

©01

```
21239436  ---ITDITVDHNGFNGSGHQITASPGVGFPAFLFNGNAGNAAPPVLVSLTGLGI
      300 310 320 330 340 350
cry2ab2_820.  DPLDTPFVR---SSDREGVAVVWQTESPET-TIGLSGAFIARGNSVFPDYFI
21239436  FRTLSNRYRITILGSGVNNQELFVLDSQTERFASLTINLPSITTIYRGVDSL-DVIP
      360 370 380 390 400 410
cry2ab2_820.  RNYISGVPLVVRNEDLRRLNHEIRNTA-PSGTGGARAYVSVNRRKNINHAVHENGSM
      420 430 440 450 460 470
21239436  PDNSVP--PRAGFSLSH--VTMLSOAAAYITRAPFTSGHRAEFNNIIPSSOI
      480 490 500 510 520
cry2ab2_820.  --IHLAPNDYTGFTISPIHATQNNQTRTFISEKFGNQSURFQNNNTARYTIRGNGN
21239436  TQIPTKTNLNGSGTSVVKPGFTGGD--ILRTSPQISITLRV--NIYASOR---
      530 540 550 560 570
cry2ab2_820.  SYNLVRSSISGNTIRVTINGRVVATNTVNTTNDGNDNGARFESNLINNVVASNS
21239436  -YRVRIRVASTINLQPHISIDGRPINQGNFSATWSS-GSNLQSGSRVIGFTIRPFNSNG
      580 590 600 610 620
cry2ab2_820.  DVPLDINV-TLNSGTQFDLMNIMLPTNISPLY
21239436  SSVFTLSAHVFNSGNEVYIDRIEFVPAEVTEAEYDLERAQKAVNELTSSNIGLKTVD
      630 640 650 660 670
cry2ab2_820. pep
NR4A:46359602
lentimorbus)

SCORES  Init1: 117  Initn: 150  Opt: 261  z-score: 290.7 E(): 6.7e-08
>>NR4A:46359602
  Initn: 150  Init1: 117  Opt: 261  z-score: 290.7 expect(): 6.7e-08
Smith-Waterman score: 261; 24.5% identity in 530 aa overlap
(76-573:84-568)

cry2ab2_820.  KNNHSLYLDPIVGVASFLKKVGLSVGKRLSELNLIFFSGSTNLMQDLRETEKFL
46359602  AIAEAVGLSIDILAEIHYLYGFPPIASFLTRALSALQGLFSSGT-LMQHI-----EQLI
      680 690 700 710 720
cry2ab2_820.  NQRLNTDTLAVNAELTGLQANVEEFNRQVDNFIINPVRNAVPLS--ITSSVNTMQQLFLN
      730 740 750 760 770
46359602  NQIAEYRANKALAEFQGRGQGLYLEADSW-EQRJUSQPHKERVQRITRLDINSFIS
      780 790 800 810 820
cry2ab2_820.  RLPQFOMQGYQLLLPLFAQANLHLSFIRDVILNADMGISAAITRYRDLKN--YTR
46359602  SIPSFAYRNYEVPLLSVYADANLHLLILRDSYIYGAFWGFDEDEY--YRNYAQIRLSA
      830 840 850 860 870
```

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170 180 190 200 210 220
cry2ab2_820.  DYSNYCINTYQSAFKGIN-TRIHDMLE---FRTYMFNVFEYVSWLSFKYQSLVSSGA
      230 240 250 260 270
46359602  EVANHCITWQTGLRLQGRATRWNNFRREMTLVIDLICALFSSYDIPS-----
      280 290 300 310 320
cry2ab2_820.  NIYASGSPQQTQSFTSQDMPFLYSLFQVNSYVNLGFGSGARLNTFPNIVGLPGSTTTH
      330 340 350 360 370
46359602  --YPMGTIKIQTREIYTD--PVVHSDMLQSTSPGLISFSS--LENL--VVRAPHLFT--
      380 390 400 410 420
cry2ab2_820.  ALLAAVNYSGTSSGIDGASFPNQF-----NCSTFLPPLL--TPFVRSWLDS
      430 440 450 460 470
46359602  --WLSRVITDITGLISTVIGGQVNNNFWRTHYQTLRTTGTGTSFOSFYVGSTAFPIQRTNT
      480 490 500 510 520
cry2ab2_820.  GSDREGVAVTNMOTSFETTLGRSGAFTAR-GNSNY-----FPDYFIRNIGVPLV
      530 540 550
46359602  LTFSGDVITYES-SVVTSSSLYGANSVAFTGTRSLYENPTVYVPAKLIHELPGVDSS
      560 570 580 590 600
cry2ab2_820.  VYRNE-DLRRPLHNEYRNTA-SPSGTGGARAYVSVNRRKNINHAVHENGSMIHLAPND
      610 620 630
46359602  RNNATNYSRLSYISGSLGYSFSGT-GLVYGMTSTATTRENNITL--DDRIVQL-PA-
      640 650 660 670
cry2ab2_820.  YTGFTISLHNVNNTQTRTFISEKFGNQSURFQNNNTARYTIRGNSYNYLVRVS
      680 690 700
46359602  --YKGRSNNNQVVKGTGFTG-GDWLKPNNNGTFSMFAFRSAYTHFRIRYA
      710 720 730
cry2ab2_820. pep
SW:8469134

8469134 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AB (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIC(B)) (CRYSTALLINE ENTOMOCIDAL (BO)OXIN) (133 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar galleriae"
source="swissprot_prot" version="NA type="prt"

SCORES  Init1: 147  Initn: 147  Opt: 260  z-score: 290.5 E(): 6.7e-08
>>SW:8469134
  Initn: 147  Init1: 147  Opt: 260  z-score: 290.5 expect(): 6.7e-08
Smith-Waterman score: 290; 21.6% identity in 603 aa overlap
(57-630:41-601)

cry2ab2_820.  PFSQKSLDVTQKEMTEWKKNNHSLYLDPIVGVASFLKKVGLSVGKRLSELNLIFF
8469134  PYNCLSNPEILLDGERISTGNSSIDISLSLVQLLVSNFVPGGGLVNG--LLDFVWGIIVG
      870 880 890 900 910
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cry2ab2_820. 90 100 110 120 130 140
PSGSTNLMDILRETEKFNORLNTDTLARVNAELTGLQANVEEFNRQVDFN----LNPN
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PSPWDAFLVQI-----EQLINERIAAARSAASINLEGLGNN--FNIYVEAFKEWEDPD
70 80 90 100 110 120

cry2ab2_820. 150 160 170 180 190 200
RNAVPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVLNADEW
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NPVTRVVDREFRILDLGLERDIPSFRIAGFEVPLLSVYAQAANLHLSFIRDSSIFGARW
130 140 150 160 170 180

cry2ab2_820. 210 220 230 240 250
GISAATLRTYRDLKMYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMFNVFE
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GLTINNVENYRNLIRHIDEYANHCAITYNRGLNMLPKSTYQDMWITYNRLRDLTLVLD
190 200 210 220 230 240

cry2ab2_820. 260 270 280 290 300 310
YVSIWLSFKYQSLVSS--GANLYASGSGPQQTOSTSQDWPFYLSLFQVNSNYVL--NGF
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
IAAFFSYDNRRYPQISQVGLTREIYTDPLIT--FNPQ-----LQSVACLPTFNMESNAI
250 260 270 280 290

cry2ab2_820. 320 330 340 350 360
SGARLSNTFPNI-----VGLPGSTTTHALLAARVNSYSGISSGDIQ-----ASFPNQ
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RTPHLFDVLNLTITFDWFSVGRNFYMGCHRVISNRIG--GGNITSPIYGREANQEPFRSF
300 310 320 330 340 350

cry2ab2_820. 370 380 390 400 410
NFNCSTFLP---PLLTFFVRSLDSDSGREGVATVNMQTESFETTLGLRSGAFTAGNS
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
TFNGPVFRLSNPTFRLOQPWPAPPFNLRGV-----EGVEFSTFLNSFTYRGRGIV
360 370 380 390

cry2ab2_820. 420 430 440 450 460 470
YVSIWLSFKYQSLVSS--GANLYASGSGPQQTOSTSQDWPFYLSLFQVNSNYVL--NGF
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
IAAFFSYDNRRYPQISQVGLTREIYTDPLIT--FNPQ-----LQSVACLPTFNMESNAI
420 430 440 450 460

cry2ab2_820. 480 490 500 510 520 530
AVHENGSMIHLAPNDYTGFTISPIHATOVNQTRTFISEKFGNQGDSLRFEQNNITARYT
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PDVTHQIPLVAFNLTSGTSGVRGFGTGGDIIRTNVNSVLMS--SLNF--SNTTLQRVR
470 480 490 500 510 520

cry2ab2_820. 540 550 560 570 580 590
LRGNGSNLYLRVSSISGNTSTIRVTINGRVATVNTTNDG--VNDNGARSDINIGN
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
VR-----VRYASQTMVMSVIVGSGTIGNQGPSTWANGALTSQSGPFAEFVPG-
540 550 560 570 580 590

cry2ab2_820. 600 610 620 630
VWASSNSDVPLDINVLNSGTQ--FOLMMIMLVPTNISPLY
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
ISAGSQQA--SISISNNVGROMFHLDRIFELPVTSTFEEDYDLERAGEAVNALFTSTNQ
580 590 600 610 620

8469134 LGKTDVTDVHDIDQVSNLVECLSDFECLDEKRELSEKVKHAKRLSDERNLLQQRNFRSIN
630 640 650 660 670 680
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cry2ab2_820.pep
NRAA:8469134
8469134 source="GENBANK PROT" Pesticidal crystal protein cryIcB (Insecticidal
delta-endotoxin CryIc(b)) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)

SCORES Initl: 147 Initn: 147 Opt: 260 z-score: 290.5 E(): 6.9e-08
>NRAA:8469134
initn: 147 initl: 147 opt: 260 z-score: 290.5 expect(): 6.9e-08
Smith-Waterman score: 290; 21.6% identity in 603 aa overlap
(57-630:41-601)

cry2ab2_820. PFSFQHSKLDTVQKIEWTEWKKNNHSLYLDPIVGIVASFLKKVGLSVKRISELNLI
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PYNCLNPEELLGGERISITGSSSIDISLSVLQLLVSNFVPGGFLVG--LLDFWVGIVG
20 30 40 50 60 70 80

cry2ab2_820. PSGSTNLMDILRETEKFNORLNTDTLARVNAELTGLQANVEEFNRQVDFN----LNPN
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
PSPWDAFLVQI-----EQLINERIAAARSAASINLEGLGNN--FNIYVEAFKEWEDPD
70 80 90 100 110 120 130 140

cry2ab2_820. RNAVPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVLNADEW
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
NPVTRVVDREFRILDLGLERDIPSFRIAGFEVPLLSVYAQAANLHLSFIRDSSIFGARW
130 140 150 160 170 180

cry2ab2_820. GISAATLRTYRDLKMYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF---RTYMFNVFE
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GLTINNVENYRNLIRHIDEYANHCAITYNRGLNMLPKSTYQDMWITYNRLRDLTLVLD
190 200 210 220 230 240

cry2ab2_820. YVSIWLSFKYQSLVSS--GANLYASGSGPQQTOSTSQDWPFYLSLFQVNSNYVL--NGF
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
IAAFFSYDNRRYPQISQVGLTREIYTDPLIT--FNPQ-----LQSVACLPTFNMESNAI
250 260 270 280 290 300 310

cry2ab2_820. SGARLSNTFPNI-----VGLPGSTTTHALLAARVNSYSGISSGDIQ-----ASFPNQ
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RTPHLFDVLNLTITFDWFSVGRNFYMGCHRVISNRIG--GGNITSPIYGREANQEPFRSF
300 310 320 330 340 350 360

cry2ab2_820. NFNCSTFLP---PLLTFFVRSLDSDSGREGVATVNMQTESFETTLGLRSGAFTAGNS
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
TFNGPVFRLSNPTFRLOQPWPAPPFNLRGV-----EGVEFSTFLNSFTYRGRGIV
360 370 380 390 400 410

