman score: 255.7 25.2% identity in 202 aa overlap
(70-263.54-246)

cry2ab2_820. KEMTEWKKNNHSLYDPIVGNASPSKKVGSINWKRLLSELRNLIFFSGSTNIMODILR
40 50 60 70 80 90
M73251_1 DGERISTGSSIDISLSVQSVSNFVPGGFLVG-LQDFWGIWGSQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNQLNTDTLARVNAELTGLQNVENROYNFI--NPNRNVPSITSSVN
100 110 120 130 140 150
M73251_1 --EQLINERIAE--FAR--NAAIANLEGIGNNFNLYKAFKEWEDOPNNVTRTH--IDNER
80 90 100 110 120 130
cry2ab2_820. TMQQLFLNRLFPQFMQGYQLLLPLFAQAANLHLSFYRDVILNADENGISAATLTIRDY
160 170 180 190 200 210 220 230 240 250 260 270
M73251_1 ILDGLERDIPSRISGFEVFLLSVYAQAANLHLSFYRDVILNADENGISAATLTIRDY
140 150 160 170 180 190 200 210 220 230 240 250
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMPFLANFVEXVWSLRYQAL
220 230 240 250 260 270
M73251_1 LIRHIDEYADHCANTYNRGLNLPKSTYQDMITVNRLLRDLTLVLDIAAPFPNRYR
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQQTOSTSQDWPFVLSFQVNSVNLGFSGARLSNTPFNIGLP
280 290 300 310 320 330
M73251_1 PIQPGQLTRVETDPLNFINFQLOSVAQLPTFNWESSAIRNPHLDILNLTITFDWF
260 270 280 290 300 310
cry2ab2_820. pep
TXNS:AF177675_1

Description: AF177675 synthetic construct Synthetic construct Cry 1Ac
Accession/ID: AF177675
=====General comments=====
LOCUS AF177675.1 [AF177675]
DEFINITION Synthetic construct Cry 1Ac insecticidal toxin gene, complete cds;

SCORES Initl: 128 Inltn: 128 Opt: 237 z-score: 252.8 E(): 3.6e-08
>TXNS:AF177675_1
Initn: 128 Inltn: 128 Opt: 237 z-score: 252.8 expect(): 3.6e-08
Smith-Waterman score: 265; 23.1% identity in 584 aa overlap
(60-604.15-565)

cry2ab2_820. FOHKSLOTDVQKEMTEWKKNNHSLYLDPIVGTIVASFLKKVGSIVGKRLISLRNLIFPSG
30 40 50 60 70 80
AF177675_1 MAJETGYTPIIDISLSLTQFLLSBF--VPGAGFVLGLVDIWIWGI
10 20 30 40
cry2ab2_820. SINLMQDLIRETEKFLNQLRNTDTLARVNAELTGL-----QANVEEFNRQVDNPLNPRNA
90 100 110 120 130 140
```

```
AF177675_1 GPSQDAFLVQIEQLINQRLNFAARNAISRLGSLNLYQIYAESFREWEADPTNP---A
50 60 70 80 90
cry2ab2_820. VPLSITSSVNTWQOLFNLRLPQFMQGYQLLLPLFAQAANLHLSFYRDVILNADENGIS
150 160 170 180 190 200
AF177675_1 LREMRIQFNDMSNALTALPLFAVQNIQVPLSVYQAANLHLSFYRDVSVFGQRMGFD
100 110 120 130 140 150
cry2ab2_820. AATLRTRDYLNKTYTRDYSNYCINTYQSAFK---GLNTRLHDMLE---EERTYMFNLNVEPY
210 220 230 240 250
AF177675_1 AATINSRYNDLTRLIGNVTDYAVRWYNTGLERVMGPDNR--DMVRYNQFRRELTLTLDI
160 170 180 190 200 210
cry2ab2_820. VSIWSLUF---KYQSLVLS--GANLYASGSGPQQTOSTSQDWPFVLSFQVNSVNLGPF
260 270 280 290 300 310
AF177675_1 VALFPNYDSRRYPRTVTSQTLREIYTPVLENFQSGFSGAQGIERSIRSPHLMIDLNSI
220 230 240 250 260 270
cry2ab2_820. SGARLSNTPFNIGLPSTTTHALLAARVNSGGISS---GDIGASPFNQNFCST---
320 330 340 350 360
AF177675_1 II--YTDHARGYYWSG-----HOIMASPVGSGPEFTFFLYGTMGNAAPQQRIVLAQLQGG
280 290 300 310 320 330
cry2ab2_820. FPLPPLTPVRSMWSDSDSDEGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYIR
370 380 390 400 410 420
AF177675_1 VYRLSLSLYRRPFNIGINNQQL--SVLDGTEFAYGTSSNLPSSAVYRKSGTIVSLDEIPPO
340 350 360 370 380 390
cry2ab2_820. NISGFLPVRNEDSRRHYNEIRNIAISPGTGGARAYWS--VHNK--NNIHAVEH--
430 440 450 460 470 480
AF177675_1 N--NNVP--PROGFRSLSDYSNFRSGSSNSV--SIIRAPMFSWIHRSAEFNIIIASDSIT
400 410 420 430 440
cry2ab2_820. -----NGSMILNRYNYTGFTLIRHITQVNNOTRTFISEKFGNGQDSLRFEQN
500 510 520 530
AF177675_1 QIEPAVKGFLNFSVLS--GPG--ETLVYRLNS--GNR--ONGYIEVP-----IHPF--
450 460 470 480 490
cry2ab2_820. NITARYTLREGNSYN--LYLRV--SIGSTIRVWIRNRYTATNTNTI--ND--GVNDNGAR
540 550 560 570 580 590
AF177675_1 STSTRYVRVRVASVTPIHLNVR--WGNSSIFS--NTVHATISLDNLQ--SDISYFESANA
500 510 520 530 540 550
cry2ab2_820. FSDINICNVASSNSDVPDLINVTLSGTFQFLMIMHNTNISPPLY
600 610 620 630
AF177675_1 FTS--SIGNIVGVNRPSTGAGVIIDREFEIPVTATLE
560 570 580
cry2ab2_820. pep
TXNS:CIGA_BACTU
Description: Q45746 bacillus thuringiensis, pesticidal crystal protein cryIa
(insecticidal)
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U63378_1 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
FTS-SGIVGRNPGAGVVIIDREFEIPVTATLE
580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820.pep
TXNS:O32306
Description: O32306 bacillus thuringiensis. delta-endotoxin. 6/2001
Accession/ID: O32306
General Comments:
ID O32306 PRELIMINARY;
AC O32306;
DT 01-JAN-1998 (TRENDEL. 05, Created)
SCORES Initl: 128 Initn: 128 Opt: 237 Z-score: 252.4 E(): 3.7e-08
>>TXNS:O32306
initn: 128 initl: 128 opt: 237 Z-score: 252.4 expect(): 3.7e-08
Smith-Waterman score: 257; 22.6% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820. FOHKSLOTQKEMKNNHSLYLPDPIGVTVASPLKKGSLVKGKRLSELNLIFFPG
30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200
O32306 IPYNCLSNPEVEVLGGRIETGTPIDISLSTQFLUSEP--VFGAGFVLGLVDIIWGIF
20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200
cry2ab2_820. STNLMDILRETEKFLNQLNLTDLARVNAELTGL---QANVEEFNRQVDNLFNADENGIS
90 100 110 120 130 140 150 160 170 180 190 200
O32306 LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRMGFD
130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLIQIYAESFREWEADPTNP---A
70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. AATLRTYRDYLNKNTYDSNYCINTYOSAFK---GLNTRLHMDL---EFTYMFNLNVEY
210 220 230 240 250
O32306 AATINSRYNDLTRLIGNYTHAVRWNTGLERVWGPDSR--DWIRYMQFRRELTIVLDI
190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. VSLTSSLFYQSLVSSGANL---YASGSGPQQTQSFTSQDMPFLSLFQVNSNYLVNGF
260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSPFGSAQIGEGSIRSPLHMDILNSI
250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. SGARLSNFPNIVGLPGSTTHALLAARVNSGGISS---GIGASFPNQFNCSF---
320 330 340 350 360
O32306 T-----IYDAHREGYWGSQHGMASPVGFGSGPEFTFPLYGTMGNAAFPQORVLAQLGQG
310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. FLPLPLTFFVRSLDSDGREGVATVNWQTESPETTLGLRSCAFTAGNSYFDFYFIR
370 380 390 400 410 420
O32306 VYFTLSLYRRFPNIGLNQQQL--SVLDGTETFACTSSNLFPSAVYKSGTIVDSLEIPFQ
360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
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cry2ab2_820. NISGVFLVWNEDLRRPLHYNEIRNIASPSGTFPGGARVMVS-VHNRK--NNIHAVHE--
430 440 450 460 470 480
O32306 N-NNVP--PROGFSHELSHVSMFSGFSSSV-SIIRAPMFWSIHRSAEFNNIIASDSIT
420 430 440 450 460 470
cry2ab2_820. -----NGSMHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNGDGLRFEQN
490 500 510 520 530
O32306 QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNNGNNIQRNGYIEVP-----IHFP--
480 490 500 510 520
cry2ab2_820. NITARYTLRNGNSYN-LYLRVSSISGSTRVINGRVYATVNTTINND-GVNDNGAR
540 550 560 570 580 590
O32306 SISTRIRYRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLONLQSSDFGYFESANA
530 540 550 560 570
cry2ab2_820. FSDINIGNVVASNSDVPLDINVTLNNGTQFDLMNMLVPTNISPLY
600 610 620 630
O32306 FTS-SLGNIVGVNFGSTAGVIIDRFEPFVPTATLEAYNL
580 590 600 610
cry2ab2_820.pep
TXNS:Y09787_1
Description: Y09787 Bacillus thuringiensis B.thuringiensis cryIA(c) gene;
infectious crystal
Accession/ID: Y09787
General Comments:
LOCUS Y09787.1 (BSCRYDEL)
DEFINITION B.thuringiensis cryIA(c) gene;
SCORES Initl: 128 Initn: 128 Opt: 237 Z-score: 252.4 E(): 3.7e-08
>>TXNS:Y09787_1
initn: 128 initl: 128 opt: 237 Z-score: 252.4 expect(): 3.7e-08
Smith-Waterman score: 257; 22.6% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820. FOHKSLOTQKEMKNNHSLYLPDPIGVTVASPLKKGSLVKGKRLSELNLIFFPG
30 40 50 60 70 80
Y09787_1 IPYNCLSNPEVEVLGGRIETGTPIDISLSTQFLUSEP--VFGAGFVLGLVDIIWGIF
20 30 40 50 60 70 80
cry2ab2_820. STNLMDILRETEKFLNQLNLTDLARVNAELTGL---QANVEEFNRQVDNLFNADENGIS
90 100 110 120 130 140
Y09787_1 GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLIQIYAESFREWEADPTNP---A
70 80 90 100 110 120 130 140
cry2ab2_820. VPLSITSSVNTMQQLFNLKLPQFMQGYQLLLPLFAQAANLHLSFIRVILNADENGIS
150 160 170 180 190
Y09787_1 LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQRMGFD
130 140 150 160 170 180 190
cry2ab2_820. AATLRTYRDYLNKNTYDSNYCINTYOSAFK---GLNTRLHMDL---EFTYMFNLNVEY
210 220 230 240 250
Y09787_1 AATINSRYNDLTRLIGNYTHAVRWNTGLERVWGPDSR--DWIRYMQFRRELTIVLDI
190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. VSLTSSLFYQSLVSSGANL---YASGSGPQQTQSFTSQDMPFLSLFQVNSNYLVNGF
260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
VSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDGSPFGSAQIGEGSIRSPLHMDILNSI
250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. SGARLSNFPNIVGLPGSTTHALLAARVNSGGISS---GIGASFPNQFNCSF---
320 330 340 350 360
Y09787_1 T-----IYDAHREGYWGSQHGMASPVGFGSGPEFTFPLYGTMGNAAFPQORVLAQLGQG
310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cry2ab2_820. FLPLPLTFFVRSLDSDGREGVATVNWQTESPETTLGLRSCAFTAGNSYFDFYFIR
370 380 390 400 410 420
Y09787_1 VYFTLSLYRRFPNIGLNQQQL--SVLDGTETFACTSSNLFPSAVYKSGTIVDSLEIPFQ
360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
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190      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      540      550      560      570      580      590
cry2ab2_820. VSIWLFYQSLVSSGANL-----YASGGPQQTQSTQSDMPFLYSFQVNSVNLNGF
Y09787_1      VSLFNYSRTYPIRTVTSQLTREIYTNFVLENFDGSGFRGSAQIEGSIKRSPLHMDLNSI
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      540      550      560      570      580      590
cry2ab2_820. SGARLSNTFPNIVGLPGSTTTHALLAARVNVSGISS-----GDIGASPNQFNCSF---
Y09787_1      T-----IYDAHRGEYWSGHOIMASPVGSGPEFTFPFLYGTMGNAAPQRIVAQLGQG
310      320      330      340      350      360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530      540      550      560      570      580      590
cry2ab2_820. FLFPPLTFPVRSMLDGSDREGVATVWVQTESPETTLGLRSAGFTARGNSNYPPDYFIR
Y09787_1      VYRTLSSTLYRRPENGINNQOL-SVLGDTEFAXGTSSNLPASAVYKSGTVDSDLEIPPO
360      370      380      390      400      410      420      430      440      450      460      470      480      490      500      510      520      530      540      550      560      570      580      590
cry2ab2_820. NLSGVPLVRNEDRLPHLYNEIRNISPSTGGARAYMVS-VNHRK--NNIHAVHE--
Y09787_1      N--NNYP--PROGFSHRLSHVSMFRSGFNSSV-SIIRAPMFWIHRSAEFNNIIASDSIT
420      430      440      450      460      470      480      490      500      510      520      530      540      550      560      570      580      590
cry2ab2_820. -----NGSMIHLAPNDYGTFTSPIHATOVNNOIRTFISEKFGNQGDSLRFEQN
Y09787_1      QIPAVKGNFLNGSVIS-GEF-FTGDDLVRLNSGNNIQNGYIEVP-----IHPF--
480      490      500      510      520      530      540      550      560      570      580      590
cry2ab2_820. NTATRYTLRGNSYN-LXLRVSSIGNSTIRVTINGRVYATNVTNNTND-GVNDNGAR
Y09787_1      STSTRYRVRYASVTPPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYESANA
530      540      550      560      570      580      590
cry2ab2_820. FSDINIGNVASSNSDVPIDINVLNSGTQFDLMNIMLVPTNISPLY
Y09787_1      FTS-SLGNIVGVNFGSGTAGVIIDRFEPFIVTATLEAYNL
580      590      600      610      620      630
cry2ab2_820.pgp
TXN5:X07518_1