cry2ab2_820. NYFPDYFRINISGVPLVVRNEDLRRPLHYNEIRNIASPSGTGGARAYMVSVHNRKNNH
8469134 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DSLTELPPEDNSVFP---REGYSHRLCHATFVQBSGTFPLITGPFVFSWTHRSATDRNIY
410 420 430 440 450 460 470
```

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CRY2ab2_820. AVHNGEMHIANPDTFTSPHATQVNNQTRTFISEKFGNGOGSLRFEQNNITARYT
8469134 PDVINGFLVAFNLTSQSVRGPGTGDRIIRNVGSLVM--SLAF-SNITLQYR
540 480 490 500 510 520
CRY2ab2_820. LRGNNGNINLVSVSISIRATNGRVYATNVNTTNDG-VNDGARGFSINIGN
8469134 VR-----VRYSQOTWASVGGSTTNGSGFPTMSANGALTSQSFAFPVG-
600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800
CRY2ab2_820. VVASSNDVLDINVLNSGTG-PDANNIMLQVNTNIPLY
8469134 ISAGSOGA--SISISNVGROMPHLRIPRLPVTSTFEFEXDLERACQAVNALETSTNQ
600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800
8469134 LGLKTDVTDYHDQVSNLVECLSDFCLOKREMERAKHAKLSLDEANLQDRNPRIN
630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800
CRY2ab2_820.pcp
NRAA:1942525
1942525 source="GENBANK_PROT" Insecticidal Toxin: Structure And Channel
Formation
SCORES Initl: 128 Initn: 168 Opt: 255 z-score: 289.8 E(): 7.6e-08
>NRAA:1942525
Initn: 168 Initl: 128 opt: 255 z-score: 289.8 expect(): 7.6e-08
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:13-581)
CRY2ab2_820. FQKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLVGRKILSELRLNIPFG
1942525 IETGVTPIDISLSTQPLSEF--VFGAGFVLGLVDIINGIF
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
CRY2ab2_820. STNLMDILRETEKFLNQLNTDTLARNVAELTGJ---QANVEENRQVONFLNPRNA
1942525 GPSQWDAFLVQIEQLINORIEEFARNOAISRLGLSLNLYQIYAESFREWADPTNP---A
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
CRY2ab2_820. VPLSITSSVNTWQFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDIVLNADENGIS
1942525 LREEMRIQFNDMNSALITPAIPLAVONQVPLLSVYVQAANLHLSVLRDVSVFGQWGF
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
CRY2ab2_820. AATLRTYDLYANTRYDYNVCINTYOSAFK---GLNTRLHML---ERTYMLNLFVEY
1942525 AATINSKYNDLTRLIGNTYDIAVRWYNTGLERVMGPDSP--DWVRYNQPRRELTTLVDI
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
CRY2ab2_820. VSIWLSLF--KQSLVSS--GANLYASGSGPQQTSTSDWDFLVSFLPVQNSVNLNGF
1942525 VALFSNVDSRRYPRTYSQLTREIYTNPVLENFDSGFRGWAQRIEQNIRQPHLMDILNSI
220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400

CRY2ab2_820. SGARLSNTPFNIVGLPGSTTTHALLAARVNYSGGISS-----GDIG--ASFPNQNFNCSTF
1942525 T-----IYTDVHRGFNWSGHOITASPVGFSGPEFAFFPLFGNAGNAPPVLVLSITGLGI
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
CRY2ab2_820. LPPLLTFVRSW-LDSGSDREGVATVNNQTESFET-TLGLRSGAFTARGNSNPPDYFI
1942525 FRTLSSPLVRRILGSGPNQOEL-FVLDTGTEFSASLTTLNLPSTIYRQGTVDLSL-DVIP
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
CRY2ab2_820. RNISGVPLVVRNEDLRRPLHYNEIRNIASPSGTGCGARAYVMSVHNRKNNIHAVHENGSM
1942525 FQDNSVP--PRAGFSHRLSH---VTMLSOAGAVVTLRAPTFSMOHSAEAFNNIIPSSQI
390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600
CRY2ab2_820. --IHLAPNDYGTFTSPHATQVNNQTRTFISEKFGNGOGSLRFEQNNITARYLNGNG
1942525 TQPLTKSNLGSSTGVVKGPGFTGGD--ILARTSPQISTLRV--NITAPLSQR---
450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600
CRY2ab2_820. SYNLILRVSSIGNSTIRVTINGRVYATNVNTTNDGVDNGARFSDINIGNVASSNS
1942525 -YRVRVASTNLNLFQHTSIDGRPINQGNFSATWSS-GSNLQSGSFRVGTTPFNFSNG
500 510 520 530 540 550 560 570 580 590 600
CRY2ab2_820. DVPLDNN-TLMSGQFDLNNIMLVPTNISPLY
1942525 SSVTLISAHVNSNNEVIDRIEFVPAEVTFEAEYDLER
560 570 580 590 600
CRY2ab2_820.pcp
NRAA:46359600
46359600 source="GENBANK_PROT" Aggaporal crystal protein [Paenibacillus
lentimorbus]
SCORES Initl: 193 Initn: 193 Opt: 260 z-score: 289.5 E(): 7.9e-08
>NRAA:46359600
Initn: 193 Initl: 193 opt: 260 z-score: 289.5 expect(): 7.9e-08
Smith-Waterman score: 260; 22.6% identity in 230 aa overlap
(74-297:96-324)
CRY2ab2_820. EWKKNHSLYLDPIVGTVASFLKKVGLVGRKILSELRLNIPFGSTNMODILNSTER
46359600 TRSLEIAVAVGVRIHSITIFRLLGVFPYSAQGEQLFSFLLTLNLSGNTQ--EETPRHAE
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
CRY2ab2_820. FLNORLNTDLARNVAELTGLQANVEENRQVNDNLF--NENNAVPLSITSVNVWQOLLS
46359600 LINEQVDPVTRTKALAEITLDGNLNLKYLAAFAEDWKKENSSQSEVTRVIDRNFISGLF
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

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[illegible][illegible]

CRY2AB2_820. VILNADWGISATLTYRDKYKNTYRDYNYCINTYQSFA---KGLNRLHDLML-EFRT
2982744 AVSGGGLDIATVNNHNLINLHRYTEHCLDTYNOGLENLGTNTQSRFQWFR
cry2ab2_820. YMFNLVFNVSINWVWGLVSSGGLNLYSGSGPQOQSFTSQDMPFLYSLFQVNSNY
2982744 EULVLVDLVALPNDADAPYPTDISSOL---TREIYTSVI-EDSP-----VSAN-
cry2ab2_820. VLNGSGARLNTFPNVLGSGSTTHALLAARVNYSGG---ISSGDIGASPPNQFNCSST
2982744 IPNGFRAFGVVRPHLMDFMNSLFTATVRSQTVAGGHVSSRNTAGNIN--FPIYG
cry2ab2_820. FFPPLLT-----PFVRSWLDGSDREGVAT---VNWQTESFETTLGRSGAFTARG
2982744 INPGGAIWIAEDDPREFVRLTSDPFRVGGFGNPHYVLGLRGVGFQOQTGNTNTRTPRNSG
cry2ab2_820. GNSNYFPDYFIRNISGVPLVRNEDLRRL-HYNEIRNIASPGTPGCGARAYWYVSHNRKN
2982744 GTDLSLDEIPQDNGSGAPW---NDYSHVLNHVTFVRMPEIAGSDSW-RAPMFSTHRS
cry2ab2_820. NNHVAHENGSMIHLAPNDYTGFTISPIHATQVNNOTRIFISEKFGNGSLRFEQNNIT
2982744 ADRTNI-----INFNIIT--QIPAVKAHNLHSGSTVVRGFGTG--GOLLRRITNGTF
cry2ab2_820. A--RYTLRGN--GNSYNYLRVSSIGNSTIRVTINGRYVYATVNTTNNQGVNDNGARFS
2982744 ADIRVNIITGLPSQRYRYRYASTTDLQFTRINGTSVNOGNFQRTNMRGNLESN-PR
cry2ab2_820. DINIGNVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
2982744 TAGSTPFSFNSAQSTFTLTQAFNSQEVYIDRIEFVPAEVTFAESDLERAQKAVNALF
2982744 TSTSLGLKTNVTGYHIDQVSNLVACLSDFCLEKRELSEKVKHAKELSKENLQDNP
cry2ab2_820.pep
SW:8469133

8469133 Description="PESTICIDIAL CRYSTAL PROTEIN CRY11B (INSECTICIDAL
DELTA-ENDOTOXIN CRY11(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 189 Initn: 216 Opt: 259 z-score: 289.4 E(): 8e-08
>>SW:8469133
initn: 216 initl: 189 opt: 259 z-score: 289.4 expect(): 8e-08
Smith-Waterman score: 330; 22.1% identity in 611 aa overlap

(46-634:26-602)
cry2ab2_820. ICDAVNAVAHDPTSFQHKSLDTVQKTEWKNNHSLYLDPIVGTVASFLKKVGLVKGK
8469133 MKNNTQNCQVPCVNCISNPVEITLSEERSTGELPLD-ISLSLTFLLSEFVPGVG-
cry2ab2_820. RILSELRLNLIFFPGSGTNLMQDILRETEKFNQELNLTDTLARVNAELTGLQANVEEFNRQV
8469133 -VAFGLFWIGFITPSEWSFLQIQLEQRIETLERNAITTLRGLADSYEVYLEAL
cry2ab2_820. DNFL-NPNNNAVPLSITSSVNTMQQLFLNRLPOFOMQGYQLLLIPLFAQANLHLSFIRD
8469133 REWEENPNNAQLREDVRIRFATDIDALITAINNFITLISFEIPLLSVIVQAANLHLSLRD
cry2ab2_820. VILNADWGISATLTYRDKYKNTYRDYNYCINTYQSFA---KGLNRLHDLML-EFRT
8469133 AVSGGGLDIATVNNHNLINLHRYTEHCLDTYNOGLENLGTNTQSRFQWFR
cry2ab2_820. YMFNLVFNVSINWVWGLVSSGGLNLYSGSGPQOQSFTSQDMPFLYSLFQVNSNY
8469133 EULVLVDLVALPNDADAPYPTDISSOL---TREIYTSVI-EDSP-----VSAN-
cry2ab2_820. VLNGSGARLNTFPNVLGSGSTTHALLAARVNYSGG---ISSGDIGASPPNQFNCSST
8469133 IPNGFRAFGVVRPHLMDFMNSLFTATVRSQTVAGGHVSSRNTAGNIN--FPIYG
cry2ab2_820. FFPPLLT-----PFVRSWLDGSDREGVAT---VNWQTESFETTLGRSGAFTARG
8469133 INPGGAIWIAEDDPREFVRLTSDPFRVGGFGNPHYVLGLRGVGFQOQTGNTNTRTPRNSG
cry2ab2_820. GNSNYFPDYFIRNISGVPLVRNEDLRRL-HYNEIRNIASPGTPGCGARAYWYVSHNRKN
8469133 GTDLSLDEIPQDNGSGAPW---NDYSHVLNHVTFVRMPEIAGSDSW-RAPMFSTHRS
cry2ab2_820. NNHVAHENGSMIHLAPNDYTGFTISPIHATQVNNOTRIFISEKFGNGSLRFEQNNIT
8469133 ADRTNI-----INFNIIT--QIPAVKAHNLHSGSTVVRGFGTG--GOLLRRITNGTF
cry2ab2_820. A--RYTLRGN--GNSYNYLRVSSIGNSTIRVTINGRYVYATVNTTNNQGVNDNGARFS
8469133 ADIRVNIITGLPSQRYRYRYASTTDLQFTRINGTSVNOGNFQRTNMRGNLESN-PR
cry2ab2_820. DINIGNVASSNSDVPLDINVTLNSGTQFDLMNIMLVPTNISPLY
8469133 TAGSTPFSFNSAQSTFTLTQAFNSQEVYIDRIEFVPAEVTFAESDLERAQKAVNALF
cry2ab2_820. TSTSLGLKTNVTGYHIDQVSNLVACLSDFCLEKRELSEKVKHAKELSKENLQDNP
cry2ab2_820.pep
SW:8469133

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8469133      AGFTPTPSFNAQSTTTGTFQAFNQSVYDRIEFVPAVTFEASDLERAQKAVNALFT
              570      580      590      600      610      620

8469133      STSQLGKTKVTGYHDQVSNVLACLSDEFCLDEKRELSKVKHAKELSKENLLQDDNF
              630      640      650      660      670      680

cry2ab2_820.pep
NRAA:6650206

6650206 source="GENBANK PROT" crystal protein CryIb [Bacillus thuringiensis
serovar morrisoni|gi|8469133|sp|066377|CryIb_BACIM Insecticidal crystal protein
cryIb [Insecticidal delta-endotoxin CryIb(b)] (Crystalline entomocidal protoxin)
(132 kDa crystal protein)

SCORES      Initl: 189      Initn: 216      Opt: 259      z-score: 289.4      E(:): 8e-08
>>NRAA:6650206
      Initn: 216      Initl: 189      Opt: 259      z-score: 289.4      expect(:): 8e-08
Smith-Waterman score: 330;      22.1% identity in 611 aa overlap
(46-634:26-602)

cry2ab2_820      ICDAYNVAADHPFQHKSLDTQKWTWKNNHSLYLDPIVGVTVASFLKKVGSVLGK
              20      30      40      50      60      70
6650206      MKNNIQOCVPYNCLSNPEVEILSEERSTGRPLD-LSLSTRELFSEFVPGV-
              10      20      30      40      50
              60      70      80      90      100      110

cry2ab2_820      RIUSELRNLIFPGSGTNLMQDILRETEKFLNQRLNMTDTRVNAELTGIQANVEFNQV
              120      130      140      150      160      170      180      190
6650206      -VAFGLFDLWGFIPPSWSLFLQEQLEIQRIETLERNAITTLRLGLADSYEVLEAL
              200      210      220      230      240      250
              260      270      280      290      300      310      320      330

cry2ab2_820      DNFL-NNPNNAVPLSITSSVNTMQQLFNLRLPQFMQGYQLLLPLPFAQANLHLSFIRD
              340      350      360      370      380      390      400      410
6650206      REWEEPNNAQLREDVRIRFANTDDLAITAINNFLTSLFSPILSLVYVQAANLHLSLRD
              420      430      440      450      460      470      480      490
              500      510      520      530      540      550      560      570

cry2ab2_820      VILNADWEGISAALTRYRDYLNKTRDYSNYCINTQSFAF--KGLNRLHMDL-EFT
              580      590      600      610      620      630      640      650
6650206      AVSFGQWGLSDIATVNNHYNRLNLIHRYTEHCLDITVQGLEMLRGTTNTRQMSFFQFR
              660      670      680      690      700      710      720      730
              740      750      760      770      780      790      800      810

cry2ab2_820      YMLNFVEVSIWLSLFXQYQLLVSSGNALYASGSGPOQTSTSOQDFLYSLVFNQVSNY
              820      830      840      850      860      870      880      890
6650206      ELTLTDLIDVALFNYDARAYFIQTSSQ-----TREIYTSVVI-EDSP-----VSAN-
              900      910      920      930      940      950      960      970
              980      990      1000      1010      1020      1030      1040      1050

cry2ab2_820      VILNFGSGLRLSNITFNVLGSLPGSTTHALLAARVNYSGG--TSSGDIAGSPFNQNCST
              1060      1070      1080      1090      1100      1110      1120      1130
6650206      IPNGFNRAEFGRVPRHLMFMNSLVTAFTVRSQTVMGWGLHSSRNATGAPINFPFY-GV
              1140      1150      1160      1170      1180      1190      1200      1210
              1220      1230      1240      1250      1260      1270      1280      1290

cry2ab2_820      370      380      390      400      410
FLIPLLT-----PVRSWLDSGSDREGVAT---VTNMQTSETFTLGRSGATARG
              420      430      440      450      460      470      480      490
6650206      FNPGGAIWAEDPRPPYTLTSLPDPVFGVGNGFNHYVLGRGVGQQGTQNHTRTFRNSG
              500      510      520      530      540      550      560      570
              580      590      600      610      620      630      640      650

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cry2ab2_820. NSNYFPDYFRNISGVPLVVRNEDLRRL-HYNEIRNIASPGTGGARAYVMVSYYHNKRN
      : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : :
6650206 TDSLETFPODNGSGAP---NDYSHVLNHVTFFVRWFGTEAGSDSW-RAPMFSWTHRSA
      400   410       420       430       440       450

cry2ab2_820. NIHAVHENGSMIHLAENDYTGTFTSPIAHQTQNNOTRTFISEKFGNQGSLSRFEQNNTTA
      480   490       500       510       520       530
6650206 DRTNI-----INENIIT--QIPAKVAHNHLSGTSVVRRPGFTG-GDLLERTNTGTGA
      460   470       480       490       500

cry2ab2_820. --RYTLGRGN-GNSYNLYLRSVSSIGNSTIRVTINGSVYATNVNTINNDDVNDNGARPSD
      540   550       560       570       580       590
6650206 DIRVNITGPLSQRYRVRIKYASTDLQOFFRINGTSVNOGNFORTNRGNSLESNG-FRT
      510   520       530       540       550       560

cry2ab2_820. INIGNVASSNDVDLDINVLTNGSTGFDLMIMILVPNTISPLY
      600   610       620       630
6650206 AGFTSPFSNAQSITGDTQFOQNSGYVIDRIEFPVPAIFEAESDLERAQKAVNALFT
      570   580       590       600       610       620

6650206 STSQLGLKTNTGYHIDIOVSNLVACLSEDFCLDEKRELSKVHKARLSDKRNLLQDPNF
      630   640       650       660       670       680

cry2ab2_820.psp
NRRAA:295866

295866 source="GENBANK_PROT" crystal protein [Bacillus
thuringiensis]g[27436034[gB|AAO13295.1] crystal delta-endotoxin [Bacillus
thuringiensis]
      Scores Initl: 189 Initn: 216 Opt: 259 Z-score: 289.3 E(): 8e-08
      >>NRRAA:295866
      Initn: 216 Initl: 189 Opt: 259 Z-score: 289.3 expect(): 8e-08
      Smith-Waterman score: 331, 22.1% identity in 612 aa overlap
      (46-634;26-602)

cry2ab2_820. ICDAYNVAADHPFSQKHSLDTVQKEWTWKKNHHSYLDPITGVVASFLKKVGSIVGK
      20    30    40    50    60    70
295866 MKNNIQNCQYPVCNCLNSEVEILLSERSTRGLPLD-ISLSLTRFLSELSEFVG-VG-
      10    20    30    40    50

cry2ab2_820. RILSELRLNLIFFSGSTNLMODILRETEKFLQRANTDTLARVNAELTGLOANVEFNROV
      80    90    100   110   120   130
295866 -VAFGLFDLWGFIPTSENFLFLQEIEQLRLETERRAITTLRGADSVSEVYLEAL
      60    70    80    90    100   110

cry2ab2_820. DNFL-NPENEVAPLSITSSVNTMQOLFNLRFQPMOGVOLLLLPLFAQANLHLSFIRD
      140   150   160   170   180   190
295866 REMEEPNNAQLREDVRIRFANTDDALITAINTLTSTFEISLPYSVYQAANHLSLIRD
      120   130   140   150   160   170

cry2ab2_820. VILNADENGISAILRTYRDYLKNTRYDSNYCINTYQSAF---KGLNTRLHML-EPRIT
      200   210   220   230   240   250
      : : : | | : : : | | : : : | | : : : | | : : : | | : : : | | : : :

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295866 AVSFGCGGLDNTAVNNHYNRLINLHRYTEHCLDYNOCLENLFGNTNRQWSRFNQFRR
190 200 210 220 230
cry2ab2_820. YNPNVFFVSTFIRLKYQSLNLSANLVSAGSGQOQTSQTSQDHPFYLSFQVNSNY
270 280 290 300 310
295866 ELTLNLDLWALFADNAPYFIQTSSD---TREIYTSVVI-EDSP-----VSAN-
240 250 260 270
cry2ab2_820. VLVNGSGARLNTFPFIVLPGSTTIRLILARVNTSSG---SSGDIGASFPNQFNCSCT
320 330 340 350 360
295866 IPNGNRAEFVGFPHLMDFANSDEVTAELRSCWGGHLYSSRWAGNPIN--FPIYG
280 290 300 310 320 330
cry2ab2_820. FLPPLLT-----PFVRSWLDGSGDRENAI---VNVYTESFETTLGLSGASTAR
370 380 390 400 410 420 430 440 450 460 470 480 490 500
295866 IPNPGATWIAEDPRPFYRTLSDFVVRGGFGNPNVLSLGRVAFQOQTNRTRTFNS
340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500
cry2ab2_820. GNSNYFPDYFRNISGVPLVWRNEDLRPL-HYNEIRNIASPGTF-CAAYVMVSVHFK
420 430 440 450 460 470 480 490 500
295866 GTLSDLEIPQDNGSGPW----NDYSHVLNHVTFVRMPGETAGSDSW-RAPWFWNTHRS
400 410 420 430 440 450 460 470 480 490 500
cry2ab2_820. NNHIAVHNGSMHLAPNDYTGTFISPIHATQVNNOTRIFISEKMGQSGLSAFEQNNIT
480 490 500 510 520 530
295866 ADRTNI-----INFNIIT--QIPAVKAHLNLSGSGTVVRGGFTG-GOLLARTNTGTF
460 470 480 490 500
cry2ab2_820. A--RYTLRGN-GNSYNLVRSSIGNSRTVINGRVATVATVNTTNNQVNDNGARES
540 550 560 570 580 590
295866 ADIRVNIITGLPSQRYVRIRYASTTDLOPFRINGTSVNGQNFQRTWNRGNLESQ-PR
510 520 530 540 550 560
cry2ab2_820. DINIGNVASSNDVPLDINVLNLSGTQFDLMIMLVPTNISPLY
600 610 620 630
295866 TAGFSTPFPSFNAQSTFTLTGQAFSNQEVYIDRIEFVPAEVTFEAESDLERAQKAVNALF
570 580 590 600 610 620
295866 TSTSGLKTNVTGYHIDQVSNLVACLSDPECLDEKRELSEKVKHAKELSDKRNLLQDPN
630 640 650 660 670 680
cry2ab2_820.pap
NRAA:62433238
62433238 source="GENBANK_PROT" Cryhime1 [paenibacillus popilliae]
SCORES Initl: 191 Initn: 191 Opt: 259 z-score: 288.4 E(): 9.1e-08
>>NRAA:62433238
Initn: 191 Initl: 191 Opt: 259 z-score: 288.4 expect(): 9.1e-08
Smith-Waterman score: 259; 22.6% identity in 230 aa overlap
(74-297:96-324)
cry2ab2_820. EWKKNHSLYLDPIVGVASFLKKVGLVGRILSELNLIFFPSGSLNQDILRETEK
50 60 70 80 90 100

62433238 TRSPETDAVAVGVRISHTIFRLLGVPSYSAQEQFLSFLDLTLNLEGNTO-WHEELMRHAE
70 80 90 100 110 120
cry2ab2_820. FVNGELNLTDLARVNAELTGLCANVEEFNQVDNF--NPNENAVPLSITSSUNTMOQLFL
110 120 130 140 150 160
62433238 LINEQIDPYVRTKALAEIILGNINLYIAAFEDWKRNPSSQEVTRIVDRNILDGLFE
130 140 150 160 170 180
cry2ab2_820. NRPLOFQMGVQLLLPLFAQAANLHLSFIRDVILNMADEWGISATLRTYRDYLNKYTRD
170 180 190 200 210 220
62433238 AYLPSFAVPGVEVPLLSVYVANVNIHLVLRDSSIHGLDWGLSSTSVDDNNYNFQORNSAT
190 200 210 220 230 240
cry2ab2_820. YSNYCINTYQSAFKGNL---TRLHDMLEPRTYMFNLNVEFVSWLSLKYQSLLVS-SGA
230 240 250 260 270
62433238 YAIHCTWYQTGLQRLQSGDASSWVNNYNNRFRREITLIVLIDICALFSYDVRYSYPIQLRGE
250 260 270 280 290 300
cry2ab2_820. NLYASGSPQOQTOSTSQDWPFLYSLSFQVNSVNLNGFSGARLSNTFPNIVGLPGSTTTH
280 290 300 310 320 330
62433238 LTRGIYTDPAVFSGTSGYSLSQAPSPAETENIATREPSPNFTMANYARVTTGTGLEVLSSK
310 320 330 340 350 360
cry2ab2_820.pap
SW:8469143
8469143 description="PESTICIDIAL CRYSTAL PROTEIN CRYIHB (INSECTICIDIAL
DEUTERATOXIN CRYIHB) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA CRYSTAL
PROTEIN) "library=NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot" version=NA type=PRT
SCORES Initl: 222 Initn: 247 Opt: 256 z-score: 286.0 E(): 1.2e-07
>>SW:8469143
Initn: 247 Initl: 222 Opt: 256 z-score: 286.0 expect(): 1.2e-07
Smith-Waterman score: 256;
(64-279:46-260)
cry2ab2_820. SLDTVQKEWTEKKNNHSLADPIVAVALLKXVGLSKRLSELNLIFFPSGSLNL
40 50 60 70 80 90
8469143 KNPKEMLDIEGLISSRSRQRELSGLTRRDESL-LPGASFGELFDLIWVGIGPDQ
20 30 40 50 60 70
cry2ab2_820. MODILRETEFLNQRINTDLARVNAELTGLCANVEEFNQVDNF-LNPNRNVAFPSITS
100 110 120 130 140 150
8469143 WSLFTIQLEQLIDQRIEAVHRNQATISRLGLEGLSDSYNITELREWBHSPNRESLOQDARN
80 90 100 110 120 130
cry2ab2_820. SYNTHQQFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNMADEWGISATLRTYRDYLNKYTRD
160 170 180 190 200 210 220
8469143 RPSNTDNALITAPILREOGGFEIPLLTVYQAAANLHLSLRDADYVFGQWGGDTAVNNH
140 150 160 170 180 190
cry2ab2_820. RQYLNKNTYRDSNYVCNTYQSAFKGNLRLHDMLEPRTYMFNLNVEFVSWLSLKYQSLL
220 230 240 250 260 270

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8469143      YNRLINLINTYSDHCAQWNRGLNFGVWTARYLDPFQREVTSIVLDIVALFPNYDIRTP
              200   210   220   230   240   250
cry2ab2_820. VSSGANLYASGSPQQTOSTFSDMPFLYSLFQVNSNYLVNFGSGARLNTFPNVGLPG
              280   290   300   310   320   330
8469143      IQTISQLTREIVTSPVAEPFGASLNVDLRNLREPHLMDFLRLVIYTGQGGIYHWAGHE
              260   270   280   290   300   310
cry2ab2_820.psp
NR2A:8469143

8469143 source="GENBANK_PROT" Pesticidal crystal protein cryIb (Insecticidal
delta-endotoxin CryIIb) (Crystalline entomocidal protoxin) (131 kDa crystal
protein)gi|1022728|gb|AAA79694.1| crystal toxin

SCORES      Init1: 222      Initn: 247      Opt: 256      Z-score: 286.0 E(): 1.2e-07
>>NRAA:8469143
Initn: 247 Init1: 222 Opt: 256 Z-score: 286.0 expect(): 1.2e-07
Smith-Waterman score: 256; 21.2% identity in 217 aa overlap
(64-279:46-260)

cry2ab2_820. SLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKXVSLGKRLSELRLNLPSPSGTNL
              40    50    60    70    80    90
8469143      KNPKIEMLDIEGISSRSREQVAEISLGLTRFLLESLLPGASFGFLDIWVGPDQ
              20    30    40    50    60    70
cry2ab2_820. MODLIRETEKELNORLNTDLARVNAELTGLQANVEENRQVNF-LNPNRNAVPLSTIS
              100   110   120   130   140   150
8469143      WSLFTQIEQLIDQIEARVNRQAISSLESGDSYEYIESLREWRASPNESLQDVNRN
              80    90   100   110   120   130
cry2ab2_820. SVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVLNADWGISAAATLRTY
              160   170   180   190   200   210
8469143      RFSNTNALITAIPIRLREQGEIPLITVYVQAANLHLSLLRDVYFGQWGLDTATVNNH
              140   150   160   170   180   190
cry2ab2_820. RDKLYKNTRYDYSNYCINTYQSAFAGLNRLHDMLEFRYTMFLNVFEVSIWSLPKYQLL
              220   230   240   250   260   270
8469143      YNRLINLINTYSDHCAQWNRGLNFGVWTARYLDPFQREVTSIVLDIVALFPNYDIRTP
              200   210   220   230   240   250
cry2ab2_820. VSSGANLYASGSPQQTOSTFSDMPFLYSLFQVNSNYLVNFGSGARLNTFPNVGLPG
              280   290   300   310   320   330
8469143      IQTISQLTREIVTSPVAEPFGASLNVDLRNLREPHLMDFLRLVIYTGQGGIYHWAGHE
              260   270   280   290   300   310
cry2ab2_820.psp
NRAA:5901703

5901703 source="GENBANK_PROT" 135 kDa insecticidal protein (Bacillus
thuringiensis serovar kurstaki)

SCORES      Init1: 128      Initn: 168      Opt: 255      Z-score: 284.8 E(): 1.4e-07
>>NRAA:5901703
```

```
Initn: 168 Init1: 128 Opt: 255 Z-score: 284.8 expect(): 1.4e-07
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)

cry2ab2_820. FQHKSLDTQKEWTEWKKNNHSLYLDPIVGTVASFLKXVSLGKRLSELRLNLPSPSG
              30    40    50    60    70    80
5901703      IPYNCLSNREVEVLGGRIERTPIDISLITQELLSEF--VPGAGFVLGLVDIINGIF
              20    30    40    50    60
cry2ab2_820. STNLMQDILRETEKELNORLNTDLARVNAELTGL---QANVEEFNRQVDFNLPNRNA
              90   100   110   120   130   140
5901703      GPSQWDTFLVQIEQLINRIEIEFARNAQISRLGSLNLYQIYAESFREWEADPTNP---A
              70    80    90   100   110   120
cry2ab2_820. VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVLNADWGIS
              150   160   170   180   190   200
5901703      LREEMRIQFNNDNNSALTTAIDLAVQNYQVPLLSYVQAANLHLSVLRDVSVFGQWGF
              130   140   150   160   170   180
cry2ab2_820. AATLTRYDLYKNTRYDYSNYCINTYQSAFK---GLNTRLHDMLE---BERTYMFNLVFEY
              210   220   230   240   250
5901703      AATINSRYNDLTRLICGNVTDYARVWNTGLERVWGPDNR--DWRVYNQFRRELTITVLDI
              190   200   210   220   230   240
cry2ab2_820. VSIWSLF---KYQSLLVSS--GALYASGSPQQTOSTFSDMPFLYSLFQVNSNYLVNFG
              260   270   280   290   300   310
5901703      VALFSNDYRRPIPTISQTLTRYINPVLNFDFGSGFMAQRIEQNIQPHLMDILNSI
              250   260   270   280   290   300
cry2ab2_820. SGARLSNTPFNIVGLPGSTTHALLAARVNSYSGISS---GDIG--ASPFNQNFNCSTF
              320   330   340   350   360
5901703      T-----IVTDVHRGFNWSGHQITASPVGFSGPEFAFFLFGNAGNAAPPVILVSLTGLGI
              310   320   330   340   350
cry2ab2_820. LPPLLTPFVRSM-LDSGSDREGVATVNNQTESFET-TLGRSGAFTARGSNYFPDYFI
              370   380   390   400   410   420
5901703      FRTLSSFLYRRIILGSGPNQOEL-FVLDGTEFSASLTTLNLPSTIYRQIGVDSL-DVIP
              360   370   380   390   400   410
cry2ab2_820. RNISGVPLVVRNEDLRRLPHVNEIRNIASPSGTGPGARVYMSVHNRKNNHVAHENGSM
              430   440   450   460   470   480
5901703      PQDMSVY--PRAGFSHRLGH--VTMLSAQAGAVYLRAPTFWQHRSAEFNNIIPSSQI
              420   430   440   450   460   470
cry2ab2_820. --IHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQSGSLRFEQNNITARYTLRNGN
              490   500   510   520   530   540
5901703      TQIPLAKSNLGSSTVVKVGPFGTGGD--ILRRTSPQIGISTLRV---NITAPLSQR---
              480   490   500   510   520
cry2ab2_820. SYNLYLRLVSSIGNSTIRVTINGRVYATVNTTNNQDNDNGARFSDINIGNVVASNS
              550   560   570   580   590   600
5901703      -YRVRIRASTNLQFHTFSIDGRPINQGNFSATMSS--GSNLQSGSRFRTVGTPTPFNSNG
              530   540   550   560   570
```

©07

~~CRY2462 620 DVPJUN-N-TLNSGOFDLMNIMLVPTNISPLY
: : : : : : : : : : : :
SSVTLSSWYFNGSGEVITISIERPVAFFEAEDYTSSNQIGLKTDV~~

cry2ab2_820.pep
NRAA:535781

535781 source="GENBANK_PROT" insecticidal crystal protein [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 168 Opt: 255 Z-score: 284.8 E(1): 1.4e-07
 >NRJAA:535781
 initn: 168 Init1: 128 Opt: 255 Z-score: 284.8 E(1): 1.4e-07
 Smith-Waterman score: 286: 21.8% identity in 600 aa overlap
 (60-634:41-609)

30 40 50 60 70 80
cry2ab2.820. FOHSLDTVOKEWTKKNNHSLYLDIVGTVAFLKKVGSVGRKUSELNUIFPSG
535781 TPYNCLSNPEVEVLGGERITGYTPIDISLSTQELSEF-VFGAGFVGLGDIWGLP

```

          90      100      110      120      130      140
cy2ab2.820. STNMQDIURETEKFLNRLNRTDITLARVNAELTGL----QANVEEFNRQVDIFLAPNRR
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
535781      GPSQWDAFLVQIEQLINORIEEFNARQASRLSEGLSNLYIAESFREWEADPTNP---A
          70      80      90      100      110      120

```

```

cry2ab2_820. VPLSITSSVNTTQQQLFLNRLPQFMQGYQLLLLPFAQAANLHLSIFRVLNADEWGIS      150      160      170      180      190      200
          :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
LREMERIQFDNMSALTTAIPLAQNQYVPLLSVYVQAANLHLSVRDVSFVGORMGCFD      130      140      150      160      170      180

```

[illegible][illegible]

```

320      330      340      350      360
CRY2AB2_820.  SGARLNTFPNIVGLPGSTTHALLAARYNYSGLSS---GDIG--ASFPNQNFNCSTF
               : : : : : : : : : : : : : : : : : : : : : : : : : : : :
535781  T-----IYDVHRGNFYNSGHQITASPVGFSGPEAFPLFGNAGNAAPPLVLSITGLGI
               310      320      330      340      350

```

370 380 390 400 410 420
 cry2ab2_820 LPPLLTPFKVRK-LDGGSDREGVATINMQTESFET-TLGRSGCAFTARGNSYFPDVF
 535781 FRTLSPLPRLVILGSGNNQEL-FVLDTGESFASLTNPLPTIYRQGTVDLSL-DVLP

cry2ab2_820. RNISGVPLVRNEDLRRLPHYNIRNIASPSGTPGARAYVMSVHNRKNNIHAVHENGSM

```

535781      : : : | : | : : : | : | : : : : : :
      PDONSVP--PRAGFSHRLSH---VTMLSQAGAVYTLFAPTFSWQHRSAEFNIIIPSSQI
      420      430      440      450      460      470

```

```

cry2ab2_820.      --ILAPNDYGTFTSPIAHQVNNQTRTFSEKFGQDLSLFEQNNTARTYLRGNNGN
                    | | | | | | | | | | | | | | | | | | | | | |
535781            TQPLTKSNLGSVTVKPGFTGGD--ILRTSPGQISLTV---NITAPLSR---
                    490    490    510    510    520    520

```

CRY2AB2_820. SYNLVLRVSSIGNSRIRVTINGRVYATNTVNITNNDGVNDGARESDINIGVVAVSSNS
 : : | :
 -YRVRIVASTTNLQFSTIDSGPRFNQGNFASMTSS--GSNLQSGSFRTVGTPTTFPSNG

```

535781      SSVFTLSAUFVNSGNEVYDRIEFVPAEYFEAYDLERAQKAVNELFTSSNGIGLKTDV
610      590      620      610      620      610      620      610      620
cry2ab2_820.  DVPIDINV.TLNSGTFDLNMIMLVPTNISPLY
610      620

```

~~sty2ab2_820.pep~~
~~NRAA:743635~~

```
> seqA=seq46365  
Initn: 128      Initrn: 168      Opt: 255      z-score: 284.8 E(): 1.4e-07  
(1176 aa)  
Initn: 98      Initrn: 138     opt: 255 z-score: 284.8 expect(): 1.4e-07  
(1176 aa)  
Initn: 98      Initrn: 138     opt: 255 z-score: 284.8 expect(): 1.4e-07  
(1176 aa)
```

(60 634 43 609)
 30 50 60 70 80
 cry2ab2_020_F0HKSJDTQKIEWEMKNNHSLYLPVIGTVASFLLKGVSLVGRILSEHNLIPSG
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100
 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

cy2ab2_820. STNMOILREKRLQVRLMUTLBYNNAEISGL ---QANVEENRQVNF.LNPRNA

~~ant60~~

[illegible]

260 270 280 290 300 310
cry2ab2_820. VSTWLF---KYQLSVLLVS-GANLTYASGGPQQTSTSDMPFLYS.FQVNSNYVNGF

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cry2ab2_820.. 320 330 340 350 360
SCARLSNTFNIIVGLPGSTTTTHALLAARNYSGGISS-----GDIG--ASPPNQNFNCSTF
743635 T-----IYTDVHRGFNYWSGCHQITASPVGFGSFPFAFLFGNAGNAAPVLIVSLTGLGI
310 320 330 340 350
370 380 390 400 410 420
cry2ab2_820.. LPPLLTFFVRSM-LDSGSDREGVATVNMQTESFET-TLGLRSGAFTARGNSNYPFDYFI
743635 FRTLSSEPLYRRIILGSGPNQOEL-FVLDGTFFSFASLTITNLPSTIYRQGTVDLSL-DVIP
360 370 380 390 400 410
390 440 450 460 470 480
cry2ab2_820.. RNISGVPLVRNEDLRPLHNEIRNIASPSGPGARAYMVSVHNRKNNIHAVHENGSM
743635 PQDNSVP--PRAGFSHRLSH---VTMLSQAGAVYTLRAPTFWSQHRSAEFNNIIPSSQI
420 430 440 450 460 470
490 500 510 520 530 540
cry2ab2_820.. --IHLPNDVTGFTISPIHATQVNNQTRTFISEKFGNOGDSLRFQEQNNITARYTLRNGN
743635 TQIPLTKSTNLGSGTSVVKPGFTGGD--ILRRTSPGQISTLRV--NITAPLSQR----
480 490 500 510 520
550 560 570 580 590 600
cry2ab2_820.. SYNLYLRVSSIGNSTIRVTINGRVYTAIVNTTINNCGVNDNGARFSDINIGNVVASNS
743635 SSVFTLSAHVFNSGNEVIDRIEFVPAEYTFEAEYDLERAQKAVNELFTSSNQIGLKTIDV
580 590 600 610 620 630
cry2ab2_820.pep
NRAA:6687073
6687073 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 168 Opt: 255 z-score: 284.8 E(): 1.4e-07
>NRAA:6687073 (1176 aa)
Initn: 168 Initl: 128 Opt: 255 z-score: 284.8 expect(): 1.4e-07
Smith-Waterman score: 286; 21.8% identity in 600 aa overlap
(60-634:41-609)
30 40 50 60 70 80
cry2ab2_820.. FOHKSLLDTQKWEKTEWKKNNHSLYLDPIVGTAVASFLLKKKGLVGGKILSELRLNIPSG
6687073 IPYNCLSNPEVEVLGGERIETGTPIDISLTQFLISEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60
90 100 110 120 130 140
cry2ab2_820.. STNLMQDILRETEKFLNQRLNTDTLAVRNAELTGL-----QANVEENRQVDNLFNPNNA
6687073 GPSQWDAFLVQIEQLINQRIEFPARNQAISRLGLESLNLYQIYAESFREWEADPTNP--A
70 80 90 100 110 120
150 160 170 180 190 200
cry2ab2_820.. VPLSITSSVNTMQQLNRLNLPFQFMQGYQLLLPLFAQAANHLHSIRTRDVILNADEWGIS
```