Description: X07518 Bacillus thuringiensis Bacillus thuringiensis gene for
delta-endotoxin: p
Accession/ID: X07518
=====General comments=====
LOCUS X07518_1 [BTEOXD]
DEFINITION Bacillus thuringiensis gene for delta-endotoxin; ...

SCORES Initl: 200 Initn: 200 Opt: 239 z-score: 249.3 E(): 5.6e-08
>TXN5:X07518_1
Initn: 200 Initl: 200 Opt: 239 z-score: 249.3 expect(): 5.6e-08
Smith-Waterman score: 239; 24.8% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KEWTEWKNNHSLYLDPIVGTVASFLKVKVSLGKRIILSELRLNLIFFSGSTNLMQDILR
40      50      60      70      80      90
```

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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      540      550      560      570      580      590
X07518_1      DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGVGFSQWDAFLVQI--
30      40      50      60      70
cry2ab2_820. ETEKFLNRINTDTLARVNAELTGLQANVEENRQVDMFL---NPNNAVPLSITSSVN
X07518_1      --EOLINERIAE--FAR-NAAIANLEGLNPNFIYVEAFKEWEEDPNNPETRTTRVIDRFR
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      540      550      560      570      580      590
cry2ab2_820. TMOQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAAATLRTYRDY
X07518_1      ILDGLLERDIPSGFRISGFEVFLLSVYAQAANLHLALRDSVIFGERWGLTTINVAENYNR
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      540      550      560      570      580      590
cry2ab2_820. LKNITRDYSNYCINTYQAFKGL-NTRLHDMLEF--RTYMLNVFEYVSIWSLFKYQSL
X07518_1      LIRHIDEYAHCAVTYRGLNLPKSTYQDMITYNLRRLRDLTLTVDIAAFAFPNRY
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      540      550      560      570      580      590
cry2ab2_820. LVSSGANLYASGSGPQQTQSTQSDMPFLYSFQVNSVNLNGFSGARLSNTEFPNIVGLP
X07518_1      PLOPVGQLTREYVTDPLINFPNLOQSVAQLPTFNWESSRIRNPHELDILNLTITPTDMF
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      540      550      560      570      580      590
cry2ab2_820.pgp
TXN5:X09872_1

Description: U9872 Bacillus thuringiensis Bacillus thuringiensis CryIac
delta-endotoxin gene
Accession/ID: U9872
=====General comments=====
LOCUS U9872_1 [BTEOXD]
DEFINITION Bacillus thuringiensis CryIac delta-endotoxin gene, complete cds. ...

SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 247.2 E(): 7.3e-08
>TXN5:U9872_1
Initn: 128 Initl: 128 Opt: 237 z-score: 247.2 expect(): 7.3e-08
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(160-604:41-591)

cry2ab2_820. FQHKSLDTVQKEWTEWKNNHSLYLDPIVGTVASFLKVKVSLGKRIILSELRLNLIFFSG
U9872_1      IPYNCILSNPEVEVLGGERIETGTPIDISLSTQELLSEF--VPGAGFVLGLVDIWIIF
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      540      550      560      570      580      590
cry2ab2_820. STNLMQDILRETEKFLNCRINTDTLARVNAELTGL---QANVEENRQVDMFLNPNRNA
U9872_1      GPSQWDAFLVQIEQLINQRIIEEFARNQALISRLGLSNLYQIYAESFREWEADPTNP---A
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      540      550      560      570      580      590
cry2ab2_820. VPLSITSSVNTMQQLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGIS
U9872_1      LREEMRIQNDMNSALITATPLFAVQNVQVFLLSVYQAANLHLSVIRDSVFGQWGF
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      540      550      560      570      580      590
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cry2ab2_820. AATLRTYRDYKXNYTRDYSNYCINTYOSAFK---GLNTRLHDM---EFTYMFVNFVEY
U89872_1 AATNSRNDLRLGNVYVAVWYNTGLERVWGPDSR--DWVRYNQFRRLTLVLDI
cry2ab2_820. VSIWMLF--KYOSLLVSS--GANLYASGSGPOOTQSTFSDMPFLYSLFQVNSNYLVNGF
U89872_1 VALFNDYSRRYFIRYTSQLTREIYTPVLENFDSFGSQAQGIERSIRSPHMLDILNSI
cry2ab2_820. SCARLSNTFFNIVGLPGSTTTHALLAARVNVSGISS---GDIGASPFNQNFNCST---
U89872_1 TI--YTDHRYGYWWSG---HQIMASPGVSGPEFTFPLGYGTMGNAFQQRIVAQLOGG
cry2ab2_820. FLPLPPLTPFVRSWLDGSDREGVATVWVWQTESFETTLGLRSGAFTAGNSNYFPDYFIR
U89872_1 VYRTLSSTLYRRFPNIGINNCOOL--SVLDGTEFAVGTSSNLPSPALRYNSGTVDSLDLEIPQ
cry2ab2_820. NISGVPLVVRNEDLRLPLHNEIRNIASPGTGGARAYNVS--VHNRK--NNIHAVEH--
U89872_1 N--NNVP--PRQGFSHRLSHVSMFSGFNSSV--SIIRAPMFSWIRSAEFNIIASDSIT
cry2ab2_820. NGSMIHLAPNDYTGFTTSPHATOVNVNQTFTFISEKFGNGDGLRPEQN
U89872_1 QIPAVKGNFLNGSVIS--GPG--FTGCDLVRNLSSGNNIQRGVIEVP-----IHFP--
cry2ab2_820. NTTARYTLRNGNSYN--LYLRVSSIGNSTIRVYTINGRVYATNVNTTND--GYNDNGAR
U89872_1 STSTRYRVRYASVTPHILNVN--WGNSSIFS--NTVPATATSLONLQSSDFGYFESANA
cry2ab2_820. FSDINIGNVASSNSDVPLDINVTLSGTFQDLMNIMLVFTNISPLY
U89872_1 FTS--SLGINVGRVNFSGTAGVIDRFPFVPTATLEAYNLERPAQKAVNALFTSTNOLGL
cry2ab2_820.pcp
TXN5:U87793_1
Description: U87793 Bacillus thuringiensis subsp. kurstaki Bacillus
thuringiensis kurstaki in
Accession/ID: U87793
=====General comments=====
LOCUS U87793.1 [BTU87793]
DEFINITION Bacillus thuringiensis kurstaki insecticidal delta-endotoxin
SCORES Initl: 128 Initn: 128 Opt: 237 Z-score: 247.2 E(): 7.3e-08
>>TXN5:U87793_1
initn: 128 initl: 128 opt: 237 Z-score: 247.2 expect(): 7.3e-08
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
```

```
(60-604:41-591)
cry2ab2_820. FQHKSLDTVQKEWTEWKNNHSLYLDPIVGTVASFLLKKVGSVLGKRIILSELNLIFFSG
U87793_1 IPYCNLSNEVEVLGGERIETGVTPTDISLSITQFLISEF--VPGAGFVLGLVDIIGCIF
cry2ab2_820. STNLMDILIRETEKFLNQRLTNTDLARVNAETGL---QANVEEFNRQVDNPLNPRNA
U87793_1 GPSQWDAFLVQTEQLINQRIEEFARNQAIISRLGSLNLYQIYAESFREWEADPTNP---A
cry2ab2_820. VPLSITSSVNTMOQLFLNRLPQOMOGYQOLLLPLFAQAANLHLSFIRDVILNADEMGIS
U87793_1 LREMRIQFNDNMNSALITAIPLFAVQNYQVPLLSVYVOANLHLSVLRDVSFVGORGWGF
cry2ab2_820. AATLRTYRDYKXNYTRDYSNYCINTYOSAFK---GLNTRLHDM---EFTYMFVNFVEY
U87793_1 AATINSRYNDLRLGNVYVAVWYNTGLERVWGPDSR--DWVRYNQFRRLTLVLDI
cry2ab2_820. VSIWMLF--KYOSLLVSS--GANLYASGSGPOOTQSTFSDMPFLYSLFQVNSNYLVNGF
U87793_1 VALFNDYSRRYFIRYTSQLTREIYTPVLENFDSFGSQAQGIERSIRSPHMLDILNSI
cry2ab2_820. SCARLSNTFFNIVGLPGSTTTHALLAARVNVSGISS---GDIGASPFNQNFNCST---
U87793_1 TI--YTDHRYGYWWSG---HQIMASPGVSGPEFTFPLGYGTMGNAFQQRIVAQLOGG
cry2ab2_820. FLPLPPLTPFVRSWLDGSDREGVATVWVWQTESFETTLGLRSGAFTAGNSNYFPDYFIR
U87793_1 VYRTLSSTLYRRFPNIGINNCOOL--SVLDGTEFAVGTSSNLPSPALRYNSGTVDSLDLEIPQ
cry2ab2_820. NISGVPLVVRNEDLRLPLHNEIRNIASPGTGGARAYNVS--VHNRK--NNIHAVEH--
U87793_1 N--NNVP--PRQGFSHRLSHVSMFSGFNSSV--SIIRAPMFSWIRSAEFNIIASDSIT
cry2ab2_820. NGSMIHLAPNDYTGFTTSPHATOVNVNQTFTFISEKFGNGDGLRPEQN
U87793_1 QIPAVKGNFLNGSVIS--GPG--FTGCDLVRNLSSGNNIQRGVIEVP-----IHFP--
cry2ab2_820. NTTARYTLRNGNSYN--LYLRVSSIGNSTIRVYTINGRVYATNVNTTND--GYNDNGAR
U87793_1 STSTRYRVRYASVTPHILNVN--WGNSSIFS--NTVPATATSLONLQSSDFGYFESANA
cry2ab2_820. FSDINIGNVASSNSDVPLDINVTLSGTFQDLMNIMLVFTNISPLY
```

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U87793_1
FTS-SIGNIVGVNFSGTAGVIIDRFEFIPVTATLEAYNLERAKVNALETSTNQLGI
580 590 600 610 620 630

cry2ab2_820.pep
TXN5:C1AC BACTK

Description: P05068 bacillus thuringiensis (subsp. kurstaki). pesticidal crystal protein cry
Accession/ID: P05068

```
=====General comments=====
ID  CIAC_BACTK  STANDARD;  PRT;  1178 AA.
AC  P05068; . . .
```

```

SCORES      Init1: 128      Intn: 128      Opt: 237      z-score: 247.2 E(): 7.3e-08
>ixXNS:ClAC_BACTK
Init1: 128      Intn: 128      Opt: 237      z-score: 247.2 expect(): 7.3e-08
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(60-604:41-591)

```

cry2ab2_820. FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTASFLKKVGSVLGKRIISLSELNLIIPFSG
 30 40 50 60 70 80
 CIAC_BACTK IPNYCISNPEVGLGGERITGVTPIDISLTSQFLSEF--VPGAGFVLGVLVDIWGIF
 20 30 40 50 60 70 80

```

90      cry2ab2_820.          100    110    120    130    140
STNIMDILRETEKELQNRINTDTLARVNAELTGL---QANVEEFNRQVDNFLPNRNA
:   :   :   :   :   :   :   :   :   :   :   :   :   :
70      GP5OWDAFLVQTEQLNQINRTEEFARQAQTSRLGLESLNYLVIAEFSFMEAEPTNP---A

```

```

cry2ab2_820. VPSITSSYNTQQQLNRLPQFMQGYQLLLPLFAQAANHLSTROVLINADWGIS      150    160    170    180    190    200
               :   |   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
CIAC_BACTK LREMRIQFNDMSNALTTAIPFLAVQNYQVPLFSYVQAANHLHLSVRDVSVFGRWGWF      130    140    150    160    170    180

```

[illegible]

```
cry2ab2_820_VSTWSLF--KYQSLVSS-GANYASGGPQQOTSOTSDWFLYSLFQNNSNVLNGF  
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::  
VALFPNYSRRPYRTVSQTREIYNPLENFDSFGSQAQGISRSRPHLMIDLSI  
CIAC_BACTK      260    270    280    290    300    310
```

```

320      330      340      350      360
SGARLNTFPNVLPGSTTHALLAARVNVSGISS-----GDIGASPPNQNFNCST---
: : : : : : : : : : : : : : : : : : : : : : : : : : : :
T1--YTDARHGYVWSG-----HOIMASPVGSGPEFFPLFYLTGMGVAAPQOIRVAQLGQG

```

CIA_C_BACTK

370	380	390	400	410	420
FLPPLLTPVRSRLDSDSGREGVATVMNQTESFETTLGLRGSAGFTARGNSNYFDYFIR	:	:	:	:	:
VYRTLSSTLYRPFGINNNQOL-SVLDDGTFFAYGTSNLPASVARYKSTCVDSLDITPPQ	:	:	:	:	:
376	380	384	390	400	410
430	440	450	460	470	480

[illegible]

```
cyt2ab2_820.      -----NGSMIHAFNDYGTISPIHATOVNQTTRTISEKFGNOGDSJREFQN  
                   ||||| :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|: | :|  
  
CIAC_BACTK       QIPAVKGNFLFNGVS-GPG-FTGGDLVRLNSNNNTQNRGYIEVP-----IHPF--  
                   480    490    500    510    520
```

[illegible]

```

cry2ab2_820.   FSDINTNGVWASSSDVFDLNTVLTMSGQFDLMNIMLVPTNISPLY
                ||:|:|:|:|:|
CIAC_BACTK    FIS-SLGNITGVYRNSGTAGVIIDREFEFTVATLEAYNLAKRAVNAFLTSTNOIGL
                580      590      600      610      620      630

```

cry2ab2_820.pep
TXN5:U43606_1

```

Description: U43606 Bacillus thuringiensis Bacillus thuringiensis cryIA(c)
gene, partial cds:
Accession/ID: U43606
=====General Comments=====
LOCUS      U43606_1 [BTU43606]
DEFINITION Bacillus thuringiensis cryIA(c) gene, partial cds. . .

```

SCORES Initl: 128 Initn: 128 Opt: 231 z-score: 246.2 E(): 8.3e-08
 >>RXNS:U43606.1
 initn: 128 initl: 128 opt: 231 z-score: 246.2 expect(): 8.3e-08
 Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
 (60-604:41-590)

```
cry2ab2_820. FQKSLDTVQKEWTEWKNNHSDYLDPIGVTVASFLIKVKVSGLVGRILISRLNLIFFPSG
IPNCLSNEPEVLGGRIETGYPIDTISLQTFLLSE--VPGAGFVLGVLDIINGIF
U43606_l      20   30   40   50   60   70   80
```

```

90      100      110      120      130      140
cry2ab_820. STNLMQDLIRETKFNLRINTDTLARVNAELTG----QANVEFPRQVNFINPNNRA
          :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
U43606 1     GPSSDAFIIVTEQLINVRTEEFARNQAISRLGTSNIYGVAESEFRFEWADTNP-----

```

```

cry2ab2_820. VPLSITSSVNTMOQLFLNRLPQFMQOGYQLLLFLPQAANLHLSFIRDVLINADENGIS
150 160 170 180 190 200
LREMRIQPNMNSALTTALFLAVONTQVFLSVYQVAANLHLSVLREDSVVFQRMGFD
130 140 150 160 170 180
U43606_1

```

```

210      220      230      240      250
AATLRTYRDYLKNYTRDYSNCINTYQSAFK--GLNTRLHDLML--EFRYTMFLNVFEY
||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
AATINSRNDUTRLIGNTYDYAVRNVTGLSRVGGPDSR--DWVRNQFRELLETLVTDI
UA43606_1

```


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```
cry2ab2_820. 190 200 210 220 230 240
cry2ab2_820. 240 250 260 270 280 290 300 310
U43606_1 250 260 270 280 290 300 310
cry2ab2_820. 320 330 340 350 360
U43606_1 320 330 340 350 360
cry2ab2_820. 370 380 390 400 410 420
U43606_1 370 380 390 400 410 420
cry2ab2_820. 430 440 450 460 470 480
U43606_1 430 440 450 460 470 480
cry2ab2_820. 490 500 510 520 530
U43606_1 490 500 510 520 530
cry2ab2_820. 540 550 560 570 580 590
U43606_1 540 550 560 570 580 590
cry2ab2_820. 600 610 620 630
U43606_1 600 610 620 630
cry2ab2_820.pcp
TXNS:Q45721
Description: Q45721 bacillus thuringiensis. cryIIa(c) (fragment). 6/2001
Accession/ID: Q45721
ID Q45721; PRELIMINARY;
AC Q45721; PRT; 607 AA.
DT 01-NOV-1996 (TRENDEL. 01, Created)

SCORES Initl: 128 Initn: 128 Opt: 231 z-score: 246.2 E(): 8.3e-08
>>TXNS:Q45721
Initn: 128 Initl: 128 Opt: 231 z-score: 246.2 expect(): 8.3e-08
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. 30 40 50 60 70 80
FOHKS LDTVQKEWTEWKKNNHSLYLDPIVGTAVASFLKKVGLGKRLISELRNLIFPSG
```

```
Q45721 IPTNCLSPVEVLGGERIETGYTPIIDISLSTOFLSEF--VPGAGFVLGLVLIWGIF
20 30 40 50 60
cry2ab2_820. 90 100 110 120 130 140
cry2ab2_820. 150 160 170 180 190 200
Q45721 GQSDMDALVQIEQLINQRIEFARNOAISLEGSLNLYQIYAESFEWEADPTNP--A
70 80 90 100 110 120
cry2ab2_820. 150 160 170 180 190 200
Q45721 LREEMRIQFNDMSALITAIPLAVQNYQVPLLSVYVQANLHLSVLRDVSFGQWGF
130 140 150 160 170 180
cry2ab2_820. 210 220 230 240 250
Q45721 AATLRYDYRLKNTYRDSNYCINTYQSAFK---GLNTRLHDML---EFTYMFNVFEY
210 220 230 240 250
cry2ab2_820. 260 270 280 290 300 310
Q45721 VALFNYDSRRYPIRTVYQUTREIYINPVLENFQSGPRGSAQGIERSIRSPHLMILNSI
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350
Q45721 SGANLNTFNVIPVLPSTTHALLAARVNVSGGSS---GDIGASPENQNCST---
320 330 340 350
cry2ab2_820. 370 380 390 400 410 420
Q45721 VRTLSSTNRRPFIINQNL--VLDGTEFAVGTSSNLPASAVYRKSGTVDSLOEIPPQ
370 380 390 400 410 420
cry2ab2_820. 430 440 450 460 470 480
Q45721 N-NNVP--PROGFSRLSHVSMFSGSSSVSI--IRAPMFSWIHRSAEFNNIISDSIT
430 440 450 460 470 480
cry2ab2_820. 490 500 510 520 530
Q45721 QIPAVKGNFLNGSVIS-GPG-FTGGDLVAVNSGNNIQNGYIEVP-----IHFP--
490 500 510 520 530
cry2ab2_820. 540 550 560 570 580 590
Q45721 NTARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGKRVYTNNTITND-GVNDGAR
540 550 560 570 580 590
cry2ab2_820. 600 610 620 630
Q45721 STSTRYRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLNLSQSDFGYFESANA
600 610 620 630
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cry2ab2_820.pep
TXN5:Q45737

Description: Q45737 bacillus thuringiensis. cryIIa(c) insecticidal crystal
protein (lepidopteran)
Accession/ID: Q45737
=====General comments=====
ID Q45737 PRELIMINARY; PRT; 618 AA.
AC Q45737;

SCORES Initl: 128 Initn: 128 Opt: 231 z-score: 246.0 E(): 8.5e-08
>>TXN5:Q45737
initn: 128 initl: 128 opt: 231 z-score: 246.0 expect(): 8.5e-08
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKXVGLVKGKILSELNLIFFPSG
30 40 50 60 70 80
420 430 440 450 460 470

Q45737 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIMGIF
20 30 40 50 60
480 490 500 510 520

cry2ab2_820. STNLMDILRETEKFLNQRLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPNRNA
90 100 110 120 130 140
490 500 510 520 530

Q45737 LREEMRIQFNQDMSALTTAIPLLAVQNYQVPLLSVYVQAANHLHSLVRDVSFVGQWGF
130 140 150 160 170 180
540 550 560 570 580 590

cry2ab2_820. AATLRTYRDYLNKNTDYSNYCINTYQSAFK---GLNTRLHDM---EFTYMLFNVEY
210 220 230 240 250
590 600 610 620 630

Q45737 AATINSRYNDLTRIGNYTDYAVRWNTGLERVWGPDSR--DWVRNQFRRLTLVLDI
190 200 210 220 230 240
640 650 660 670 680 690

cry2ab2_820. VSTWLSF---KYQSLVSS--GANLYASGSPQQTQSTQSDWPFYLSLFQVNSYVLMGF
260 270 280 290 300 310
700 710 720 730 740 750

Q45737 VALFPNYSRRYPRTVSQLTREIYTNPVLENFQSGFRGSAQGIERSIRSPHLMILNSI
250 260 270 280 290 300
760 770 780 790 800 810

cry2ab2_820. SGARLSNTPFNVLGPGSTTHALLAARVNSGGISS-----GDIGASPNQNFNCST---
320 330 340 350 360
820 830 840 850 860 870

Q45737 TI--YTDARHGYWWSG---HQIMASPVGSGGPEFTFPLYGTMGNAAPQQRVAQLQGG
310 320 330 340 350
880 890 900 910 920 930

cry2ab2_820. FLPLLTTPVRSWLDSDREGVATVWNQTESFETTLGLRSQAFRTAGNSYFPDYFIR
370 380 390 400 410 420
940 950 960 970 980 990

Q45737 VYRTLSSTFYRRFPFNIGINNQQ--SVLDGTETEFAYGTSSNLPSPVAYRKSQSTVDSLDLPIPPQ
360 370 380 390 400 410
1000 1010 1020 1030 1040 1050

cry2ab2_820. NISGVPLVVRNEDLRRLPHYNEIRNIASPGTPGGARAYMVS--VHNK--NNIHAVH--
430 440 450 460 470 480
1060 1070 1080 1090 1100 1110