```

6687073 LREMRIQFNDNNSALTTATPLAVQNYQVPLLSVTOAANHLHSVLRDVSFVGQRMGFD
130 140 150 160 170 180
210 220 230 240 250
cry2ab2_820.. AATLTRYRDYKKNYTRDYSNCINTYQSFAK---GLNTRLHML---EERTYMFNLVPEY
6687073 AATINSRYNDLRLICGNVTDVAVRWYNTGLERVWGPDSR--DWVRNQFRRELITLTLDI
190 200 210 220 230 240
260 270 280 290 300 310
cry2ab2_820.. VSIWSLF---KTQSLVSS-GANLYASGSGPOQTOSTFSQDWPFLYSLFQVNSNVLNGF
6687073 VALESNDSSRYPIRTVSQLTREIYTNVLENFDGSGFRGMAQRIEQNIHQPHLMDILNSI
250 260 270 280 290 300
320 330 340 350 360
cry2ab2_820.. SGARLSNTFNIIVGLPGSTTTTHALLAARNYSGGISS-----GDIG--ASPPNQNFNCSTF
6687073 T-----IYTDVHRGFNYWSGCHQITASPVGFGSFPFAFLFGNAGNAAPVLIVSLTGLGI
310 320 330 340 350
370 380 390 400 410 420
cry2ab2_820.. LPPLLTFFVRSM-LDSGSDREGVATVNMQTESFET-TLGLRSGAFTARGNSNYPFDYFI
6687073 FRTLSSEPLYRRIILGSGPNQOEL-FVLDGTFFSFASLTITNLPSTIYRQGTVDLSL-DVIP
360 370 380 390 400 410
430 440 450 460 470 480
cry2ab2_820.. RNISGVPLVRNEDLRPLHNEIRNIASPSGPGARAYMVSVHNRKNNIHAVHENGSM
6687073 PQDNSVP--PRAGFSHRLSH---VTMLSQAGAVYTLRAPTFWSQHRSAEFNNIIPSSQI
420 430 440 450 460 470
490 500 510 520 530 540
cry2ab2_820.. --IHLPNDVTGFTISPIHATQVNNQTRTFISEKFGNOGDSLRFQEQNNITARYTLRNGN
6687073 TQIPLTKSTNLGSGTSVVKPGFTGGD--ILRRTSPGQISTLRV--NITAPLSQR----
480 490 500 510 520
550 560 570 580 590 600
cry2ab2_820.. SYNLYLRVSSIGNSTIRVTINGRVYTAIVNTTINNCGVNDNGARFSDINIGNVVASNS
6687073 -YRVRIYASTTNLQFHTSIDGRPINQGNFSATMSS-GSNLQSGSFRTVGTTPFNFSG
530 540 550 560 570
610 620
cry2ab2_820.. DVPIDINV-TLNSGTQFDLMNIMLVPTNISPLY
6687073 SSVFTLSAHVFNSGNEVIDRIEFVPAEYTFEAEYDLERAQKAVNELFTSSNQIGLKTIDV
580 590 600 610 620 630
cry2ab2_820.pep
NRAA:41688283
41688283 source="GENBANK_PROT" putative mosquitoicidal toxin [Bacillus thuringiensis serovar entomocidus]
SCORES Initl: 205 Initn: 205 Opt: 251 z-score: 284.1 E(): 1.6e-07
>NRAA:41688283 (686 aa)
Initn: 205 Initl: 205 Opt: 251 z-score: 284.1 expect(): 1.6e-07
Smith-Waterman score: 268; 22.1% identity in 592 aa overlap
```

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41688283 cry2ab2_820. PSFQKSLDTVQKWEKNNKSLYLDPIVGTAVSFLLKKGSLVGRKILSELRLNLF
630 640 650 660 670 680
41688283 cry2ab2_820.pap
NRAA: 67089177
67089177 source="GENBANK_PROT" CryIAa [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 168 Opt: 254 z-score: 283.7 E(1): 1.6e-07
>NRAA: 67089177
initn: 168 opt: 254 z-score: 283.7 expect(1): 1.6e-07
Smith-Waterman score: 285; 21.8% identity in 600 aa overlap
(60-634:34-602)
cry2ab2_820. FQKSLDTVQKWEKNNKSLYLDPIVGTAVSFLLKKGSLVGRKILSELRLNLFPSG
67089177 IPYNCLSNPEVGLGERIETGYTPIDISLUTQFLSEF--VFGAGFVLGLVDIIMGIF
10 20 30 40 50 60
cry2ab2_820. STNLMQDILRETEKFLNORLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPENA
90 100 110 120 130 140
67089177 GPSQMDAFLVQIEQLINORIEEFARQCAISRLEGLSNLYQIYAESREWEADPTNP---A
70 80 90 100 110
cry2ab2_820. VPSKSSVNTMQQLFNRLPQOMQGYQLLLPLFAQANLHLSFIRVILNADMGIS
150 160 170 180 190 200
67089177 LREMRVQPNNSALITTAIPALAVQYVPLLSVYQAAHLNLSVLRDVSFVGQMGFD
120 130 140 150 160 170
cry2ab2_820. RATIRYDILKNYTRNSNCTINTYQSAFK--GLNTRLDML---ERTYMLNVEFY
180 190 200 210 220 230
67089177 LATINSRYNDLTELAVYTDYVARNNTGLERVWGPDSR--DWVRNQFRRLITLVLDI
260 270 280 290 300 310
cry2ab2_820. VSIWLSF--NQSIVSS--SAYVYSGSGPOSTSTSDMPFLYSFQVNSVNLNGF
240 250 260 270 280 290
67089177 VALFSNYDSRRYPITVQSQRREIYVNDLNFQDGSFSGAQRIGONIRQPHLMILNSI
320 330 340 350 360 370
cry2ab2_820. SGARLSNTPFNIVGLPGSTTHALLARVNSGGIS--GIDIG--SPFNQFNCSFT
300 310 320 330 340 350
67089177 T-----IYDVHRGFNWSGHQITASPVGSGPPEAPPLFGNAGNAAPVPLSLGLGI
370 380 390 400 410 420
cry2ab2_820. LPPLTPFVRSW-LDSSGSDREGVATVNMOTESPET-TLGLSGCATARGNSVTPYFI
430 440 450 460 470 480
67089177 FRTLSSPLVRRILLGSGFPNNOEL-FVLDGTFSPASLTTLNLPSTIYVQSGVDSIAVVI
410 420 430 440 450 460
cry2ab2_820. RNISGVLVVRNEDURPLHYNEIRNIASPGTGGARAVSVNHRNNIHAHVHNSCM
430 440 450 460 470 480
67089177 PQNSVFP--PRAGFSHLRSH---VTMLSQAGAVYTLRAFTFSWHRSAEFNNIIPSSQI
410 420 430 440 450 460

41688283 cry2ab2_820. PSFQKSLDTVQKWEKNNKSLYLDPIVGTAVSFLLKKGSLVGRKILSELRLNLF
630 640 650 660 670 680
41688283 cry2ab2_820.pap
NRAA: 67089177
67089177 source="GENBANK_PROT" CryIAa [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 168 Opt: 254 z-score: 283.7 E(1): 1.6e-07
>NRAA: 67089177
initn: 168 opt: 254 z-score: 283.7 expect(1): 1.6e-07
Smith-Waterman score: 285; 21.8% identity in 600 aa overlap
(60-634:34-602)
cry2ab2_820. FQKSLDTVQKWEKNNKSLYLDPIVGTAVSFLLKKGSLVGRKILSELRLNLFPSG
67089177 IPYNCLSNPEVGLGERIETGYTPIDISLUTQFLSEF--VFGAGFVLGLVDIIMGIF
10 20 30 40 50 60
cry2ab2_820. STNLMQDILRETEKFLNORLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPENA
90 100 110 120 130 140
67089177 GPSQMDAFLVQIEQLINORIEEFARQCAISRLEGLSNLYQIYAESREWEADPTNP---A
70 80 90 100 110
cry2ab2_820. VPSKSSVNTMQQLFNRLPQOMQGYQLLLPLFAQANLHLSFIRVILNADMGIS
150 160 170 180 190 200
67089177 LREMRVQPNNSALITTAIPALAVQYVPLLSVYQAAHLNLSVLRDVSFVGQMGFD
120 130 140 150 160 170
cry2ab2_820. RATIRYDILKNYTRNSNCTINTYQSAFK--GLNTRLDML---ERTYMLNVEFY
180 190 200 210 220 230
67089177 LATINSRYNDLTELAVYTDYVARNNTGLERVWGPDSR--DWVRNQFRRLITLVLDI
260 270 280 290 300 310
cry2ab2_820. VSIWLSF--NQSIVSS--SAYVYSGSGPOSTSTSDMPFLYSFQVNSVNLNGF
240 250 260 270 280 290
67089177 VALFSNYDSRRYPITVQSQRREIYVNDLNFQDGSFSGAQRIGONIRQPHLMILNSI
320 330 340 350 360 370
cry2ab2_820. SGARLSNTPFNIVGLPGSTTHALLARVNSGGIS--GIDIG--SPFNQFNCSFT
300 310 320 330 340 350
67089177 T-----IYDVHRGFNWSGHQITASPVGSGPPEAPPLFGNAGNAAPVPLSLGLGI
370 380 390 400 410 420
cry2ab2_820. LPPLTPFVRSW-LDSSGSDREGVATVNMOTESPET-TLGLSGCATARGNSVTPYFI
430 440 450 460 470 480
67089177 FRTLSSPLVRRILLGSGFPNNOEL-FVLDGTFSPASLTTLNLPSTIYVQSGVDSIAVVI
410 420 430 440 450 460
cry2ab2_820. RNISGVLVVRNEDURPLHYNEIRNIASPGTGGARAVSVNHRNNIHAHVHNSCM
430 440 450 460 470 480
67089177 PQNSVFP--PRAGFSHLRSH---VTMLSQAGAVYTLRAFTFSWHRSAEFNNIIPSSQI
410 420 430 440 450 460

cry2ab2_820. --HILANDYGTETSPHATQVNNQTRTFISEKFGNGDLSRFEQNNTARYTIRNGN
490 500 510 520 530 540
67089177 TQIPLTSTNLSGSGSVVKGPGFTGGD--ILRRTSPGQISTLRV--NITAPLSOR---
470 480 490 500 510

cry2ab2_820. SYNLYLRVSSIGNSTIRVTINGRVYATVNTTNNQDNGVNGARSDINIGVASSNS
550 560 570 580 590 600
67089177 -YRVIRYASTNLQFHTSIDGRPIQNGFNSATMSS-GSNLQSGSFRTVGTTPPNSG
520 530 540 550 560 570

cry2ab2_820. DVPLDINV-TLNSGTQFDLMIMLVPTNISPLY
610 620 630
67089177 SSVFTLSAHVFNSSGNEVYIDRIEFPVPAEVTFEAEYDLERACKAVNELFTSSNQIGLXTDV
580 590 600 610 620 630

cry2ab2_820.pap
NRAA:13173240

13173240 source="GENBANK_PROT" insecticidal crystal protein BTRX28 [Bacillus
thuringiensis serovar KunthalarX28]

SCORES Init1: 128 Initn: 168 Opt: 253 z-score: 282.9 E(): 1.8e-07
(1118 aa)
Initn: 168 Init1: 128 Opt: 253 z-score: 282.9 expect(): 1.8e-07
Smith-Waterman score: 279; 21.1% identity in 602 aa overlap
(60-634;41-610)

cry2ab2_820. FQHSLSLTQKTEWTKNNHSLYLDPIVGTVASFLKKVGLSVKRIILSELRNLIIPSG
30 40 50 60 70 80
13173240 IPYNCLSNPEVVLQGERIETGYTPIDISLSLTQFLSEF--VFGAGFVLGLVDIINGIF
20 30 40 50 60

cry2ab2_820. STNLMQDILFRETKEFLNRLNTDTLARVNAELTGL---QANVEEFNRQVDNPLNPNRA
90 100 110 120 130 140
13173240 GPSQWDAFLVQIEQLINQRIEFPARNQALSRLEGLSNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQQLFNLRLPQFQMGYQLLLPLFAQAANLHLSFTRVILNADWGIS
150 160 170 180 190 200
13173240 LREEMRIQFNDMNSALTITAIPLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF
130 140 150 160 170 180

cry2ab2_820. AATLRTYRDYLNKYTRDYSNYCINTYOSAFK--GLNTRLHDML---EERTYMLNVEFY
210 220 230 240 250
13173240 AATINSYNDLTELIGNYTDYAVRWNTGLRWGPDGR--DWRVYNQFRITILVLDI
190 200 210 220 230 240

cry2ab2_820. VSIWLSFKYGLSVSSGANL---YASGPGQQTQSFTSQDWPFPLYSLFQVNSVYLVNGP
260 270 280 290 300 310
13173240 VALFPNVDSTRTYPIRTVSQLTREIYTNFVLENFDGSRGSAQGTFSIRSPLHMLNSI
250 260 270 280 290 300

320 330 340 350 360

cry2ab2_820. SGARLSNTFNPINVLPGSTTTTHAL--LAARVNYSGGISSGIGASP---FNQNFNGSTF
490 500 510 520 530 540
13173240 TIYRMH--JEDIIICQIKKLLLEGFQONSFLYICRGEMQLHFNRLNLLNKVRACIEH
310 320 330 340 350 360

cry2ab2_820. LPPLLPFVRSWLDGSDREGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYFIRN
370 380 390 400 410 420
13173240 YRPL---YTEDLFKEGINNQL-SVLDGTEFAYGTSSNLPSAVYKSGTVDSLDEIPQN
370 380 390 400 410

cry2ab2_820. ISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVSVNRKNNIHAVHENGSMIH
430 440 450 460 470 480
13173240 -NNVP--PRQGFSHLSHVSFMRSGFSNSSV-SIIRAPMFSW-----IHRSAEFNN
420 430 440 450 460

cry2ab2_820. LAPNDYGTISPI-HATQVNNQTRTFISEKFGNGDLSRFEQNNTARYTIRGN-----
490 500 510 520 530 540
13173240 IIPS--SOITQIPLTKSNLGSSTSVKPGFTG-GDLRRTSPGQIS--TLRVNITAPL
470 480 490 500 510

cry2ab2_820. GSNLYLRVSSIGNSTIRVTINGRVYATVNTTNNQDNGVNGARFSDINIGVASS
550 560 570 580 590 600
13173240 SORYVRIRYASTNLQFHTSIDGRPIQNGFNSATMSS-GSNLQSGSFRTVGTTPPNS
520 530 540 550 560 570

cry2ab2_820. NSDVPYLDINV-TLNSGTQFDLMIMLVPTNISPLY
610 620 630
13173240 NGSSVFLLSAHVFNSSGNEVYIDRIEFPVPAEVTFEAEYDLERACKAVNELFTSSNQIGLKT
580 590 600 610 620 630

13173240 DVTVDHIDQVSNLVECLSDFECLDEKQELSEKVKHAKELSDERNLLQDPNFRGINQLDR
640 650 660 670 680 690

cry2ab2_820.pap
NRAA:1922253

1922253 source="GENBANK_PROT" cbm72 mosquitoicidal toxin [Clostridium
bifermentans]gi|10719926|sp|O05102|Cl7AA_CLOBI Pesticidal crystal-like protein
cry17Aa (insecticidal toxin CryxvIIA(a)) (Cbm72 mosquitoicidal toxin)

SCORES Init1: 69 Initn: 102 Opt: 248 z-score: 281.5 E(): 2.2e-07
(618 aa)
Initn: 102 Init1: 69 Opt: 248 z-score: 281.5 expect(): 2.2e-07
Smith-Waterman score: 248; 25.8% identity in 229 aa overlap
(56-269;43-259)

cry2ab2_820. DPFSFQHSLSLTQKTEWTKNNHSLYLDPIVGTVASFLKKVGLSVKRIILSELRNLI
30 40 50 60 70 80
1922253 EYNSNLDIQPRELNTINGLVFTGATVSIILPLIGTTA--VVPVVGVIQ--IIAALLPVI
20 30 40 50 60

cry2ab2_820. FPSGST---NLMDILRETEKFLNORLNTDTLARVNAELTGLQAA--NVEEFNRQVDNFLN
90 100 110 120 130 140
1922253 WPAQTSSNDNLFDVAVKXTENIDEXISEYV--VNDANTFELSILYLDYVYLSKDFWE
70 80 90 100 110 120

[illegible]

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crv2ab2_820. VNRKNKIHAVHENGSMIHLAFNDYTGFTISPHATQV-----NNQTRTFISEKFG-NQ
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MGPTTQDPVPVY--SWTHQSA-DRIN-TINSDRITQPLVKAHTIQLSGTTVWKGPGFTG
      480      490      500      510      520

crv2ab2_820. GDSLRFEQNNTTAYTLRNGN--SYNLYLRVSSIGNSTIRTVNGRVYVATNVTITIN
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
GDILRTSGGPFASFNVDLNFSLQRYRARIYASTTITRLRYIVTVAGERIFAGQFDKTMW
      530      540      550      560      570      580

crv2ab2_820. NDGVNDNGARFSDINIGNVASSNSDVLDPINV-TLNSGTG-----FDLMNMLVPTNIS
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
A-CAPUTTQGSFVSATINTAFTTPERSSSLTGADTFSSGNEVVDVDFELIQVATPEARS
      590      600      610      620      630      640

crv2ab2_820. PLY
8469141      DLRARAKVALFTSNPRGLTVDYTHIDQVSNLVECLSDDEFCKDKRELLFEVKYAK
      650      660      670      680      690      700

crv2ab2_820.pcp
SW:8469141

8469141 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAK (INSECTICIDAL
DELTA-ENDOTOXIN CRYIAK(A)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (I37 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar morrisoni"
source="swissprot_prot" version="NA type=PRT

SCORES      Init1: 148      Initn: 177      Opt: 252      Z-score: 281.1 E(): 2.3e-07
>>SW:8469141
      initn: 177      init1: 148      opt: 252      Z-score: 281.1 expect(): 2.3e-07
Smith-Waterman score: 257;      23.3% identity in 622 aa overlap
(56-626:73-636)

crv2ab2_820. 30      40      50      60      60      60      60      80
8469141      EGNIDPFVSASTVQTGISIAGRILGVIGVPFAGQALSFY----SFLAGE-----L
      50      60      60      60      60      60      60      80

crv2ab2_820. 90      100      110      120      130      140
crv2ab2_820. FPGSGTNLMQDILRETFEXFLNQRINTDITLARVN-AEUTGLQANVEEFNRQVDNPLNPNR
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WFSGR-DWEIPEFHEVQEIVRQOQDITSDVDRDTARLEGIRGYSYQQALETWLDNRND
      90      100      110      120      130      140

crv2ab2_820. 150      160      170      180      190      200
crv2ab2_820. AVPLSITSSVNTMQQL-FLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVLNADG
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AKRSRIIRERYALELDTITAIPLFSIRNEEVPLMRYAQAANLHLLLRDASLFGSEWG
      150      160      170      180      190      200

crv2ab2_820. 210      220      230      240      250
crv2ab2_820. ISAAATLRIRDYLNKTYRDSNYCINTYQSAFKGLNTRLHDML-----EFTYMLNVPEY
8469141      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
MSSADVNGYQOEIRYITEYSNHCVQWYNTGLNRLRGTTAETWRYNQCFRDLTLGLVDL
      210      220      230      240      250      260

      260      270      280      290      300

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cry2ab2_820. VSIWLFKYQLLVSSGML---YA--SG---SGPQOTQ-----SPTSD-----WPFLY
      270      280      290      300      310      320
8469141 VALFPSYOTRYPIPTTAOLTEVYTPDNGVAGNNWSFRNCASFSAIENAIIRPHLY
      330      340      350      360      370
cry2ab2_820. SLF-----QVNSYVLNGFSGARLSNTFPNVGLPGSTTHALLAARVNYSGGIS
      380      390      400      410      420
8469141 DFLNLTIYTRRSQVGT--IMNLWAGHRI--TFNRIOG--GSTSEWYGAI---INPVS
      330      340      350      360      370
cry2ab2_820. 360      370      380      390      400      410
8469141 VSDI---:---:---:---:---:---:---:---:---:---:---:---:---:---:---:---:
      380      390      400      410      420
cry2ab2_820. GAFTARGNSYFPDYFIRNISGPLVVRNEDLRRLHYNEIRNIASPGTGGCARAYMVS
      430      440      450      460      470
8469141 GLF-----YHFGH-----AGIATQVKSDELTPETTPQPNRYAFSHLLS-----HLS
      430      440      450      460      470
cry2ab2_820. 480      490      500      510      520
8469141 VHRKNNTHAVHENGSMHLAPNDYTGFTISPIHATQV-----NNQRTFISEKFG-NQ
      480      490      500      510      520
cry2ab2_820. MGPTQDQVPVY---SWTHQSA-DRTN--TINSDRITQIPLVKAHTLQSGTIVWKVGGFTG
      480      490      500      510      520
cry2ab2_820. 530      540      550      560      570      580
8469141 GDILRTSGGFPAPSNVLNDFNLQSRYRARIYASITNLRIYVYAGERIFAGQFQKTWD
      530      540      550      560      570      580
cry2ab2_820. 590      600      610      620      630
8469141 A-GALPTFGSVATINTAFTFPERSSSLTGATTFSSGNEVYVDREFELQVTAPEAES
      590      600      610      620      630
cry2ab2_820. PLY
cry2ab2_820. 650      660      670      680      690      700
8469141 DLRARKAVNALFTSNPRGKLTVDYHIDQVSNLVECLISDEFCLDKKRELLSEVVKYAK
      650      660      670      680      690      700
cry2ab2_820.pwp
SW:61221640
61221640 description="Pesticidal crystal protein cryIaA (Insecticidal
delta-endotoxin CryIa(a)) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar entomocidus"
source="swissprot_prot" version="NA type="PRT
SCORES Init1: 128 Initn: 168 Opt: 251 z-score: 280.2 E(): 2.6e-07
>>SW:61221640
Initn: 168 Init1: 128 opt: 251 Z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 282; 22.1% identity in 560 aa overlap
(100-634:79-609)
70 80 90 100 110 120