Q45737 N--NNVP--PRQGFSLRSHSVSMFRSGSSSVSI--IRAPWFSWTHRSASFENIIASDSIT
430 440 450 460 470 480
1120 1130 1140 1150 1160 1170
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cry2ab2_820. -----NGSMHILAPNDYTGFTISPIHATQVNNOTRTFISEKFGNQDSLRFQEQN
490 500 510 520 530
540 550 560 570 580 590

Q45737 QIPAVKGNFLPNSVIS--GPG--FTGGDLVRLSSGNNIQNGYIEVP-----IHFP--
480 490 500 510 520
600 610 620 630 640 650

cry2ab2_820. NNTARYTLRGNGSYN--LYLRAVSSIGNSTIRVTINGRVYVATNTVNTTND--GVNDNGAR
540 550 560 570 580 590
600 610 620 630 640 650

Q45737 SISRIVRVRYASVTPHLLVN--WGNSSIFS--NTVPAITASIDNLQSSDGFYFESANA
530 540 550 560 570 580 590

cry2ab2_820. FSDINIGNVVASNSDVPLDINVTINSQTQFDLMNIMLVPTNISPLY
600 610 620 630
640 650 660 670 680 690

Q45737 FTS--SLGNIYGVNFSGTAGVIIDRFEFIPVPTATLEAYNLE
580 590 600 610
700 710 720 730 740 750

cry2ab2_820.pep
TXN5:AF081248_1

Description: AF081248 Bacillus thuringiensis Bacillus thuringiensis
plasmid-encoded lepidoter
Accession/ID: AF081248
=====General comments=====
LOCUS AF081248.1 (AF081248)
DEFINITION Bacillus thuringiensis plasmid-encoded lepidoteran-specific toxin.

SCORES Initl: 128 Initn: 157 Opt: 235 z-score: 245.1 E(): 9.6e-08
>>TXN5:AF081248_1
initn: 157 initl: 128 opt: 235 z-score: 245.1 expect(): 9.6e-08
Smith-Waterman score: 261; 22.5% identity in 609 aa overlap
(60-634:41-609)

cry2ab2_820. FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKXVGLVKGKILSELNLIFFPSG
30 40 50 60 70 80
420 430 440 450 460 470

AF081248_1 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIMGIF
20 30 40 50 60
480 490 500 510 520

cry2ab2_820. STNLMDILRETEKFLNQRLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPNRNA
90 100 110 120 130 140
540 550 560 570 580 590

AF081248_1 GPSQWDAFLVQIEQLNQRIEIEFARNQAIISLEGLSNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
600 610 620 630 640 650

cry2ab2_820. VPLSITSVNTMQQLFNRLPQFMQGYQLLLPLFPAQANHLHSLFIRDVILNADEWGIS
150 160 170 180 190 200
660 670 680 690 700 710

AF081248_1 LREEMRIQFNQDMSALTTAIPLLAVQNYQVPLLSVYVQAANHLHSLVRDVSFVGQWGF
130 140 150 160 170 180
720 730 740 750 760 770

cry2ab2_820. AATLRTYRDYLNKNTDYSNYCINTYQSAFK---GLNTRLHDM---EFTYMLFNVEY
210 220 230 240 250
780 790 800 810 820 830

AF081248_1 AATINSRYNDLTRIGNYTDYAVRWNTGLERVWGPDSR--DWVRNQFRRLTLVLDI
190 200 210 220 230 240
840 850 860 870 880 890

cry2ab2_820. VSTWLSF---KYQSLVSS--GANLYASGSPQQTQSTQSDWPFYLSLFQVNSYVLMGF
260 270 280 290 300 310
900 910 920 930 940 950

AF081248_1 VALFPNYSRRYPRTVSQLTREIYTNPVLENFQSGFRGSAQGIERSIRSPHLMILNSI
250 260 270 280 290 300
960 970 980 990 1000 1010

cry2ab2_820. SGARLSNTPFNVLGPGSTTHALLAARVNSGGISS-----GDIGASPNQNFNCST---
320 330 340 350 360
1020 1030 1040 1050 1060 1070

AF081248_1 TI--YTDARHGYWWSG---HQIMASPVGSGGPEFTFPLYGTMGNAAPQQRVAQLQGG
310 320 330 340 350
1080 1090 1100 1110 1120 1130

cry2ab2_820. FLPLLTTPVRSWLDSDREGVATVWNQTESFETTLGLRSQAFRTAGNSYFPDYFIR
370 380 390 400 410 420
1140 1150 1160 1170 1180 1190

AF081248_1 VYRTLSSTFYRRFPFNIGINNQQ--SVLDGTETEFAYGTSSNLPSPVAYRKSQSTVDSLDLPIPPQ
360 370 380 390 400 410
1200 1210 1220 1230 1240 1250

cry2ab2_820. NISGVPLVVRNEDLRRLPHYNEIRNIASPGTPGGARAYMVS--VHNK--NNIHAVH--
430 440 450 460 470 480
1260 1270 1280 1290 1300 1310

AF081248_1 N--NNVP--PRQGFSLRSHSVSMFRSGSSSVSI--IRAPWFSWTHRSASFENIIASDSIT
430 440 450 460 470 480
1320 1330 1340 1350 1360 1370
```

CIAG_BACTU IPYNCLSNPEVEVLGERIETGYTPDIDSLSITQFLSEF---VPGAGFVLGLVDLWIGFI
 20 30 40 50 60
 cy2ab2_820 STNLMODILRETEKFLNORLNTDTLARVAELTGL---QANVEFNQVDNFLAPNRNA
 90 110 120 130 140
 CIAG_BACTU GPSQWDAFLVOIEQLINRIEFPARQCAISRLEGLSNLYQIYAESFREWEADTPV---A
 70 80 90 100 110 120
 cy2ab2_820 VPLSITSSVNTMOQLFLNRLFOFOMQYQLLLPLFAQAANHLHSFTRIVILNADWGIS
 150 160 170 180 190 200
 CIAG_BACTU LREEMRIQOFNDMNSALTITAPLLAVONYQVELLSVYVQAANHLHSVLRLDVSVFGRGWGF
 130 140 150 160 170 180
 cy2ab2_820 AATLRTYRDVLYKNRYDRVSNICINTYQSAFK---GLNTRLHML---EFTYFNFLNVEFY
 210 220 230 240 250
 CIAG_BACTU AATINSRYNDLRLTGINGYTDYAVRWNTGLERAWGPDGR---DWRYNQRFRELTITVLADI
 190 200 210 220 230 240
 cy2ab2_820 VSIWSLF---KYQSLLVSS-GANLYAS-----GSGPQOTQSFQ-DWPELSLFOVN
 260 270 280 290 300
 CIAG_BACTU VALFSYDSSRPITVTSQLTREIYINPVLENFDSFGMAQRIEPEYQPHLMOLLNSI
 250 260 270 280 290
 cy2ab2_820 GNY--VLNGF---SGARLSNTPFNIVGLPGSTITHALLAARVNSYSGISGDIGASPNQ
 310 320 330 340 350 360
 CIAG_BACTU SYLTDVHRGNYWSGHOITTS-P-VGSGPEFTPLXYGVNAAPORIAQTGLGIFR-
 310 320 330 340 350
 cy2ab2_820 NFNGSFTPLPLTPFRWMLSGSDREGVATVNNQTESPT-TLGRSGAATARGNSY
 370 380 390 400 410 420
 CIAG_BACTU ---TLGSL---YRNILSGPNQEL-FVLGDTEFSASLTPLPSTIYRQRTGVS
 360 370 380 390 400 410
 cy2ab2_820 FPDYFENAGVPLVAFVTPRRLPHNERENIASPSTPGGARAYMVSVHNRKNHIAV
 430 440 450 460 470 480
 CIAG_BACTU L-DVIPPQUNSP-PRAGFRISH---VPMISORAGVTVLRASFLLL-----VILLI
 420 430 440 450
 cy2ab2_820 HENGSMIHLAPNDYTGFTISHLAOWNQVTF SEFGNODS-RFQNNNTARYTLR
 490 500 510 520 530 540
 CIAG_BACTU HARSIFNNIIPSSQITQSFX-----HLISVSVKPGFTG-DILRPSGLIS-TLR
 460 470 480 490 500 510
 cy2ab2_820 GN-----GNSYNLYLRVSSIGNSIRTVINGRYVTAIVNNNTINNVDNGAREFSANI
 550 560 570 580 590
 CIAG_BACTU VNITAPLSQRYRVIRYAFTTNLQFTSIDGRFINQGNFYATNS- GSNLSGFTVGVF
 520 530 540 550 560
 cy2ab2_820 GNVVASSNSDVPDLNV-TLNSGTQFDLMNMLVNTNISPLY
 600 610 620 630
 CIAG_BACTU TTPFNFGSSSVFTLSAHVFNSGNEVVIDRIEFVFAEYTFEAYDLERAQNGVNLQTSVS
 580 590 600 610 620 630
 CIAG_BACTU NOIGLKTGDGYDHIDOVNLVECLSDPEFCLDEKOELSEKVVKHAKRISDERNLLODPNFRG

cry2ab2_820.pep
TXN5:Q9S4B5

Description: Q9S4B5 bacillus thuringiensis, insecticidal protein cryIac (fragment), 6/2001
Accession/ID: Q9S4B5
=====General comments=====

ID Q9S4B5 PRELIMINARY: PRT; 723 AA.
AC Q9S4B5;

SCORES Init1: 128 Initn: 128 Opt: 231 z-score: 244.8 E(): 1e-07
>TXN5:Q9S4B5
Initn: 128 init1: 128 opt: 231 z-score: 244.8 expect(): 1e-07
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FQKSLDTQKWEKWKNNHSLYDPIGVGVASFLKKVGLSKRILSELNLIFFPSG
30 40 50 60 70 80

Q9S4B5 IFYNCLSNPEVEVLGGERIETGTPIDISLSLQFLSEF--VPGAGFVLGLDIWIGIF
20 30 40 50 60

cry2ab2_820. STNLMQDILRETEKFLNRLDTILARVNAELTGL---QANVEEFNQVDNLFNRRNA
90 100 110 120 130 140

Q9S4B5 GPSQWDAFLVQIEQLNQRIEFANQAIKRLGLSLNLYQIYVAESFREWADPTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSVNTMOQLFNRLPQFMQGYQLLLPLFLPAQANLHLSFIRDFILNADEWGIS
150 160 170 180 190 200

Q9S4B5 LREMRIQFQNDMSALTTAIPLLAQVQVPLLSVYVQAANLHLSVLRDYSVFGQRMGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTYRDYKRYTRDYSNYCINTYOSAFK---GLNTRLHML---EFRTYMLNVEFY
210 220 230 240 250

Q9S4B5 AATINSRYNDLTGLIGNYTDYAVRWYNTGLERYMGPDNR--DMVRYNQPRRELTTLVDI
190 200 210 220 230 240

cry2ab2_820. VSIWSLF--KYQSLVSS--GANLVASGSGPQQTQSFTSDPPLYSLFQVNSNYVLNGF
260 270 280 290 300 310

Q9S4B5 VALFNYDSRRYPIRTVYSQITREIYTPVLENFDGSGFRGSAQGIERSRPHLMDILNSI
250 260 270 280 290 300

cry2ab2_820. SGARLSNTFFNIIVGLFGSTTHALLAARVNSGGISS---GDIGASFPQNFNCST---
320 330 340 350 360

Q9S4B5 TI--YTDAHRYGYYWSG---HQIMASPVGFSGFPEFTFLPYGTMGNAAPQRIVAQLGQG
310 320 330 340 350

cry2ab2_820. FLPLPLTFVRSWLDGSDRGVATVNNMQTESFETTLGLRSGATARGNSNFPFYFIR
370 380 390 400 410 420

Q9S4B5 VYRTLSSTFYRRFFNIGINNQOL--SVLDGTEFAYGTSNLPVAVYRSGTGVDSLDLPIPPQ
360 370 380 390 400 410

cry2ab2_820. NISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVS--VHNRR--NNIHAVHE--
430 440 450 460 470 480

Q9S4B5 N-NYVP--PROGFSHRLSHVSMERSGSSSVSI--IRAPMFSWIHRSAEFNNIIASDSIT
420 430 440 450 460 470

cry2ab2_820. -----NGSMIHLAPNDYGTFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQN
480 490 500 510 520 530

Q9S4B5 QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNLSGNNIQRGYIEVP-----IHFP--
480 490 500 510 520

cry2ab2_820. NITARYTLRNGNSYN-LYLRVSSIGNSIIRVTNGRYVYATNNTITNNND-GVNDNGAR
540 550 560 570 580 590

Q9S4B5 STSTRYRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYESANA
530 540 550 560 570

cry2ab2_820. FSDINIGNVASSNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPLY
600 610 620 630

Q9S4B5 FTS-SLGNIVGVRFSGTAGVIIDREFIPVPTATLEAEYNLEBAQAVNALETSTNQLGL
580 590 600 610 620 630

cry2ab2_820.pep
TXN5:X07423_1

Description: X07423 Bacillus thuringiensis Bacillus thuringiensis israelensis
bt8 gene for 13

Accession/ID: X07423

=====General comments=====

LOCUS X07423_1 [BT0XKD2]
DEFINITION Bacillus thuringiensis israelensis bt8 gene for 130 kDa crystal . . .

SCORES Init1: 142 Initn: 166 Opt: 233 z-score: 243.3 E(): 1.2e-07
>TXN5:X07423_1
Initn: 166 init1: 142 opt: 233 z-score: 243.3 expect(): 1.2e-07
Smith-Waterman score: 244; 22.8% identity in 254 aa overlap
(30-266:11-264)

cry2ab2_820. MQAMDNSVLNSGRITICDAYNVAADPFQFQHKSLDTVQKEWTEWKKNNHSLYLDPI---
10 20 30 40 50

X07423_1 MNSGYPLANDLQSGMKNTNYKDWLWAMCENNOQYGVNPAIN
10 20 30 40

cry2ab2_820. ---VGF---VASFLKKVGLVK---RIUSELRNLIIPSGSTN---LMDILRETEKFLN
60 70 80 90 100

X07423_1 SSSSVTALKVAGAILKFPVNPAGTIVTLVLSAVLPILMPTNTPTPERVWDFNTGNTGLID