```

CRY2ab2_820. GSLVGRKILSELNLIFFSGSTNLMDILRETEKELNORLNTDTLARVNAELTGL----Q
160 170 180
16221640 EFVPGAGFVLGLVDIIMWIFQPSQWDAFFVQIEQINQRIIEFARNQAIISRLGSLNLYQ
80 90 100
CRY2ab2_820. ANVEEFNRQVDNLFNPNPNAVPLSITSSVNTMQQLFNRLPQFMQYQQLLLPLFAQAA
130 140 150 160 170 180
61221640 IYASFPREWEADPTNF--ALREEMRIQFNDMNSALTTAIPLLAVQYQVPLLSVYVQAA
110 120 130 140 150 160
CRY2ab2_820. NLHLSFIRDVILNADWEGISATLTYRDYKNIYRDYSNYCINTYQSAPK---GLNTRL
130 140 150 160 170 180
61221640 NLHLSVLDRDVSFVGQWGFDAATINSYNDLRLGNYTDYAVRWYNTGLERVAGPDSR-
170 180 190 200 210 220
CRY2ab2_820. DMPLYSGLFQVNSNYLVNGFSGCARLSNTPFNIVGLPGSTTHALLAARVNSGGIS--
300 310 320 330 340 350
61221640 AORTEQNIQPHLMILNSIT-----IYDVHRGFNYWNGHQTASPVGSGPFAFPL
290 300 310 320 330
CRY2ab2_820. -GDIG--ASFPNQFNCSITFLPPLTFVRSM-LDSGDRGVATVNNQTESFET-TLG
360 370 380 390 400
61221640 FGNAGNAAPVLSVLTGLGIFRLSSFLYRRIILGSGPNQEL--FVLDTGTEFSFASLTN
340 350 360 370 380 390
CRY2ab2_820. LRSAGTARGNSYFPDYFIRNISGVPLVRNEDLRRLHYNRIINIASPSTPGGARAY
410 420 430 440 450 460
61221640 LPSTIYRQGTVDLSL-DVIPPQNSVP--PRAGFSHRLSH--VTMLSQAGAVYTRAP
400 410 420 430 440 450
CRY2ab2_820. MVSVHNRKNNIHAVHENG--SMIHLAPNDYTGFTISPIHATQVNNQTRIFISEKFGNQGD
470 480 490 500 510 520
61221640 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGDD--ILRTSPGQIS
460 470 480 490 500
CRY2ab2_820. SLRFEQNTTARYTLRNGNSYNYLRYRVSSIGNSTIRVTINGRYVYATVNTTNNQGVN
530 540 550 560 570 580
61221640 LOSGSFRTVGTTPFPNSGSSVFTLSAHVNSGNEVYIDRIEFPVAFVFAEYDLERA
560 570 580 590 600 610
61221640 OKAVNELFTSSNQIGLKDVTVDHIOQVSNLVECLSDPEFCLEKQELSKVYHAKRLSDE
620 630 640 650 660 670
CRY2ab2_820.pep
510 520 530 540 550

NRAA:142765
142765 source="GENBANK_PROT" crystal protein
SCORES Initl: 128 Initn: 168 Opt: 251 z-score: 280.2 E(): 2.6e-07
>NRAA:142765
initn: 168 initl: 128 opt: 251 z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 282; 22.1% identity in 560 aa overlap
(100-634:79-609)
CRY2ab2_820. GSLVGRKILSELNLIFFSGSTNLMDILRETEKELNORLNTDTLARVNAELTGL----Q
142765 EFVPGAGFVLGLVDIIMWIFQPSQWDAFFVQIEQINQRIIEFARNQAIISRLGSLNLYQ
50 60 70 80 90 100
CRY2ab2_820. ANVEEFNRQVDNLFNPNPNAVPLSITSSVNTMQQLFNRLPQFMQYQQLLLPLFAQAA
130 140 150 160 170 180
142765 IYASFPREWEADPTNF--ALREEMRIQFNDMNSALTTAIPLLAVQYQVPLLSVYVQAA
110 120 130 140 150 160
CRY2ab2_820. NLHLSFIRDVILNADWEGISATLTYRDYKNIYRDYSNYCINTYQSAPK---GLNTRL
130 140 150 160 170 180
142765 NLHLSVLDRDVSFVGQWGFDAATINSYNDLRLGNYTDYAVRWYNTGLERVAGPDSR-
170 180 190 200 210 220
CRY2ab2_820. DMPLYSGLFQVNSNYLVNGFSGCARLSNTPFNIVGLPGSTTHALLAARVNSGGIS--
300 310 320 330 340 350
142765 AORTEQNIQPHLMILNSIT-----IYDVHRGFNYWNGHQTASPVGSGPFAFPL
290 300 310 320 330
CRY2ab2_820. -GDIG--ASFPNQFNCSITFLPPLTFVRSM-LDSGDRGVATVNNQTESFET-TLG
360 370 380 390 400
142765 FGNAGNAAPVLSVLTGLGIFRLSSFLYRRIILGSGPNQEL--FVLDTGTEFSFASLTN
340 350 360 370 380 390
CRY2ab2_820. LRSAGTARGNSYFPDYFIRNISGVPLVRNEDLRRLHYNRIINIASPSTPGGARAY
410 420 430 440 450 460
142765 LPSTIYRQGTVDLSL-DVIPPQNSVP--PRAGFSHRLSH--VTMLSQAGAVYTRAP
400 410 420 430 440 450
CRY2ab2_820. MVSVHNRKNNIHAVHENG--SMIHLAPNDYTGFTISPIHATQVNNQTRIFISEKFGNQGD
470 480 490 500 510 520
142765 TFSWQHRSAEFNNIIPSSQITQIPLTKSTNLGSGTSVVKGPGFTGDD--ILRTSPGQIS
460 470 480 490 500
CRY2ab2_820. SLRFEQNTTARYTLRNGNSYNYLRYRVSSIGNSTIRVTINGRYVYATVNTTNNQGVN
530 540 550 560 570 580
142765 TLRV--NITAPLSQR-----YRVIRVASTINIQFHTSIDGRPINQGNFSATMSS-GSN
510 520 530 540 550

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117531      LPSTIYQRGTVDLSL-DVIPQDMSVP--PRAGFSHRLSH---VTMLSQAAGNAVYTLRAP
          400       410       420       430       440       450

cry2ab2_820. MYSVHNKNNIHAVHENG--SMILHNDYTGFTISPIHATQVNVNQTRTFISEKFNQGD
          470       480       490       500       510       520

117531      TFSWQHRSASFNNIIIPSSQIQIPLTKSTWLGSGTGVVKGFPGTDG-ILLRTPSPGOIS
          460       470       480       490       500       510

          530       540       550       560       570       580

cry2ab2_820. SURFEQNNTTARILRGNGNSYNLYLRVSSIGNSTRIRTVINGRYTTATNNTITNNQGVN
          :|||   |||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
117531      TLRW---NITAPLSQR-----YRVRIEYASTTNLOFHSTIDGRFINQGFMATSS-GSN
          510       520       530       540       550       560

          590       600       610       620       630       640

cry2ab2_820. DNGARFSDINIGNVASSNSDPVDINV-TLNSGTQFDLMIMLVLPNTISPLY
          :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
117531      LOSGSFRIVCGFTTFPNFGSNGSVFTLSAHVFNSGENEVDIRIEFVPAVETFEAYDLERA
          560       570       580       590       600       610

          620       630       640       650       660       670

117531      QKANVELFTSSNOGLUKTDTVDYHDQVSNLVECLDSDFCULDEKQELSEKVHKAKRLSDE
          620       630       640       650       660       670

SW:8488967

8488967 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL
PROTEIN)." library=NA species=Bacillus thuringiensis serovar sotto"
source="Swissprot_prot version=NA type=PRT

SCORES Init1: 128 Initn: 168 Opt: 251 Z-score: 280.2 E(): 2.6e-07
>>SW:8488967
Initn: 168 init1: 128 opt: 251 Z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 282; 22.% identity in 560 aa overlap
(100-634:79-609)

              70           80           90          100          110          120
cry2ab2_820. GSLVGKRIILSELNRNLIFPFGSTNIQMQLIRETEKFLNORLNMTDLARVAETLGL----Q
8488967      EFVPGAGFVLGLVDIIWGIFGPSQMDAFFPVQIEQLINQRIEEFARNQASLRLEGLSNLYQ
              50           60           70           80           90          100

              130          140          150          160          170          180
cry2ab2_820. ANVEEFNRQVDNFLENRNNAVPLSIITSVNTHMQOQLFNRLPFQOMQGYQLLLLPFAQAA
              :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
8488967      IYAESFWREADPTNP--ALUREEMRIQDNMNSALTITAIPELLAQVNYQVPLLSVVYVQAA
              110          120          130          140          150          160

              190          200          210          220          230          240
cry2ab2_820. NLHSFIRDVIHLNDEWGISATLRTYRDLYKNTRYDRSYNCINTYQSAPK---GLNTRL
              :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
8488967      NLHSLVRDVSVFQGRGWGFDATINSRYNDLTRNLGNITYDVAFWEVNYTGLERWVGPDSCR-
              170          180          190          200          210          220

              250          260          270          280          290
cry2ab2_820. HDML---EFFTYMFLNVFEYSVISLWF---KYOSLLVSS-GANLYAGSGPOQTOSTFSQ
              :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||   :|||
8488967      -DWRYNQCFRELTUHTDIVALEPSYDSDSRYPRTVTSQLTREITYNPVLNPFVLDGSGFRGM
              230          240          250          260          270          280

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CRY2ab2_820. DWPEYTLFOVNSVYVNGFGCARLSNTEFNVLPGSTITTHALLAARNVYGGSSIGSS---
300 310 320 330 340 350
8488967 AQRREYRPHIMLNLII-----IYDVHRGFTWNSGHQITASPVGFGSGPEAFPL
290 300 310 320 330
CRY2ab2_820. -GDIG-ASFEINNCSTAPPPLTPVRSH-LDSGSDRGVAIVTNQTESFET-TLG
360 370 380 390 400
8488967 FGNAGNAAPWAVSLTGLGISTLSCPLVRRILLGSDNNQEL-FVLDDGTESFASLTNN
340 350 360 370 380 390
CRY2ab2_820. MVSVHNKNNIIHAVHENG--SMIHLANDYTGFTISLTHSNQVNCGRITPEKFGNCSO
410 420 430 440 450 460
8488967 LRSGAFTARGNSNYFDYFIRNLSGVLVVRNRLRZPLHYNEZRNINSPSGTGGARAY
420 430 440 450 460
CRY2ab2_820. LPTSIYRQRTVDLSL-DVIPPQNSVR-LPAGFSLSLST-VTMLSRAQAVVTLRAP
400 410 420 430 440 450
8488967 TFSNQHSRAEFNNIIPSSQITQIPLTKSINLGSITSVVKGPFTGSD--LRRPFGQIS
460 470 480 490 500
CRY2ab2_820. SLRFEQNNITARYTLRGNNSYNIYLRVSSIGNSTIRVTINGRYATNVNTTNGQVN
530 540 550 560 570 580
8488967 TLRV--NITAPLSQR----YRVRIYASTINLQFHTSIDGRPIQNGFNSATMSS--GSN
510 520 530 540 550 560
CRY2ab2_820. DNGARFSDINGNVASSNSDVFLDINV-TLMSGTQFDLMNMLVFNISPLY
610 620 630
8488967 LQSGSFPTGFTPIPFNFSGNSVFIILSAHFVNSGNEVYIDRIEFVPAEVTFAEYDLERA
570 580 590 600 610
CRY2ab2_820. QKAYNELFTSSNQIGLKTDVTDYHDQVSNVECLSDFLCDKQELSKVHKHAKRLSDE
620 630 640 650 660 670
CRY2ab2_820. pep
NR044:40267
40267 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi161221638[sp|POA366|CRIA_A_BACTX_Pesticidal crystal protein
cryIAA (insecticidal delta-endotoxin CryIA(a)) (Crystalline entomocidal protoxin)
(133 kDa crystal protein)gi161221640[sp|POA368|CRIA_A_BACTE_Pesticidal crystal
protein cryIAA (insecticidal delta-endotoxin CryIA(a)) (Crystalline entomocidal
protoxin)](133 kDa crystal protein)

```

SCORES Init1: 128 Initn: 168 Opt: 251 z-score: 280.2 E(): 2.6e-07
>NRJAA:40267
Initn: 168 Init1: 128 opt: 251 z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 282: 22.% identity in 560 aa overlap
(101-634:79-609)

70 80 90 100 110 120
cry2ab2_820. GSLVGRKILSELNLNIFPGSGTNLMQDILRETEKFLNORLNTDTLAVNAELTGL---Q
40267 EFVPGSGVLGVLDIINGIFPGSOWAFPVQTEQLINRIEFPARNOATSRLEGLSLNLYO

40267 EFVFGAGFVLGVLDIINGIFGFSQDAFPVQLEQINQRIFEAFRNQATRSLEGSNLQ
50 60 70 80 90 100
130 140 150 160 170 180

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cry2ab2_820. ANVEEFNRVDNFIAPNNAVPLSITSSVNTWQOLFNLRFQFOMQCYQLLLPLFPAQAA
40267 IYAESFREWADPTNP--ALUREMIRIQFNMMNSALITAITELLAVQNYQVPLLSVYVQAA
110 120 130 140 150 160

cry2ab2_820. NUHLSFIRSDVILNADGWISATLURDYRDLNRYDYSNCTYNQSAFK---GLNTRL
40267 NUHLSVLDRDVSFGORWGFDAATINSRYNDLTRLNIGYNTDYAVRWYNTGLERWGWGDSK-
170 180 190 200 210 220

cry2ab2_820. HDML--EFTYMFNLVEYYSINSLF---KQOSLLVSS-CAMLYASGSGPOQTOSPTSQ
40267 -DWRYNQFRETULFVLDIVAUFSNYSRYPITRYSQLTREIYINPVLENFPMGDSFGRM
230 240 250 260 270 280

cry2ab2_820. DWPFYLSLFQVNSYVLYNGFSGARLSNTPFNVLGPGSTTTTHALLAARNVYSGISS---
40267 AQRTEQNIQRPMLMDLANSIT-----IYDVHRGFYMSWGHQITASPVGFGSGPEFAFPL
290 300 310 320 330 340 350

cry2ab2_820. -CDIG--ASFPNCFNCSFTPLPLTTPFRSM-LDSGDRGVATVNNQTSFT-TLG
40267 FQNGMNAAPVLVSLTGLGIFRTUSSPYLRIILGSGNNQEL-FVLDGTETFSFASLTIN
340 350 360 370 380 390

cry2ab2_820. LRSARFAGNSNYFDYFINISGVLVVRNEDLRPHLYEIRNIASPTPGGAGAR
40267 LPSTINQRTQSDSL-DVIPPQDSNP--PRAGFGRHLSH---VTMLSQAAGAVVTLRAP
400 410 420 430 440 450

cry2ab2_820. MYWNNANINHAIRNG--SMIHLANDYGTFTSPIHATQVNNQTRTIFSEKGNQGD
40267 TFSWQHSASFPNNTPSQTOYTNLTKSNLASGTSVVKVGPGFTGD--ILRKTSPGQIS
460 470 480 490 500 510 520

cry2ab2_820. SLRFEQNTVARTLRNGSYALYLRVSNSNIRVYTINGRVYATVNTTNNQDGN
40267 TLRV--NITAPLSR---YRGRYVNTNLQHSIDGRPIHQGNSFASMTSS-GSN
510 520 530 540 550 560 570 580 590 600 610 620

cry2ab2_820. DNGARFSDINIGNVVASNSVDPLNPLTNSGOFDNLMLVNTNSPLY
40267 LOSGSPFTGCTPFPNGSGSVFTLSARWNSDEVTYRIEFVPAVYVREKRWDLERA
560 570 580 590 600 610 620

cry2ab2_820. OKAVNELFTSSNOIGLKTVDVTDHIDQVSNLVECLSDFCDEKQETSXVYHAKLSE
40267
620 630 640 650 660 670 680 690 700

cry2ab2_820.pap
SW:6121638

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cry2ab2_820.pep
SW:61221638

61221638 description="Pesticidal crystal protein cryIIAa (Insecticidal delta-endotoxin CryIIA(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein)." library="NA species="Bacillus thuringiensis serovar kurstaki" source="Gibson et al. 1997" version="NA type="DPT

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SCORES   Init1: 128   Initn: 168   Opt: 251   z-score: 280.2 E(): 2.6e-07
>>SW:61221638
Initn: 168 init1: 128 opt: 251 z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 282; 22.1% identity in 560 aa overlap
(100-634:79-609)

cry2ab2_820. 70 80 90 100 110 120
GSLVGKRLSELRLNLIFFSGSTNLMDILRETEKFLNQLNDTLARNAELTGL----Q
61221638  EVVPGAGVGLVDIINGIFGPSQWDAPFQIEQLNQRIEFARNAQISRLGLSLNQ
110 120 130 140 150 160 170 180
cry2ab2_820. ANVEEFNQVDNLFNPNNAVPLSITSSVTMQOLFNLRFQFQMGVQLLLFLFAQAA
61221638  IYAESFREWEADPTNP---ALREEMRIQFNDMNSALTTAIPLLAQVNYQVPLLSVVYVQAA
110 120 130 140 150 160 170 180
cry2ab2_820. NUHLSEFIRDLNADWEGISRAATLTIRYDVLKMYTRDYSNYCINTYQSAFK---GLNTRL
61221638  NUHLSEFIRDLNADWEGISRAATLTIRYDVLKMYTRDYSNYCINTYQSAFK---GLNTRL
170 180 190 200 210 220 230 240
cry2ab2_820. HDML---EFRTYMFANVFEVVISLFL---KYQSLLVSS-GANLYASGSGPQOTQFTSQ
61221638  HDML---EFRTYMFANVFEVVISLFL---KYQSLLVSS-GANLYASGSGPQOTQFTSQ
230 240 250 260 270 280 290
cry2ab2_820. DMFFLYSLFQVNSYVNLGFGSARLSNFPNIVGLPGSTTHALLARVNSGGISS---
61221638  DMFFLYSLFQVNSYVNLGFGSARLSNFPNIVGLPGSTTHALLARVNSGGISS---
290 300 310 320 330 340 350
cry2ab2_820. -GDIG--ASPFGNQFNCFPLPLLPFRSM-LDSGSDREGVATVNWQTESFET-TLG
61221638  -GDIG--ASPFGNQFNCFPLPLLPFRSM-LDSGSDREGVATVNWQTESFET-TLG
340 350 360 370 380 390 400
cry2ab2_820. LSGAFTARGNSYFFDYFIRNIGSVPLVNRNEDLRPLHYNEIRNIASPSGTPGARAY
61221638  LSGAFTARGNSYFFDYFIRNIGSVPLVNRNEDLRPLHYNEIRNIASPSGTPGARAY
400 410 420 430 440 450 460
cry2ab2_820. MYSVHNKRNKNIHAVHENG--SMIHLAPNDVTGFTISPIHATQVNNQRTIRISEKFGNCGD
61221638  MYSVHNKRNKNIHAVHENG--SMIHLAPNDVTGFTISPIHATQVNNQRTIRISEKFGNCGD
460 470 480 490 500 510 520
cry2ab2_820. SLRFEQNNTIARTLRGNSYNYLVRVSSIGNSIRTVINGRVYVATVNTVNTNDGVN
61221638  SLRFEQNNTIARTLRGNSYNYLVRVSSIGNSIRTVINGRVYVATVNTVNTNDGVN
530 540 550 560 570 580
cry2ab2_820. TLRV---NITAPLSQR-----YRVIRVASTTNLQHTSIDGRPINQGNESATMSS-GSN
61221638  TLRV---NITAPLSQR-----YRVIRVASTTNLQHTSIDGRPINQGNESATMSS-GSN
510 520 530 540 550 560 570
cry2ab2_820. DNGARFSDINIGNVASSNSDVPFLDINV-TLNSGTQFDLMNINLVPTNISPLY
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61221638  LOGSFRVGTFTPFNFNSGVSFTLSAHVFNSGNEVYIDIRIEFVPAEVTFEAEVDLERA
560 570 580 590 600 610
61221638  QKAVNELFTSSNOIGLKTQDVTYHIDQVSNLVECLSDPECLDEKQELSEKVKHAKLSDE
620 630 640 650 660 670
cry2ab2_820.pcp
SW:8469136
8469136 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAD (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIA(D)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT"

SCORES   Init1: 151   Initn: 192   Opt: 251   z-score: 280.2 E(): 2.6e-07
>>SW:8469136
Initn: 192 init1: 151 opt: 251 z-score: 280.2 expect(): 2.6e-07
Smith-Waterman score: 295; 23.2% identity in 608 aa overlap
(60-634:41-609)

cry2ab2_820. FOKHSLDTQKENTWKNHSLYLDPIVGTVASFLKKVGSVLGKRIILSELNLIFFSG
30 40 50 60 70 80
8469136  VFYNCNDPTIEILEGERIETGYTPIDISLSLTQFLSEF--VFGAGFVLGLIDLWGFV
20 30 40 50 60
cry2ab2_820. STNLMDILRETEKFLNQLNDTLARNAELTGL----QANVEEFNQVDNLFNPNNA
90 100 110 120 130 140
8469136  GSGQDAFLVQIEQLNQRIEFARNAQISRLGLSLNQVYVQVPLLSVQVQANHLHSLVLDVSVEGQWGF
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVTMQOLFNLRFQFQMGVQLLLFLFAQANHLHSLVLDVSVEGQWGF
150 160 170 180 190 200
8469136  LTEEMRIQFNDMNSALTTAIPLFTVQNYQVPLLSVQVQVQANHLHSLVLDVSVEGQWGF
130 140 150 160 170 180
cry2ab2_820. AATLRTYRDYKMYTRDYSNYCINTYQSAFK---GLNTRLHDMML---EFRTYMFANVFEY
210 220 230 240 250
8469136  VATINSRYNDLTLELIGITDYAVRWYNTGLERVWGPDSR--DWVRYNQFRRELTITVLDI
190 200 210 220 230 240
cry2ab2_820. VSIWLSFKYQSLVSSGANL---YAS-----GSGPQOTQSTSQ-DWPFYSLFQVN
260 270 280 290 300
8469136  VSLFPNYDSITYPIRTVSQLTREITYTNPVLENFDGSGFRGMAQRIEQNPHQLMOLLNSI
250 260 270 280 290 300
cry2ab2_820. SNY---VLNGF---SGARLSNTPFNIVGLPGSTTHALLARVNSGGISGDIASPNQ
310 320 330 340 350 360
8469136  TTYTDVHRGFNWSGHOITAS-P-VGFAGPEFTFPRYGTMGNAAPVPLISITITGLGIFR-
310 320 330 340 350
cry2ab2_820. NFENCSFLPPLLTPFVRSVNLDSGSDREGVATVNWQTESFET-TLGRSGAFTARGNSY
370 380 390 400 410 420
8469136  -----TUSSEL---YRRILGSGPNQNL-FVLDDGTEFSASLTADLPSTIYRQRTVDS
360 370 380 390 400 410
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8469136      VATINSRYNDLTLLGCTYTDVAVRWYNTGLERVWGPDSR---DWVRVYNQFRRELTLLVLDI
      190      200      210      220      230      240

cry2ab2_820. VSIWLSFKYQSLVSSGANL---YAS-----GSGPQQTQSFTSQ-DWPELYSLFQVN
      250      260      270      280      290      300

8469136      VSLFVNDYSRTYPIRTVYSQLTRFATVPLENFDGSGFRGMAQRTEQNIQPHMLMOLLINSI
      250      260      270      280      290      300

cry2ab2_820. SNY--VLNGF---SGARLSNTFNPVIGLPGSTTHALLAAARVNYSGGSSGDIGASPNQ
      310      320      330      340      350      360

8469136      TIYDVRGFWYWSGHQITAS-P--VGFAGPEPTFRGTGMNAAPPVLISITGLGIFR-
      310      320      330      340      350      360

cry2ab2_820. NFNCSTLPEPLLTFVRSWMLDGSREGVATVNNQTESPET-TLGLRSGAFTARGNSNY
      370      380      390      400      410      420

8469136      -----TLSSPL--VRRILGSGPNQNL-FVLDDGTESFASLTADLPSTIYRQRGTSDS
      360      370      380      390      400      410

cry2ab2_820. PDYFIRNISGVPLVVRNEDLRPLPHNEIRNIASPSGTCGARAYVWSVHRKKNIRHV
      430      440      450      460      470      480

8469136      L-DVIFQDDNSVP--ARAGFGRRLSH---VTMLSQAGAVTLRAPTFSWR-----
      420      430      440      450      460      470

cry2ab2_820. NENGSMHLAPNDYTGFTISPIHATQVNNQTRTFISEXFG-NQGDLSIRFEQNN--TTARY
      490      500      510      520      530      540

8469136      HQAPLNSLIPS--SQITQIPUTKS-INLGSSTVSVKPGFTGGDILRTISPGQSLIRV
      480      490      500      510      520      530

cry2ab2_820. TLRGH-GNSNRLKLR--SSIGNSTRITRVINGRTVATNNITINNDGVNONGA-RFSDINI
      540      550      560      570      580      590

8469136      JIITAPSSQVLRVIRVATTHIDQPHITSIDGRPNQGNFSATMSGGNSLQSGSFRTAGTFT
      520      530      540      550      560      570

cry2ab2_820. GNVVASNSVPLDINLQSGTQDFDINLVNPNISPLY
      600      610      620      630

8469136      PFNFSNGSSITPLSHV-FNSNGNVIETIERPAPVITFEAYEDLERAQEAVALFTSSN
      580      590      600      610      620      630

8469136      QLGLKTNVTDYHDQVSNVNECSGPECLEKPISEKVRVNNLSDERILLQDNPFRGI
      640      650      660      670      680      690

cry2ab2_820.pgp
NRAA:1769867

1769867 source="GENBANK_PROT" delta-endotoxin [synthetic construct]

SCORES      Initn: 206      Initn: 206      Opt: 245      Z-score: 277.9      E(I): 5e-67
>>NRAA:1769867
      Initn: 206      Initn: 206      Opt: 245      Z-score: 277.9      expect(I): 3.5e-67
Smith-Waterman score: 245;      25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820.      KENTWKKNNHSLYLDPIVGTVASFLKKVGLSGVLGRILSELRLNLIFFPSGGSNLMQDLIR
      940      950      960      970      980      990

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cry2ab2_820. LVSSGANLYASGSGPQQTSFTSDPFFLYSLFQVNSYVLVNGSGARLNTFPNVLGSL
280 290 300 310 320 330
PIQVQGLTREYVTDPLINFPNQLQSVQALPTFNWMESSAIRNPFLFDILNNLLTFTDWF
260 270 280 290 300 310
NRAA:143227

cry2ab2_820.pep
NRAA:38231198

38231198 source="GENBANK_PROT" CytLC [Chloroplast transformation vector
pN-IC101]

SCORES Initl: 206 Inltn: 206 Opt: 245 z-score: 277.6 E(): 3.6e-07
>NRAA:38231198
inltn: 206 initl: 206 opt: 245 z-score: 277.6 expect(): 3.6e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLLLKKVGSIGVKRILSELNLIFFSGSTNLMODILR
40 50 60 70 80 90
38231198 DGERISTGSSDISLSLVQLFVSNFVPGGFLVG--LIDFVWGIVPGSQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEXFLNQRINTDLARVNAELTGLQANVEEFNRQVDNFL---NPNRNAVLSITSVSN
100 110 120 130 140 150
38231198 --EQLINERIAE--FAR-NAAIANLEGLNFNFIYVEAFKEWEDPNPATRIVDIRFR
80 90 100 110 120 130
cry2ab2_820. TMOQLFLNLRFQPMQGYQLLLPLFQAQANLHFLFDIVILNADEWGISAAITLRYDY
160 170 180 190 200 210
38231198 ILDGLLERDIPFRISGGFEVPLSLVSAQAANLHLLALRDSVIFGERWGLTINVNVNINR
140 150 160 170 180 190
cry2ab2_820. LKNYTRDYNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNLNVEYYSIWSLFGSL
220 230 240 250 260 270
38231198 LIRHIDEYADHCANTYRGLNLPKSTYQDWITYNRLRDLTLTLVLDIAAAPPVNDNRY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQQTSFTSDPFFLYSLFQVNSYVLVNGSGARLNTFPNVLGSL
280 290 300 310 320 330
38231198 PIQVQGLTREYVTDPLINFPNQLQSVQALPTFNWMESSAIRNPFLFDILNNLLTFTDWF
260 270 280 290 300 310
cry2ab2_820.pep
NRAA:143227

143227 source="GENBANK_PROT" insecticidal endotoxin

SCORES Initl: 128 Inltn: 168 Opt: 248 z-score: 276.9 E(): 3.9e-07
>NRAA:143227
inltn: 168 initl: 128 opt: 248 z-score: 276.9 expect(): 3.9e-07
Smith-Waterman score: 257; 21.4% identity in 611 aa overlap
(60-634:41-611)

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143227 SSNQIGLKTVDTHYIDQVNLVECLDSDFCLDEKKSEKVKHAKRLSDERNLLQDPNF 640 650 660 670 680 690

crv2ab2_820.psp
SM:117542

117542 description:"l31 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE
ENTOMOCIDAL PROTOXIN)." library=NA species="Bacillus thuringiensis serovar
kurstaki" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 128 Initn: 168 Opt: 248 2-score: 276.9 E(): 3.9e-07
>>SW:117542
initn: 168 initl: 128 opt: 248 2-score: 276.9 expect(): 3.9e-07
Smith-Waterman score: 257; 21.4% identity in 611 aa overlap
(60-634:41-611)

30 40 50 60 70 80
crv2ab2_820. FQKSLDTVQKEWTEWKNHNSLYLDPIGVTSFLKKVGSLSVKRILSEKRLNLPSPG
117542 IPYNCLSNFEVVLGGRIETGTPIDISLTOFLSEP--VPGAGFVLGLVDIIWGIF
20 30 40 50 60
crv2ab2_820. STNLMODILRETKFLNQRINTDTLARVNAELTGL---QANVEEFNQVDNFIENRVA
117542 SPSSOWDAFLVOIEQLINQRIETEEFARNQALISEGLSNLVQIYAESFRWEADPNP---A
70 80 90 100 110 120 130 140
crv2ab2_820. VPSITSSYNFQQLFLNRLPQFMQGYQLLLFLFAQANLHLFIIRDVLINADENGIS
117542 LREEMAIQFNDNGALNTAIPLEAVNQVPLLSVYVQAANLHLVLNRDVSFGQRMGFD
110 120 130 140 150 160 170 180
crv2ab2_820. ASFLKRYRYLKNYTVSYNCKNTQSAFK---GLNTRLHDML---EFRTYFLNLFVEY
117542 AATINRNNDITRLGLTMDVRVYNLSELSVNGPDSR--DWIRNQFRRETLTVDLDI
190 200 210 220 230 240
crv2ab2_820. VSTWSLFXKYQSLLVSSNANLNGSGSQTQFTSDQWFLSLFLQVNSVNLVNGFSGAR
260 270 280 290 300 310
117542 VSLFPNVDSRTYPIRTVSQI-----TRLEITLTPVLEKFDSSFRGSAGGIEGSI
220 230 240 250 260 270 280 290
crv2ab2_820. LSNFTFNIVGLPGSTTHALLAARVNYSGGTSGLTGAQSPQNFNCSTETPLPLTFTVR
320 330 340 350 360 370
117542 RS---PHLMDLNGITITYD-AHRGEIYW--SGHQINLSPVG--FSG---DEFTPLPFG
300 310 320 330 340 350 360 370
crv2ab2_820. SWLSDSGDEGVAIVTWQTESFETTLGLRGAFTAGNSVFPD-----VIRNIVG
380 390 400 410 420 430
117542 TMGNAAPQRIQVAGGVGVFTLSLTYLFRFNFINNQLSGPDGGGRICLMLNLLKGP
340 350 360 370 380 390
crv2ab2_820. PLVVNRDLRPLNHYEIRNIASP--SGTPGGARVYVYVHNRKNIHVAHENGSMIHLAP
440 450 460 470 480 490

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[illegible]

1234884 --EQLINERIAE--FAR-NAAIANLEGLNFIYVEAFKWEEDPNPATRTRVIDRFR
80 90 100 110 120 130
cry2ab2_820. TWQQLFLNRLPQFOMOGYQLLLPLFAQAANLHLSFIRDVLNADENGISAATLRTYDY
140 150 160 170 180 190 200 210
1234884 ILDGLEEDIPSRISGFEVPLLSVYAQAANLHLSFIRDVLNADENGISAATLRTYDY
140 150 160 170 180 190 200 210
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNVFVYSIMSLFKYQSL
220 230 240 250 260 270
1234884 LIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNYDNRYY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLIYASGSGPQQTOSTFSQDWPLFLSLFQVNSNYVNGFSGARLNTFTDMF
280 290 300 310 320 330
1234884 PIQPVQGLTREVTDLINFNPLQSVQAQLPTFNWESSAIRNPHLFDILNNLTFTDMF
260 270 280 290 300 310
cry2ab2_820.pgp
NRAA:40356
40356 source="GENBANK_PROT" unnamed protein product (Bacillus thuringiensis)
SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 276.0 E(): 4.4e-07
>>NRAA:40356
Initn: 206 Initl: 206 Opt: 245 z-score: 276.0 expect(): 4.4e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)
cry2ab2_820. KEWTEWKKNNHSLYLDPIVGTVASFLKKVGLKVLGKRLSELNRLIFPPSGSTNLMODILR
40 50 60 70 80 90
40356 DGERISTGSSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNORLNTDLARVNAELTGLQANVEEFNRQVDNPL---NPNRNAVPLSITSSVN
100 110 120 130 140 150
40356 --EQLINERIAE--FAR-NAAIANLEGLNFIYVEAFKWEEDPNPATRTRVIDRFR
80 90 100 110 120 130
cry2ab2_820. TWQQLFLNRLPQFOMOGYQLLLPLFAQAANLHLSFIRDVLNADENGISAATLRTYDY
160 170 180 190 200 210
40356 ILDGLEEDIPSRISGFEVPLLSVYAQAANLHLSFIRDVLNADENGISAATLRTYDY
140 150 160 170 180 190 200 210
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNVFVYSIMSLFKYQSL
220 230 240 250 260 270
40356 LIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNYDNRYY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLIYASGSGPQQTOSTFSQDWPLFLSLFQVNSNYVNGFSGARLNTFTDMF
280 290 300 310 320 330
40356 PIQPVQGLTREVTDLINFNPLQSVQAQLPTFNWESSAIRNPHLFDILNNLTFTDMF
260 270 280 290 300 310
cry2ab2_820.pgp
NRAA:40356
40356 source="GENBANK_PROT" Crylaa (Bacillus thuringiensis)
SCORES Initl: 128 Initn: 168 Opt: 246 z-score: 274.5 E(): 5.4e-07
>>NRAA:37781497
Initn: 168 Initl: 128 Opt: 246 z-score: 274.5 expect(): 5.4e-07
Smith-Waterman score: 277; 21.7% identity in 600 aa overlap
(60-634:41-609)
cry2ab2_820. FOHKSLOTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLKVLGKRLSELNRLIFPPSG
30 40 50 60 70 80
37781497 IPYNCLNPEVVLGERIETGYTPIDISLSLTQFLISEF--VPGAGFVLGLVDILNLTFTDMF
20 30 40 50 60
cry2ab2_820.pgp
NRAA:37781497
37781497 source="GENBANK_PROT" Crylaa (Bacillus thuringiensis)
SCORES Initl: 128 Initn: 168 Opt: 246 z-score: 274.5 E(): 5.4e-07
>>NRAA:37781497
Initn: 168 Initl: 128 Opt: 246 z-score: 274.5 expect(): 5.4e-07
Smith-Waterman score: 277; 21.7% identity in 600 aa overlap
(60-634:41-609)
cry2ab2_820. FOHKSLOTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLKVLGKRLSELNRLIFPPSG
30 40 50 60 70 80
37781497 IPYNCLNPEVVLGERIETGYTPIDISLSLTQFLISEF--VPGAGFVLGLVDILNLTFTDMF
20 30 40 50 60

cry2ab2_820.pgp
NRAA:7141141
7141141 source="GENBANK_PROT" toxin CryIcA6 (Bacillus thuringiensis)
SCORES Initl: 208 Initn: 208 Opt: 247 z-score: 275.6 E(): 4.7e-07
>>NRAA:7141141
Initn: 208 Initl: 208 Opt: 247 z-score: 275.6 expect(): 4.7e-07
Smith-Waterman score: 247; 25.3% identity in 202 aa overlap
(70-263:54-246)
cry2ab2_820. KEWTEWKKNNHSLYLDPIVGTVASFLKKVGLKVLGKRLSELNRLIFPPSGSTNLMODILR
40 50 60 70 80 90
7141141 DGERISTGSSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNORLNTDLARVNAELTGLQANVEEFNRQVDNPL---NPNRNAVPLSITSSVN
100 110 120 130 140 150
7141141 --EQLINERIAE--FAR-NAAIANLEGLNFIYVEAFKWEEDPNPATRTRVIDRFR
80 90 100 110 120 130
cry2ab2_820. TWQQLFLNRLPQFOMOGYQLLLPLFAQAANLHLSFIRDVLNADENGISAATLRTYDY
160 170 180 190 200 210
7141141 ILDGLEEDIPSRISGFEVPLLSVYAQAANLHLSFIRDVLNADENGISAATLRTYDY
140 150 160 170 180 190 200 210
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNVFVYSIMSLFKYQSL
220 230 240 250 260 270
7141141 LIRHIDEYADHCANTYNGRLNPKSTYQDWITYNRLRDLTLVLDIAAFFPNYDNRYY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLIYASGSGPQQTOSTFSQDWPLFLSLFQVNSNYVNGFSGARLNTFTDMF
280 290 300 310 320 330
7141141 PIQPVQGLTREVTDLINFNPLQSVQAQLPTFNWESSAIRNPHLFDILNNLTFTDMF
260 270 280 290 300 310
cry2ab2_820.pgp
NRAA:37781497
37781497 source="GENBANK_PROT" CryIcAa (Bacillus thuringiensis)
SCORES Initl: 128 Initn: 168 Opt: 246 z-score: 274.5 E(): 5.4e-07
>>NRAA:37781497
Initn: 168 Initl: 128 Opt: 246 z-score: 274.5 expect(): 5.4e-07
Smith-Waterman score: 277; 21.7% identity in 600 aa overlap
(60-634:41-609)
cry2ab2_820. FOHKSLOTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLKVLGKRLSELNRLIFPPSG
30 40 50 60 70 80
37781497 IPYNCLNPEVVLGERIETGYTPIDISLSLTQFLISEF--VPGAGFVLGLVDILNLTFTDMF
20 30 40 50 60

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crv2ab2_820. STNLMQDILRETEKFLNQELNTDTLARWAEITGL-----QANVEFNQRVDNPLNPRNA
37781497 GPSQMDAFLVQIEQLQINRIIEFARNOAIRLEG-SNYQIYAESFREWEDPTNP---A
70 80 90 100 110 120

crv2ab2_820. VPLSITSVNTMQQLFLNRLPQFMQGYQLLLPLFAQANLHLFSFRDVLINADWEGIS
37781497 LREMRIOFNDMNSALTITAIPLAVQNYQVPLLSVVYQAAHLHLSLRDLSDVSVFGRGWGF
130 140 150 160 170 180

crv2ab2_820. AATIKTRVDYLNKNTDRDYNVICINYYQSAFK-----GLNLRHDMLE---EFTYWFNLNVFEY
37781497 AATINSRYNDLTLEIGNYITDVAVARYNTGLERVWGDPSKR--DWRYNQCFRELLITVLIDI
190 200 210 220 230 240 250

crv2ab2_820. VSIWSLF---KYOSLIVSS-GANLYASGSGFOQTOSTSQDWPEFLYSLFQVNSVNYVLMGF
37781497 VALPSNYDSRRYPIRTVSQLTREITYTPVPLENFDSGRGMAQRTEQINRQPHLMDILMSI
260 270 280 290 300 310 320 330 340 350 360

crv2ab2_820. SGARLSNTFNNIVGLPGSTTHALLARVNYSGGSS---GDTG--ASPFNQFNCFSTF
37781497 T-----IYTDVHRGNYWSGHQITASFVGSFGEPAFLPGFNAGNAAPFLVLSLTG-LGI
310 320 330 340 350 360 370 380 390 400 410 420

crv2ab2_820. LPPLLTPFVRSW-LDSGSDREGVATVNTMQTESFET-TLGRSGAFTARGNSYPPDYFI
37781497 FRTLSSPLRYRIILGSGPNNQEL-FVLDTGTFESFASLTITNLPSTIYRQRTVDLSL-DVIP
360 370 380 390 400 410 420 430 440 450 460 470 480

crv2ab2_820. RUISGVFLVVRNEDLRPHINEIRNTASPGTGGARAYWVSVHNNKNNHAVENG--
37781497 PQDNSSVP--PRAGFSHRUSH---VTMLSQAAGAVYTLRAFTFSWOHRSASFNNIIPSSOV
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

crv2ab2_820. SMHILAPNDYTGFTSPIHATQVNNQTRTFISEKFNQGSLSRFEQNNITARTVYLRGMGN
37781497 TQIPLTKSTNLGSGTSVTKVKGPGFTGGD--TLRRTSPGQISLIRV---NITAPLSQR-----
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

crv2ab2_820. SYNLXLRVSSIGNSTIRVTINGRVYITATVNTITNDGVNONGARFSDINIGNVASNS
37781497 -YRVRIYASTTLQPHSDISDRPINOQNFSAITMCS-GSNLQSGSFVIGFTPTFPNFNG
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

crv2ab2_820. DVPIDINV-TLNSGTQFDLMLNMLVPTNISPLY
37781497 SSVFTLSAHVFNSSGNEVIDRLIEFVFEAYDLERBAQKAVNELFTSSNOIGLKTIDV
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

crv2ab2_820.pap
NRAA:61696667
61696667 source="GENBANK PROT" insecticidal crvstal protein CrvIC [Bacilli