50 60 70 80 90 100

cry2ab2_820. ORLNTDTLARNVNAELTGLQANVEEFNQVDNPL-NPNNNAVPLSITSSVNTMQQLFNRL
110 120 130 140 150 160

X07423_1 QTVTAVRTDANAKMTVVKYDILQYTKENTWKREPNNQSYRTAVITQFNLSAKLRETA
110 120 130 140 150 160

cry2ab2_820. PQFQ-MQGYQLLLPLFAQANLHLSFIRDFILNADEWGISAATLRTYDKYKNTRDYS
170 180 190 200 210 220

X07423_1 VYFSNLVGYELLPLPIVAQVANFNLLIRDLGLINAQEWSLARSAGDQLYNTVQVTKYI
170 180 190 200 210 220

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cry2ab2_820.280. NYCIYAFKGLNTRLDHM--LEFRITMFLNVFEYSIWSLFKYQSLVSSGANLYASG
X07423_1 AHSITWYKGLDLVRNKSNGOWITFNDYKREMTIQVLDILALFASDPPRYPADKIDNTK
cry2ab2_820. SGPOQTOSTSQDWPFLLYSLFQVNSVYLVNGFSGARLSNFTFNVIGPGSTTHALLAAR
X07423_1 LSKTEFTREIYATLVESPPSSKSIKIALEALTRDVLHFTWLKRVDFWNTIYQDLRFUSAN
cry2ab2_820. pep
TXNS: C4BA_BACTI

Description: P05519 bacillus thuringiensis (subsp. israelensis), pestiscidal
crystal protein
Accession/ID: P05519
ID C4BA_BACTI STANDARD; PRT: 1136 AA.
AC P05519; P16479; P11782;

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General comments=====

SCORES Initl: 142 Inltn: 166 Opt: 233 z-score: 243.3 E(1): 1.2e-07
>TXNS: C4BA_BACTI
Inltn: 166 Initl: 142 opt: 233 z-score: 243.3 expect(1): 1.2e-07
Smith-Waterman score: 244; 22.8% identity in 254 aa overlap
(30-266:11-264)

cry2ab2_820. MQAMNSVLNSGRITICDAYNVAADHFFSFQHKSLDTVQKEMTKNNHSLYLDPI---
C4BA_BACTI MNSGYPLANDLQSGMKNTNYKDWLWAMCENNOQYGVNPAAIN
cry2ab2_820. ---VGT---VASFLKKVGLVKG--RILSELNLIFFSGSTN---LMQDILRETEKFLN
C4BA_BACTI SSSVSTALKVAGAILKFNVPAGTGLTSLVSAVLPLWPTNTPTPERVWDFWNTINTGLID
cry2ab2_820. POFG-MQGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYTRDYS
C4BA_BACTI QIVTAVRIDANAKMTIVVDYLDQYITFKNTWKREPNQSYRTAVITQFNLTSAKLRETA
cry2ab2_820. POFG-MQGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYTRDYS
C4BA_BACTI VYFNSLVGYELLPLPIYAQVANFNLLLRDGLINAQWLSARSAGDQLYNTWQYTKEYI
cry2ab2_820. NYCIYAFKGLNTRLDHM--LEFRITMFLNVFEYSIWSLFKYQSLVSSGANLYASG
C4BA_BACTI AHSITWYKGLDLVRNKSNGOWITFNDYKREMTIQVLDILALFASDPPRYPADKIDNTK
cry2ab2_820. SGPOQTOSTSQDWPFLLYSLFQVNSVYLVNGFSGARLSNFTFNVIGPGSTTHALLAAR
C4BA_BACTI LSKTEFTREIYATLVESPPSSKSIKIALEALTRDVLHFTWLKRVDFWNTIYQDLRFUSAN

cry2ab2_820. pep
TXNS: X07082_1

Description: X07082 Bacillus thuringiensis Bacillus thuringiensis gene for 130
kDa delta-endo
Accession/ID: X07082
LOCUS X07082_1 [BTITOX]
DEFINITION Bacillus thuringiensis gene for 130 kDa delta-endotoxin;
=====
General comments=====

SCORES Initl: 141 Inltn: 165 Opt: 232 z-score: 242.2 E(1): 1.4e-07
>TXNS: X07082_1
Inltn: 165 Initl: 141 opt: 232 z-score: 242.2 expect(1): 1.4e-07
Smith-Waterman score: 243; 22.8% identity in 254 aa overlap
(30-266:11-264)

cry2ab2_820. MQAMNSVLNSGRITICDAYNVAADHFFSFQHKSLDTVQKEMTKNNHSLYLDPI---
X07082_1 MNSGYPLANDLQSGMKNTNYKDWLWAMCENNOQYGVNPAAIN
cry2ab2_820. ---VGT---VASFLKKVGLVKG--RILSELNLIFFSGSTN---LMQDILRETEKFLN
X07082_1 SSSVSTALKVAGAILKFNVPAGTGLTSLVSAVLPLWPTNTPTPERVWDFWNTINTGLID
cry2ab2_820. POFG-MQGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYTRDYS
X07082_1 VYFNSLVGYELLPLPIYAQVANFNLLLRDGLINAQWLSARSAGDQLYNTWQYTKEYI
cry2ab2_820. NYCIYAFKGLNTRLDHM--LEFRITMFLNVFEYSIWSLFKYQSLVSSGANLYASG
X07082_1 AHSITWYKGLDLVRNKSNGOWITFNDYKREMTIQVLDILALFASDPPRYPADKIDNTK
cry2ab2_820. SGPOQTOSTSQDWPFLLYSLFQVNSVYLVNGFSGARLSNFTFNVIGPGSTTHALLAAR
X07082_1 LSKTEFTREIYATLVESPPSSKSIKIALEALTRDVLHFTWLKRVDFWNTIYQDLRFUSAN
cry2ab2_820. pep
TXNS: Y09326_1

Description: Y09326 Bacillus thuringiensis B. thuringiensis cryII gene
Accession/ID: Y09326
=====
General comments=====

LOCUS Y09326_1 [ASCRYIJ]

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DEFINITION B.thuringiensis cryIIIM gene.
DATE 02-APR-1997

SCORES Init1: 147 Initn: 171 Opt: 232 z-score: 241.9 E(): 1.4e-07
>>TXNS:Y09326_1 (1173 aa)
initn: 171 init1: 147 opt: 232 z-score: 241.9 expect(): 1.4e-07
Smith-Waterman score: 232; 20.9% identity in 234 aa overlap
(32-264,12-242)

cry2ab2_820. QAMDNSVLNSGRITICDAYNVAADPFQFHKSLSDTVQKEWTEWKNHSLYLDPIVGTV
Y09326_1 MEISDQNIPIYPCINLNPESSEIFNARNISFGL-VSQVSSGL
10 20 30 40 50 60
70 80 90 100 110 120
cry2ab2_820. ASFLKKVGSILVKRILSELNLIFPGSGSTNLMODILRETEKFLNQRINTDTLARVNAEL
Y09326_1 TRFLLEAAVPEAGPAL--GLFDLIWGAIVGQNSLFLRQIEQLRQIEITELERNRATAIL
50 60 70 80 90
100 110 120 130 140 150
cry2ab2_820. TGLQANVEEFNRQVDNPLN--PNRNAVPLSITSSVNTWQQLFLNRLPQFMQGYQLLLPL
Y09326_1 IGLSSSYNLVVEALREWENDPNPASQERVTRPRLLTDDAIVTGLPTLAIRNLVNLVS
100 110 120 130 140 150
160 170 180 190 200 210 220 230 240
cry2ab2_820. FQAANHLHSFIRDVILNDEWGISAAILRYRDYLNKYTRDYSNYCINTVQSFAKGLNT
Y09326_1 YTOAANHLHSLRDVAIVGERMGLTQANIEDLYTRLSNTQSYDSDHCARWNOGLNEIGG
160 170 180 190 200 210
220 230 240 250 260 270 280 290 300
cry2ab2_820. RLHDMLEFRTYMLNVEYVSWSLFKYQSLLVSSGANLYASGSGPQQTQSFTSQDWPFPL
Y09326_1 ISERYLDQRDLTISVLDIVAPSPNYDIRTYPIPTQSOLTREIYTSFPVAGNINFGLSI
220 230 240 250 260 270
cry2ab2_820.pep
TXNS:A27529_1

Description: A27529 Bacillus thuringiensis B.thuringiensis PS81A2 endotoxin
gene, 9/1995
Accession/ID: A27529
=====General comments=====
LOCUS A27529_1 (A27529)
DEFINITION B.thuringiensis PS81A2 endotoxin gene. . .

SCORES Init1: 134 Initn: 134 Opt: 232 z-score: 241.9 E(): 1.4e-07
>>TXNS:A27529_1 (1174 aa)
initn: 134 init1: 134 opt: 232 z-score: 241.9 expect(): 1.4e-07
Smith-Waterman score: 269; 22.4% identity in 589 aa overlap
(73-634,50-601)

cry2ab2_820. TEWKKNHSLYLDPIVGTIVASFLKKVGSILVKRILSELNLIFPGSGSTNLMDILRETE
A27529_1 VEILGSRNSNVAAEIGLGLTRLLVSRIPLGDFILG-LPFDVIWGAIGPSQWDIFLEGIE
20 30 40 50 60 70 80 90 100
```

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cry2ab2_820. KFLNQELNTDLARVNAELTGLQANVEEFNRQVDNF--LNPNRNAVPLSITSSVNTWQQLF
A27529_1 LLIGQRIEFARNQAISRLGQSLNLYRIYNAPFQWVEVDTNFPALREEMRIQFNDMSAL
80 90 100 110 120 130
140 150 160 170 180 190
cry2ab2_820. LNRLPQFMQGYQLLLPLFAQAANHLHSFIRDVILNDEWGISAAILRYRDYLNKYTR
A27529_1 TTAIPLFSVQGVGEIPLLSVVQAAANHLHSVLREDVSVFGQWGFDAVATINSRYNDLRLIG
140 150 160 170 180 190
200 210 220 230 240 250
cry2ab2_820. DYSNYCINTVQSFAKGLNTRHDMLEFRTYMLNVEYVSWSLFKYQSLLVSSGANLYA
A27529_1 EYTDYAVRWYNT--GLN-RLPRNEGVRGMARFRRELITISVLDIISFFQNYDSRLYP
200 210 220 230 240 250
260 270 280 290 300 310
cry2ab2_820. SSGSPQQTQSFTSQDWPFPL-YSLFQVNSNY--VLNG-FSGARLSNTFPNIV-GLPGSTTT
A27529_1 IPTIYQLTREVYD--PVNIIDIRVTSPFESIESAITSPLHNDPLNIIIDTLIRGV
260 270 280 290 300 310
320 330 340 350 360 370 380
cry2ab2_820. HALLAARV--NYSGG---ISSGDIG---ASFPNQNFNCSTFLPPLTPFVRSWLDGSD
A27529_1 HYWAGHRVTSHTFGSSQVSISSPQYGITANAEP--SRTIAPSTF--PGLNLFYRTLSDPFFR
320 330 340 350 360
370 380 390 400 410 420 430 440
cry2ab2_820. R-BEVAIVTNWQTESFETILGRSGA--FTAGNSNYFDYFI---RNISGVPLVVRNED
A27529_1 RSDNIMPTGLINNVQGVGFIQPNNGEVLYRRRGTVDSLDDELPGDGENSLGVGSHRLSHVT
370 380 390 400 410 420
430 440 450 460 470 480
cry2ab2_820. LRRPLHYNEIRNIASPGTTCGARAQVMSVHNRKNNIHAVE---NGSMIHLPANDYTG
A27529_1 LTRSLYNTNITSLPTFVWTHSATDRNIYDPVITQIPLVKSFSLSLTSGTSVVRGP---G
430 440 450 460 470 480
490 500 510 520 530 540 550
cry2ab2_820. FTISPIHATQVNNQTRTIFSEKFGNQGDSLRFEQNNITARYTLRGN--GNSYNYLVRVSI
A27529_1 FTGDDIIRTNVNGNVLMS-----SLNF--SNTSLQRYVRVRVYAAASQTMVRVN-V
490 500 510 520 530
540 550 560 570 580 590 600 610
cry2ab2_820. GNSIRVTVNGRYVATVNTVITNDGVNDNGARFSDINIGNVVASNSDVPLDINVTLN
A27529_1 GGST-----TFDQGFPTMSANGSLTSQSFRFAEPFVG--ISTSGSQTG-GISISNN
540 550 560 570 580
620 630
cry2ab2_820. SGTO-FDLMMIMLVPTNISPLY
A27529_1 FGRQTFHLDRIEFIPVDATFAEYDLERAQAVNSLFTSSNQIELKTDVTDYHIDQVSNL
590 600 610 620 630 640
650 660 670 680 690 700
cry2ab2_820.pep
TXNS:C1EB_BACTA
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|| : | :||: : || :||: : || :||: :
C1EB_BACTA FTGGDIRTVNGNVLSM-----SLNF-SNTSLQRYVRVRYAASQTMMVRVN-V
490 490 500 510 520 530

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cyy2ab2_820. SGTQ-FDLMNIMLVPTNISPLY 620 630

ctv2ab2 820 pep

Description: M73253 *Bacillus thuringiensis* (cryI) gene, complete C
Accession/ID: M73253

DEFINITION	Bacillus thuringiensis (cryI(b)) gene, complete CDS. . . .
SCORES	Initl: 134 Initn: 134 Opt: 232 z-score: 241.9 E(): 1.4e-07
TYPE MATHS	