```

thuringiensis]

SCORES Init1: 206 Initn: 206 Opt: 245 z-score: 274.3 E(): 5.5e-07
>>NRAA:6196667
Initn: 206 Init1: 206 Opt: 245 Z-score: 274.3 expect(): 5.5e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

40 50 60 70 80 90
cyr2ab2_820. KEWTEKKNNHSYLDPIVGTVASFLKKVGLVCKRILSELNLIFFSGSTNLMODILR
6196667 DGERISTGSSIDISLSLVQFVSNFVPGGFLVG--LIDFVWGIVGFSQWDAPLQVI--
30 40 50 60 70
cyr2ab2_820. ETEKFLNQLRLTDTLARVNAETGLQANVEEFNRQVNFEL---NPNRNAVPLSITSSYN
100 110 120 130 140 150
6196667 --EQLINERIAE--FAR-NAALNLEGLGNFNFIYVFAFKEMEEPDPNPATFTRVYIDRFR
80 90 100 110 120 130
cyr2ab2_820. 160 170 180 190 200 210
TMQLFLNRLPQFMQGYQLLILPLFAQRANHLHSFTRDVLNADENGISATILRIYDY
6196667 ILDGLLRDIFSRISGPEVLPLSVYQAANLHLAILRDLTVIFGRWGLTITINVENNRR
140 150 160 170 180 190
LIRHIDEADVHCANTYNRGLNLPKSTYQDWITYNRLRRDLTLTLDIAAFAFPNYDNRYY
200 210 220 230 240 250
cyr2ab2_820. LKNYTRDSYCNITQSAFKGL-NTRLHDMLF---RTVMFLNFVFXVSWLSLQYSL
220 230 240 250 260 270
6196667 LIRHIDEADVHCANTYNRGLNLPKSTYQDWITYNRLRRDLTLTLDIAAFAFPNYDNRYY
200 210 220 230 240 250
cyr2ab2_820. LVSSGNLYASGSPQQTOSTSQDWDFLYSLFQVNSYVLNFCGRKLSNTPFNVLGP
280 290 300 310 320 330
6196667 PIQPVQLTRVYTDPLINFNPQLQSAVLPFTFNWMESSAIRNPHFLDILNLTITFDWF
260 270 280 290 300 310
cyr2ab2_820.pgp
NRAA:545641

545641 source="GENBANK PROT" insecticidal protein Cry I A (c) product {toxic
domain} [Bacillus thuringiensis, esp. kurstaki HD-1, peptide, 723 aa]

SCORES Init1: 128 Initn: 128 Opt: 242 z-score: 273.5 E(): 6.1e-07
>>NRAA:546641
Initn: 128 Init1: 128 Opt: 242 Z-score: 273.5 expect(): 6.1e-07
Smith-Waterman score: 268; 23.0% identity in 583 aa overlap
(60-604:41-590)

30 40 50 60 70 80
cyr2ab2_820. FOHKSLLDTVQKEWTEKKNNHSYLDPIVGTVASFLKKVGLVCKRILSELNLIFFSG
546641 IPNCLSNPEVVLGGERIEGTYPIDISLITQLLSEF--VPGAGFVLGLVDINGIF
20 30 40 50 60
cyr2ab2_820. STNLMDILRETKFLNQRLNLTDLARVNAETGL---QANVEEFNRQVDFNPNRNA
90 100 110 120 130 140
546641 GPQWDAPLVIQTLINQRIEFAFNQALSRLEGLSNLYQVAFSFEWREADPTNP---A
70 80 90 100 110 120

Monsanto Company
Financial Report
Product Characterization Center

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cry2ab2_820. 150 160 170 180 190 200
VPLSGSYVWQOLFARLPLFOMOGYQLLLPLFAQANLHLSFIRVILNADWGIS
150 160 170 180 190 200
AREMRIRQNDMSITTAIPDAVQVPLLSVYVQAAHLHLSVLRDVSFVGQWGF
210 220 230 240 250
AATLRYRDLKRYRDYSNYCINTYQSAFK--GLNTHLDM--EFTYMFNLVFEY
546641 AATINSYNDLRLTQNTYAVRWANLHLSVLRDVSFVGQWGFDS--DWRYNOFRRELTITVLDI
190 200 210 220 230 240
cry2ab2_820. 260 270 280 290 300 310
VSINSLF--KYQSLVSS--GANLYAGSGPOQTSG--EFTYMFNLVFEY
546641 VALFPNYSRRYPPIRTVSQLPREIYTNVLENFDS--EFTYMFNLVFEY
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350 360 370
SGARLSNTFPNIVGLPGSTTHALLAARVNYSGGSS--SDTASFPNYSRRYPPIRTVSQLPREIYTNVLENFDS
546641 TI--YTAHRYGVYWSG--HQAISPVGSGPEFTPLGTGTGNAPQOIRVACLG
310 320 330 340 350 360
cry2ab2_820. 370 380 390 400 410 420
FLPPLTPVRKSLDSDREGVATVNWQTESFETTLGLASGFTARGNSYFFDPIR
546641 VYRTLSSTFYRRFNIIGNOOL--SVLDGTEFAYGTSNLPVSAVYRKSFTVDSLOEIPPO
360 370 380 390 400 410
cry2ab2_820. 430 440 450 460 470 480
NISGVPLVWNEDELRPLHYNEIRNIASPGTGGARAYMVS--VHNRK--NHIHVAHE--
546641 N--NVP--PQGFHSHLHVMSFSGSSSVSI--IRAPMFSWIHRAEPNIIASDSIT
420 430 440 450 460 470
cry2ab2_820. 490 500 510 520 530
-----NGSMHILAPNDYTGFTISPIHATQVNNQTRTFISEKFGQSDSLRFEON
546641 QIPAVKGNFLNGSVIS--GPG--FTGGDLVELNSSGNNITQNGYIEVP-----IHF--S
480 490 500 510 520
cry2ab2_820. 540 550 560 570 580 590
NTTARYTLRGNGSNLYLRVSSIGNSTIRVTINGRVYATVNTVNTTND--GVNDNGARF
546641 STSTRYVRVYASVTPHENVNGNSIES--NTVPATATSCDNLQSDDFGVFESANAF
530 540 550 560 570
cry2ab2_820. 600 610 620 630
SDINIGNVASSNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPLY
546641 TS--SLGNIVGVNRVSGTAGVILDRFEFIPVTATLEAYNLERAKAVNALFTSTNQLGK
580 590 600 610 620 630
cry2ab2_820.pep
NRAA:225472
225472 source="GENBANK_PROT" endotoxin delta 1
SCORES Initl: 128 Initn: 168 Opt: 245 z-score: 273.4 E(): 6.2e-07
>>NRAA:225472 (1176 aa)
```