22.4% identity in 589 aa overlap
Smith-Waterman score: 366;
(43-634, 50-601)

ry2ab2_820. KFLNORLNSOTLHARVALTSTHJANVEEPARONDF-LAPNENAVPISTASSUNTWOOF
VALDLENNSNVAKLGUSNSNLSVKIPIGDFILG-LFDVINGAIGPSOWITFLEQIE

ry2ab2_820..LNRLPQFMQGYOLLILPFFQANLHLSPIRDIILHSEWGISARLSTYRDIKYNTR

140 150 160 170 180 190
 230 240 250 260 270 280
 DYSYCINTYQSAAGLNRHDMLEPRTYWFNFVETWISLKFQSLVLSGANLPA
 : : : : :
 230 240 250 260 270 280
 DYSYCINTYQSAAGLNRHDMLEPRTYWFNFVETWISLKFQSLVLSGANLPA
 : : : : :

250 240 230 220 210 200 290 300 310 320 330
 ry2ab2_820. SGSGPQOTSFTSQDWPL-YSLFQVNSNY--VLNG-FSGARLSTNPNTV-GDGGNTT

310 300 250 200 150 100 50 0

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[illegible]

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260      190      200      210      220      230      240
cry2ab2_820. VSIWLSLF--KYQSLVSS--GANLYASGGPQQTCSQTSQDWFLYSLFOVNSVNLNGF
Q03743      250      260      270      280      290      300
      VALFNYDSRRYPPIRTVSQLTREIYNPVLENFDSGRGSAQGIERSIRSPHLMILNSI
cry2ab2_820. 320      330      340      350      360
Q03743      370      380      390      400      410      420
      TI--YTDARHGVYWSG---HOIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLCQG
cry2ab2_820. 370      380      390      400      410      420
Q03743      430      440      450      460      470      480
      N--NNVP--PRQGFHRLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNIIASDSIT
cry2ab2_820. 490      500      510      520      530
Q03743      540      550      560      570      580      590
      QIPAVKGNFLFNGSVIS-GFG-FTGGDLVRLNSGNNIQRGYIEVP-----IHFP--
cry2ab2_820. 600      610      620      630
Q03743      640      650      660      670      680      690
      FTS-SLGNIVGVNRFSGTAGVIIDREFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
cry2ab2_820.pep
TXN5:M73248_1

Description: M73248 Bacillus thuringiensis Bacillus thuringiensis (cryIa(c)3)
gene, complete
Accession/ID: M73248
=====General comments=====
LOCUS M73248_1 [BACCRYIACC]
DEFINITION Bacillus thuringiensis (cryIa(c)3) gene, complete CDS. . .

SCORES      Init1: 128      Initn: 128      Opt: 231      z-score: 240.9 E(): 1.7e-07
>>TXN5:M73248_1
      Initn: 128      Init1: 128      Opt: 231      z-score: 240.9 expect(): 1.7e-07
Smith-Waterman score: 263;      23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FQHKSLDTQKWEKWKNNHSLYLDPIVGTVASFLKKKVGSLGKRISLRLNLIFFPSG
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M73248_1      IPYNCNLSPEVVGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIWGIF
      20      30      40      50      60
cry2ab2_820. 90      100      110      120      130      140
      STNLMQILRETEKFLNQRNLNTDLARVNAELTGL----QANVEEFNRQVDNLFNRRNA
M73248_1      150      160      170      180      190      200
      GPSQWDAFLVQIBOLLNQRIREFARNQAIISRLGSLNLYQIYAESFREWADPTNP---A
      70      80      90      100      110      120
cry2ab2_820. 150      160      170      180      190      200
      VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLPFAQAANLHLSFIRDVILNADEWGIS
M73248_1      210      220      230      240      250      260
      LREEMRIQFNDMNSALTATPILAVQNYQVPLLSVYVQAANLHLSVLDRVSVFGQWGF
      130      140      150      160      170      180
cry2ab2_820. 210      220      230      240      250
      AATLRTYRDYLNKYIRDYSNICYQSAFK---GLNRLHDML---EPRIYMFNLNVPEY
M73248_1      260      270      280      290      300      310
      AATINSYNDLRLGNITDFAVRNITGLIERVWGPDSR--DWRYNQPFRELTTLVLDI
      190      200      210      220      230      240
cry2ab2_820. 260      270      280      290      300      310
      VSIWLSLF--KYQSLVSS--GANLYASGGPQQTCSQTSQDWFLYSLFOVNSVNLNGF
M73248_1      320      330      340      350      360
      VALFNYDSRRYPPIRTVSQLTREIYNPVLENFDSGRGSAQGIERSIRSPHLMILNSI
      250      260      270      280      290      300
cry2ab2_820. 320      330      340      350      360
      SGARLSNTPFNIVGPGSTTTTHALLAARVNSGGISS---GDIGASPFNQFNCST---
M73248_1      370      380      390      400      410      420
      TI--YTDARHGVYWSG---HOIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAQLCQG
      310      320      330      340      350
cry2ab2_820. 370      380      390      400      410      420
      FLPLLTFFVRSWLDGSDREGVATVNNQTESFETTLGLSGAFTARGNSYFPDYFIR
M73248_1      430      440      450      460      470      480
      VYRTLSTFYRRPFNIGINNQQQL--SVLDGTEFAYGTSSNLPSSAVYRKSGTVDSLDEIPPO
      360      370      380      390      400      410
cry2ab2_820. 430      440      450      460      470      480
      NISGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGARAYMVS--VHNK--NNIHAVHE--
M73248_1      490      500      510      520      530
      N--NNVP--PRQGFHRLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNIIASDSIT
      420      430      440      450      460      470
cry2ab2_820. 490      500      510      520      530
      -----NGSMIHLPNDYGTFTTSPIHATQVNNQTRTFISEKFGNQGDSLRFEQN
M73248_1      540      550      560      570      580      590
      QIPAVKGNFLFNGSVIS-GFG-FTGGDLVRLNSGNNIQRGYIEVP-----IHFP--
      480      490      500      510      520      530
cry2ab2_820. 540      550      560      570      580      590
      NITARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATVNTNND-GVNDNGAR
M73248_1      600      610      620      630
      STSTRYVRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLOSDFGYFESANA
      530      540      550      560      570
cry2ab2_820. 540      550      560      570      580      590
      NITARYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRVYATVNTNND-GVNDNGAR
M73248_1      600      610      620      630
      STSTRYVRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLOSDFGYFESANA
      530      540      550      560      570
cry2ab2_820. 600      610      620      630
      FSDINIGNVASSNSDVPFLDINVTLNSGTQFDLMNIMLVPTNISPLY
M73248_1      640      650      660      670      680      690
      FTS-SLGNIVGVNRFSGTAGVIIDREFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      580      590      600      610      620      630
cry2ab2_820. 600      610      620      630
      FSDINIGNVASSNSDVPFLDINVTLNSGTQFDLMNIMLVPTNISPLY
M73248_1      640      650      660      670      680      690
      FTS-SLGNIVGVNRFSGTAGVIIDREFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
      580      590      600      610      620      630
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cy2ab2_820. 420 430 440 450 460 470
-----NGSMIHLPANDYTGFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQ
Q45768 QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSGNNIQNRGIYVP-----IHFP--
480 490 500 510 520 530
-----IHFP--
Q45768 QIPAVKGNFLFNGSVIS-GPG-FTGGDLVRLNSGNNIQNRGIYVP-----IHFP--
480 490 500 510 520 530
-----IHFP--
cy2ab2_820. 540 550 560 570 580 590
NTTARTYLRGNSGVN-LYLRVSSIGNSTIRTVNGRVYATVNTVNTTND-GVNDNGAR
Q45768 STSTRYKRVRYASVYTPHLLNVN-WGSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570 580 590
-----IHFP--
cy2ab2_820. 600 610 620 630
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 640 650 660 670 680 690
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 700 710 720 730 740 750
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 760 770 780 790 800 810
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 820 830 840 850 860 870
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 880 890 900 910 920 930
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 940 950 960 970 980 990
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1000 1010 1020 1030 1040 1050
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1060 1070 1080 1090 1100 1110
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1120 1130 1140 1150 1160 1170
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1180 1190 1200 1210 1220 1230
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1240 1250 1260 1270 1280 1290
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1300 1310 1320 1330 1340 1350
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1360 1370 1380 1390 1400 1410
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1420 1430 1440 1450 1460 1470
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1480 1490 1500 1510 1520 1530
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1540 1550 1560 1570 1580 1590
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1600 1610 1620 1630 1640 1650
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1660 1670 1680 1690 1700 1710
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1720 1730 1740 1750 1760 1770
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1780 1790 1800 1810 1820 1830
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1840 1850 1860 1870 1880 1890
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1900 1910 1920 1930 1940 1950
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 1960 1970 1980 1990 2000 2010
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 2020 2030 2040 2050 2060 2070
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 2080 2090 2100 2110 2120 2130
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 2140 2150 2160 2170 2180 2190
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 2200 2210 2220 2230 2240 2250
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 600 610 620 630
-----IHFP--
cy2ab2_820. 2260 2270 2280 2290 2300 2310
FSDINIGNVVASSNDSVPLDINVLNSGTQFDLMIMLVPTNISPLY
Q45768 FTIS-SLGNIVGVNFSGTAGVIDRFEFIPVTATLEAYNLERQAKVNAFLTSTNOLG
580 590 
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