```
initn: 168 initl: 128 opt: 245 z-score: 273.4 expect(): 6.2e-07
Smith-Waterman score: 276; 22.0% identity in 560 aa overlap
(100-634:79-609)
cry2ab2_820. 70 80 90 100 110 120
GSLVGRKILSELNRLNIPFSGSTNLMDILRETEKFLNORINTDILARVNAELTGL---Q
225472 EFPVAGAGFVLGVLDIWIINGIFGPGQWDAFFVQIEQLINQRIEERFARNQAISSLEGSLNLYQ
50 60 70 80 90 100
cry2ab2_820. 130 140 150 160 170 180
ANVEEFNRQVDFNLPRNRNAVPLSITSSVNTMQQLFLNRLPQFOMQGYQLLLPLFAQAA
225472 IYAESFREWEADPTNP--ALREEMRIQFNDMNSALTATPAIPLAVQVQVPLLSVYVQAA
110 120 130 140 150 160
cry2ab2_820. 190 200 210 220 230 240
NLHLSFIRVILNADWGISANLRYRDLKRYRDYSNYCINTYQSAFK--GLNTHL
225472 NLHLSVLRDVSFVGQWGFDAATINSYNDLRLTQNTYAVRWANLHLSVLRDVSFVGQWGFDSR-
170 180 190 200 210 220
cry2ab2_820. 250 260 270 280 290
HDM--EFTYMFNLVFEYVSIWSLF--KYQSLVSS--GANLYAGSGPOQTSGTQ
225472 -DWRYNOFRRELTITVLDI VALFNSVDSSRRYPPIRTVSQLPREIYTNVLENFDSFRGM
230 240 250 260 270 280
cry2ab2_820. 300 310 320 330 340 350
DMETVSLFQVNSVNLVNGFSGARLSNTFPNIVGLPGSTTHALLAARVNYSGGSS--
225472 AQR--QNTNQPQHLMDILNSIT-----IYDVRHGFNWSGHQITASPVFGSGPEFAPFL
290 300 310 320 330
cry2ab2_820. 360 370 380 390 400
-GD(G--AS--QVNN--NCS--FUPPLTPVRK--LDSDREGVATVNWQTESFET--TLG
225472 FQVAGNS--FPLVSLTGLG--ER--LSSPLRYRILGLSGFNQDEL--FVLDTGTEFSASLTNN
340 350 360 370 380 390
cry2ab2_820. 410 420 430 440 450 460
LRSGAFTARGNSYFFDPIR--VHNRK--NHIHVAHE--
225472 LPSTIYRQRGTVD--DAIPQ--PRAGF--VTMLSQAGAVYTLFAP
400 410 420 430 440 450
cry2ab2_820. 470 480 490 500 510 520
MVSVHNEKNIHVAHENG--SMVHNEKNIHVAHENG--SMVHNEKNIHVAHENG--
225472 TFSQWHRSAEFNIIIPSSQITQIPLIKSNLGSSTSVVNGF--FTGGD--NRRSPGQIS
460 470 480 490 500 510
cry2ab2_820. 530 540 550 560 570 580
SLRFEQNNITARYTLRGNGSNLYLRVSSIGNSTIRVTINGRVYATVNTVNTTND--GVNDNGARF
225472 TLRV--NITAPLSOR-----YRVRIYASTTNLQFHTSIDGRF--NCAFSATM--
510 520 530 540 550 560
cry2ab2_820. 590 600 610 620 630
DNGARFSDINIGNVASSNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPLY
225472 LOSGSFTVGFITTFPFGNSGVSFTLSAHVFNISGNEVYIDRIEFVPAEYTFEAYDLER
560 570 580 590 600 610
```

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225472 OKAVNELFTSSNQIGLKTDTVDYHIDQVSNLVECLSEDFCLDEQKELSEKVKHAKRLSDE
620 630 640 650 660 670

cry2ab2_820.pep
NRAA:142750

142750 source="GENBANK_PROT" cryIC(b)

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 273.3 E(): 6.3e-07
>>NRAA:142750
Initn: 206 initl: 206 opt: 245 z-score: 273.3 expect(): 6.3e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGSVGVKRLSELRLNLIFFSGSTNLMDILR
40 50 60 70 80 90
142750 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70

cry2ab2_820. ETEKFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
100 110 120 130 140 150
142750 --EQLINERIAE--FAR-NAAIANLEGLGNFNIIYVEAFKEWEEDPNNPATRIVDRFR
80 90 100 110 120 130

cry2ab2_820. LKNTYDRSYNCINTYQSAFAGL-NTRLHDMLEF--RTYMFNLNVEFYSIWSLKFYQSL
160 170 180 190 200 210
142750 LIRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVLIDIAAFFPNVDNRY
200 210 220 230 240 250

cry2ab2_820. LVSSGANLYASGGPQQTQSFTSQDWPFYLSLFQVNSNYLVNGFSGARLSNTFFPNIVGLP
260 270 280 290 300 310
142750 PIQVQGLTREVTYDPLINFPNLPQSAQLPTFNVMESSAIRNPHLPDILNLIITFDWF
320 330

cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGSVGVKRLSELRLNLIFFSGSTNLMDILR
40 50 60 70 80 90
142750 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70

cry2ab2_820. ETEKFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
100 110 120 130 140 150
142750 --EQLINERIAE--FAR-NAAIANLEGLGNFNIIYVEAFKEWEEDPNNPATRIVDRFR
80 90 100 110 120 130

cry2ab2_820. LKNTYDRSYNCINTYQSAFAGL-NTRLHDMLEF--RTYMFNLNVEFYSIWSLKFYQSL
160 170 180 190 200 210
142750 LIRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVLIDIAAFFPNVDNRY
220 230 240 250 260 270

cry2ab2_820. LVSSGANLYASGGPQQTQSFTSQDWPFYLSLFQVNSNYLVNGFSGARLSNTFFPNIVGLP
280 290 300 310 320 330
142750 PIQVQGLTREVTYDPLINFPNLPQSAQLPTFNVMESSAIRNPHLPDILNLIITFDWF
340 350

cry2ab2_820.pep
NRAA:61252387

61252387 source="GENBANK_PROT" Pesticidal crystal protein cryIcA (Insecticidal
delta-endotoxin CryIc(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
protein)

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 273.3 E(): 6.3e-07
>>NRAA:61252387
Initn: 206 initl: 206 opt: 245 z-score: 273.3 expect(): 6.3e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGSVGVKRLSELRLNLIFFSGSTNLMDILR
40 50 60 70 80 90
61252387 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70

61252387 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70

cry2ab2_820. ETEKFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
100 110 120 130 140 150
61252387 --EQLINERIAE--FAR-NAAIANLEGLGNFNIIYVEAFKEWEEDPNNPATRIVDRFR
80 90 100 110 120 130

cry2ab2_820. TMOQLFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
160 170 180 190 200 210
61252387 ILDGLLERDIPSRISGFEVPLLSVYAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
140 150 160 170 180 190

cry2ab2_820. LKNTYDRSYNCINTYQSAFAGL-NTRLHDMLEF--RTYMFNLNVEFYSIWSLKFYQSL
220 230 240 250 260 270
61252387 LIRHIDEVADHCANTYNGLNLPKSTYQDWITYNRLRDLTLVLIDIAAFFPNVDNRY
200 210 220 230 240 250

cry2ab2_820. LVSSGANLYASGGPQQTQSFTSQDWPFYLSLFQVNSNYLVNGFSGARLSNTFFPNIVGLP
280 290 300 310 320 330
61252387 PIQVQGLTREVTYDPLINFPNLPQSAQLPTFNVMESSAIRNPHLPDILNLIITFDWF
260 270 280 290 300 310

cry2ab2_820.pep
SW:8488968

8488968 description="PESTICIDIAL CRYSTAL PROTEIN CRYICA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 273.3 E(): 6.3e-07
>>SW:8488968
Initn: 206 initl: 206 opt: 245 z-score: 273.3 expect(): 6.3e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGSVGVKRLSELRLNLIFFSGSTNLMDILR
40 50 60 70 80 90
8488968 DGERISTGSSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGSPQWDAFLVQI--
30 40 50 60 70

cry2ab2_820. ETEKFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
100 110 120 130 140 150
8488968 --EQLINERIAE--FAR-NAAIANLEGLGNFNIIYVEAFKEWEEDPNNPATRIVDRFR
80 90 100 110 120 130

cry2ab2_820. TMOQLFLNRLPQFOMQGYQLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
160 170 180 190 200 210
8488968 ILDGLLERDIPSRISGFEVPLLSVYAQAANLHLSFIRDVILNADWEGISAATLRTYRDY
140 150 160 170 180 190

cry2ab2_820. LKNTYDRSYNCINTYQSAFAGL-NTRLHDMLEF--RTYMFNLNVEFYSIWSLKFYQSL
220 230 240 250 260 270
cry2ab2_820. LKNTYDRSYNCINTYQSAFAGL-NTRLHDMLEF--RTYMFNLNVEFYSIWSLKFYQSL
220 230 240 250 260 270

8489968 LIRHIDEADHCANTYNGRLNLPKSTYQDMWITYNRLRRDLTLTVLDIAFAFFPNYDRRY
240 220 230 240 250
cry2ab2_820 LVSSGANLYASGSPQOTSFTSQDWPFLYSFQVNSVNLGFGSGARLSNTFPNIVGLP
290 300 310 320 330
8489968 PIQPGQLTREVTYDDELINFPQLOSVLAQFLTFNNVMESSAIRNPHLFDILNNLTITDWF
260 270 280 290 300 310
cry2ab2_820.pep
SW:61252387
61252387 description="Pesticidal crystal protein CryIcA insecticidal
delta-endotoxin CryIC(a) (Crystalline endotoxin) [13] KDa crystal
protein." library="NA species="Bacillus thuringiensis serovar azawai"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 273.3 E(): 6.3e-07
>>SW:61252387
initn: 206 initl: 206 opt: 245 z-score: 273.3 expect(): 6.3e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

40 50 60 70 80 90
cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGLSKRLSELRLNLIFFSGSTNLMDILR
100 110 120 130 140 150
61252387 DGERISTGNSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGFSQWDAFLVQI--
30 40 50 60 70

100 110 120 130 140 150
cry2ab2_820. ETEKFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRVDILNADWGISAAITRTYDY
1189
61252387 --EQLINERIAE--FAR--NAAIANLEGNNFNIIYVEAFKEWEEDPNPATRVIDRFR
80 90 100 110 120 130

160 170 180 190 200 210
cry2ab2_820. TMOQLFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRVDILNADWGISAAITRTYDY
61252387 ILDGLERDIPSPRISGFEVPLLSVYAQAANHLAIRDSVIFGERWGLTITNNVNNR
140 150 160 170 180 190

220 230 240 250 260 270
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL--NTRLHDMLEF--RTYMFNLVFEVVSWSLFXQSL
61252387 LIRHIDEADHCANTYNGRLNLPKSTYQDMWITYNRLRRDLTLTVLDIAFAFFPNYDRRY
200 210 220 230 240 250

280 290 300 310 320 330
cry2ab2_820. LVSSGANLYASGSPQOTSFTSQDWPFLYSFQVNSVNLGFGSGARLSNTFPNIVGLP
61252387 PIQPGQLTREVTYDDELINFPQLOSVLAQFLTFNNVMESSAIRNPHLFDILNNLTITDWF
260 270 280 290 300 310

cry2ab2_820.pep
NRAA:18913153
18913153 source="GENBANK PROT" delta-endotoxin [Bacillus
thuringiensis]gi|19880135|gb|AAM00264.1| insecticidal protein CryIcA [Bacillus
thuringiensis]

SCORES Initl: 206 Initn: 206 Opt: 245 z-score: 273.3 E(): 6.3e-07
>>NRAA:18913153
initn: 206 initl: 206 opt: 245 z-score: 273.3 expect(): 6.3e-07
Smith-Waterman score: 245; 25.2% identity in 202 aa overlap
(70-263:54-246)

40 50 60 70 80 90
cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGLSKRLSELRLNLIFFSGSTNLMDILR
18913153 DGERISTGNSIDISLSLVQFLVSNFVPGGFLVG--LIDFVWGIVGFSQWDAFLVQI--
30 40 50 60 70

100 110 120 130 140 150
cry2ab2_820. ETEKFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRVDILNADWGISAAITRTYDY
18913153 --EQLINERIAE--FAR--NAAIANLEGNNFNIIYVEAFKEWEEDPNPATRVIDRFR
80 90 100 110 120 130

160 170 180 190 200 210
cry2ab2_820. TMOQLFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRVDILNADWGISAAITRTYDY
18913153 ILDGLERDIPSPRISGFEVPLLSVYAQAANHLAIRDSVIFGERWGLTITNNVNNR
140 150 160 170 180 190

220 230 240 250 260 270
cry2ab2_820. LKNYTRDYSNYCINTYQSAFKGL--NTRLHDMLEF--RTYMFNLVFEVVSWSLFXQSL
18913153 LIRHIDEADHCANTYNGRLNLPKSTYQDMWITYNRLRRDLTLTVLDIAFAFFPNYDRRY
200 210 220 230 240 250

280 290 300 310 320 330
cry2ab2_820. LVSSGANLYASGSPQOTSFTSQDWPFLYSFQVNSVNLGFGSGARLSNTFPNIVGLP
18913153 PIQPGQLTREVTYDDELINFPQLOSVLAQFLTFNNVMESSAIRNPHLFDILNNLTITDWF
140 150 160 170 180 190

cry2ab2_820.pep
NRAA:46409857
46409857 source="GENBANK PROT" CryIA type crystal protein [Bacillus
thuringiensis serovar kurstaki]

SCORES Initl: 128 Initn: 128 Opt: 242 z-score: 272.9 E(): 6.6e-07
>>NRAA:46409857
initn: 128 initl: 128 opt: 242 z-score: 272.9 expect(): 6.6e-07
Smith-Waterman score: 275; 23.8% identity in 93 aa overlap
(60-604:34-583)

30 40 50 60 70 80
cry2ab2_820. FQHKSLDTVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVGLSKRLSELRLNLIFFSG
46409857 VPYNCLSNPEVVLGGERTGTGTPTDIDLSLTQFLLSDF--HPCAGFVGLVILWGF
10 20 30 40 50 60

90 100 110 120 130 140
cry2ab2_820. STNLMQDLIRETEKFNQRLNRLTDLARVNAELTGL----QANVEEFNRQNDNNTNRDP
46409857 GFSQWDAFLVQIQLINQRIEFARNAQISRLGSLNLYQIVASFPREWADPTNP--A
70 80 90 100 110

150 160 170 180 190 200
cry2ab2_820. VPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQAANHLHSFIRVDILNADWGIS

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(60-607:23-560)

cry2ab2_820. 30 40 50 60 70 80
FQHSKLDTVOKEWTKNNHSLYLDPIVGTIVASFLKKVSLGKRIILSELRNLIFFPSG
PEVEVLGERIETGYTPIDLSLUTQFLSEF--VPGAGFVLGLVDLIMGIF
10 20 30 40 50

cry2ab2_820. 90 100 110 120 130 140
STNLMOQILRETEKFLNORLNTDTLARVNAELTGL---QANVEENRQVDMFLNPNRNA
100 110 120 130 140
GPSQWDAFLVQLEQLINORIEEFARQCATSRLEGLSNLYOIAESFREWEADTPN--A
60 70 80 90 100

cry2ab2_820. 150 160 170 180 190 200
VPLSITSSVNTWQQLFLNRLPQOMQGYQLLLPLFAQANLHLSFTROVLINADWGIS
100 110 120 130 140 150 160
LREEMRIQFNDWNSALTTAIFLFAVQYQVPLLSVYQAAANLHLSLRVDSVFGQRMGFD
110 120 130 140 150 160

cry2ab2_820. 210 220 230 240 250 260
AATILYRDYKLNTRYDSNYCINTYQSAFKGLNTRLHDMLEFRTYMFNVVEYSIWSL
100 110 120 130 140 150
RATINSYNDLTELIGNYTDVAVRWYNT--GLD-RLBRTGGLNWARFNQFRRELTISV
170 180 190 200 210 220

cry2ab2_820. 270 280 290 300 310 320
PKYQSLVSSGGANLVAASGGPQQTQSFSTQDMPFLYSLFQVNSYVLNFGSGARLNTFP
100 110 120 130 140 150
LDIISFERNYDRLSPYPTSSQLTRVYT-DFVINITYRVGSPFENISAIRS---P
230 240 250 260 270

cry2ab2_820. 330 340 350 360 370 380
NIVLPGSITTHALLAARVNYSGG--ISSGDIGASFPQNFNCSTFLPLLTPFVRSMLD
100 110 120 130 140 150
HLMDFLNNLTIDTLIRGVHVAWRVTSHTFGSSQV-----ITTP-QYGITA
280 290 300 310 320

cry2ab2_820. 390 400 410 420 430 440
SGSOREGVAITVNWQTESFETLLGKSGAFTARGNSYFPDYFRINISGVLVVRNEDLR
100 110 120 130 140 150
NAEPRTIAPSTPPGLNLFYRTL--SNPFRRSE-NITPTGLINVVGQVGFQIPNNA--
330 340 350 360 370

cry2ab2_820. 450 460 470 480 490
RPLVNEIRNISPSTGGARVAMVYHNRKNNHVAHE--NGSMHLAPNDYTGf---
100 110 120 130 140 150
-EVLYRSRGTVDSLNELDIGENSLVGYSHRLSVTLRSLYNTITSPTLFPFWTHHSAT
380 390 400 410 420 430

cry2ab2_820. 500 510 520 530 540
---TISPIHATQV-----NNQRTFISEKFGQSLRFEQNNRTARYTLIRNGNS-
100 110 120 130 140 150
NTNTINPDITQIPLVKFRLGGGTSVIKPGFTG-GBILR--RNTIGFVSLQVNWINSF
440 450 460 470 480 490

cry2ab2_820. 550 560 570 580 590 600
---YNLYLRVSSIGNSIRTVINGRYVYATVNTVNTNDGVNDGARSDINIGNVA-
100 110 120 130 140 150
ITQRYLRFRYASSRDAKITVAIGQIRVDMTEKIMEI-GESLTSRTFSYTNFNSPFSEF
500 510 520 530 540 550

cry2ab2_820. 610 620 630
SSNSDVFLDINVTLSNGSQFDLMIMLVPNTISPLY
100 110 120

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SCORES   Init1: 128   Initn: 128   Opt: 240   z-score: 270.8 E(): 8.6e-07
>>NRAA:62548840
initn: 128   init1: 128   opt: 240   z-score: 270.8   expect(): 8.6e-07
Smith-Waterman score: 247;   22.9% identity in 576 aa overlap

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6254840
RANPILTAELPARGGELYIDKIELLADATFEEDYDLERAQKAVNALFTSTNQLGK
50 570 580 590 600 610
cry2ab2_820.pep
NRAA:295862
295862 source="GENBANK_PROT" crystal protein (Bacillus
thuringiensis) [18469146] [18469146] (1166 aa)
cryIc (insecticidal delta-endotoxin CryIc) (crystalline entomocidal protoxin)
(132 kDa crystal protein)

SCORES Initl: 192 Initn: 192 Opt: 242 z-score: 270.0 E(): 9.5e-07
>NRAA:295862
Initn: 192 Initl: 192 Opt: 242 z-score: 270.0 expect(): 9.5e-07
Smith-Waterman score: 242; 20.1% identity in 249 aa overlap
(32-279:12-257)

cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADPFQHKSLDTVQKRWTEWKKNNHSLYLDPIVGT
10 20 30 40 50 60
295862 MEISDQNOQYIPYNCNLPESIFNARNNSFGL-VSQVSSGL
10 20 30 40 50 60

cry2ab2_820. ASFLKKVGSGLVKSEILSELRLNLIFFSGSTNLMODILRETEKFLNQRINTDTLARVNAEL
70 80 90 100 110 120 130 140 150 160 170 180
295862 TRFLLEAAVPEAGPAL--GLFDIINGALGVQWSLFLRQIEQLRQIEITELERNRATAIL
50 60 70 80 90 100 110 120 130 140 150 160

cry2ab2_820. TGLQANVEEFNRQVDNFLN--PNRNAVPLSITSSVNTMQQLFLNRLPQFQMOGYQLLLPL
130 140 150 160 170 180
295862 TGLSSSNLYVLEALREWENDPNPASQERVTRFLRDLDDAIVTGLPTLAIRNLEVNLSV
100 110 120 130 140 150 160 170 180 190 200 210

cry2ab2_820. YSLQANVNLNGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGIGASPF
190 200 210 220 230 240
295862 YTOANLHLISFTRDVLNADMGISATLRTYRDYLNKYTRDYSNVCINTYOSAFKGLNT
160 170 180 190 200 210 220 230 240 250 260 270

cry2ab2_820. RLHDMLEFRYTMFLNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL
250 260 270 280 290 300
295862 ISRRYLDFOEDITISVLDAIPNDYDRTPIPTQSOLTRREYTSPPVAGNINFGLSIA
220 230 240 250 260 270

cry2ab2_820. YSLQANVNLNGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGIGASPF
310 320 330 340 350 360
295862 NVLRAPHLMDFIDRIYVITNSVRSTPYWAGHEVSRRTGOGQNEIRPFLYGVAAANAEP
280 290 300 310 320 330

cry2ab2_820.pep
SN:8469146
8469146 description="PESTICIDIAL CRYSTAL PROTEIN CRYIc (INSECTICIDAL
DELTA-ENDOTOXIN CRYIc(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (132 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT

SCORES Initl: 192 Initn: 192 Opt: 242 z-score: 270.0 E(): 9.5e-07
>SW:8469146
Initn: 192 Initl: 192 Opt: 242 z-score: 270.0 expect(): 9.5e-07
Smith-Waterman score: 242; 20.1% identity in 249 aa overlap
(32-279:12-257)

cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADPFQHKSLDTVQKRWTEWKKNNHSLYLDPIVGT
10 20 30 40 50 60
8469146 MEISDQNOQYIPYNCNLPESIFNARNNSFGL-VSQVSSGL
10 20 30 40 50 60

cry2ab2_820. ASFLKKVGSGLVKSEILSELRLNLIFFSGSTNLMODILRETEKFLNQRINTDTLARVNAEL
70 80 90 100 110 120 130 140 150 160 170 180
8469146 TRFLLEAAVPEAGPAL--GLFDIINGALGVQWSLFLRQIEQLRQIEITELERNRATAIL
50 60 70 80 90 100 110 120 130 140 150 160

cry2ab2_820. TGLQANVEEFNRQVDNFLN--PNRNAVPLSITSSVNTMQQLFLNRLPQFQMOGYQLLLPL
130 140 150 160 170 180
8469146 TGLSSSNLYVLEALREWENDPNPASQERVTRFLRDLDDAIVTGLPTLAIRNLEVNLSV
100 110 120 130 140 150 160 170 180 190 200 210

cry2ab2_820. YSLQANVNLNGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGIGASPF
190 200 210 220 230 240
8469146 YTOANLHLISFTRDVLNADMGISATLRTYRDYLNKYTRDYSNVCINTYOSAFKGLNT
160 170 180 190 200 210 220 230 240 250 260 270

cry2ab2_820. RLHDMLEFRYTMFLNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL
250 260 270 280 290 300
8469146 ISRRYLDFOEDITISVLDAIPNDYDRTPIPTQSOLTRREYTSPPVAGNINFGLSIA
220 230 240 250 260 270

cry2ab2_820. YSLQANVNLNGSGARLNTFFNIVGLPGSTTHALLAARVNSGSGIGASPF
310 320 330 340 350 360
8469146 NVLRAPHLMDFIDRIYVITNSVRSTPYWAGHEVSRRTGOGQNEIRPFLYGVAAANAEP
280 290 300 310 320 330

cry2ab2_820.pep
NRAA:5916230
5916230 source="GENBANK_PROT" Cry IAC insecticidal toxin (synthetic construct)

SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 269.4 E(): 1e-06
>NRAA:5916230
Initn: 128 Initl: 128 Opt: 237 z-score: 269.4 expect(): 1e-06
Smith-Waterman score: 265; 23.1% identity in 584 aa overlap
(60-604:15-565)

cry2ab2_820. FOHKSLDTVQKRWTEWKKNNHSLYLDPIVGTVASFLKKVGSGLVKSEILSELRLNLIFFSG
30 40 50 60 70 80
5916230 MAITGTPTDLSLSTLFLSEF--VFGAGFVLGLVDILNITF
10 20 30 40 50 60

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SCORES   Init1: 128   Initn: 128   Opt: 237   z-score: 269.0   E(): 1.1e-00
>>NRAA:4090435
>init1: 128   initn: 128   opt: 237   z-score: 269.0   expect(): 1.1e-06
Smith-Waterman score: 261;   23.1% identity in 584 aa overlap
(60-604:41-591)

cry2ab2_820.  FQHKSLDTVQKEWTWKKNNHSLYLDPIVGTVASFLFKKVGSLVGVKRIISLELNRIIPFSG
30      40      50      60      70      80
100      110      120      130      140
cry2ab2_820.  STNLMDQILRETEKFLINJORLNTDTLARVNAETGL-----QANVEENRQVDNFLNPNRNA
90      100      110      120      130      140
4090435      IPYNCNLSPEVEVLGERIETGYTPDISLSLTQELSEF--VPGAGFVLGLVDIIWIGIF
20      30      40      50      60
4090435      GPSQWDAFLVQIEQLINRIIEFAAQTASRLSEGLSNLYQIYAESFREWAEPTNP--A
70      80      90      100      110      120
cry2ab2_820.  VPLSITSSVNTMOQLFNELPQFOMQOVQQLLPLFAQAAHLHSFIRDVLINLAEMGIS
150      160      170      180      190      200
4090435      LREEMRQFNDMNSALTATLPLFAVQYQVPLLSVYQAAHLHSVLRLDVSVPFGQWGF
130      140      150      160      170      180
cry2ab2_820.  AATIRYRDYLNKYTRDYSNICYQSAFK--GLNTRLHDML---EPTRYMFLNVFEY
210      220      230      240      250
4090435      AATINSRYNDLTRIGNYTDVAVRWYNTGLERVMGPDSCR--DMWRYNQFRRELTITVLDI
190      200      210      220      230      240
cry2ab2_820.  VSIKSLF--KYQSLVGS--GNLYASGSPQQTOSTSQDWPFLVSLFQVNSVNVANGF
260      270      280      290      300      310
4090435      VALFVNDRRYPIRVISQLTREILYTVLENFDGSRFGSAQGERSIRSLPHMLDLSI
250      260      270      280      290      300
cry2ab2_820.  SGARLSNTFPNIVGLPGSTTHALLAARVNYSGTSS---GDIGASPNQNFNGST---
320      330      340      350      360
4090435      TI--YTAHGRGYYWSG---HQIMASPVGSGPEFTPLFYGTMGNAAPQQRIVAQLGQG
310      320      330      340      350
cry2ab2_820.  FPLPPLTFPVRSLMDSGDREGVATVNTWQTESFTTLIGIESGAFARGNSYFPDYFIR
370      380      390      400      410      420
4090435      VYRILSLTVRRFNGINNOQL--SLVDGTGFAIGTSNLSFSAVYKSGIVSLDDEIIPPQ
360      370      380      390      400      410
cry2ab2_820.  NTSGVPLVNRNEDLRPLHYNEIRNIASPSGTPGGARAYMVS-VHNRK--NNIHAVH--
430      440      450      460      470      480
4090435      N--NVP--PRQGSRLHSHVSMFASGFSNVS--SITRAPMFSWTHRSAAFNFIIRASDIT
420      430      440      450      460      470
cry2ab2_820.  -----NGSMTHLAPNDYTGFTISPIHATQVNOTFTFISEKFGNQGSURLPQEN
490      500      510      520      530
4090435      QIPAVKGNFLFNGSVIS-GFG-FTGGDLVRKLSNNGNNLNKRGYTEVP-----IHPF--
480      490      500      510      520
cry2ab2_820.  NNTARYLRNGNSYN--LYLRYSSIGNSTIRVTINGRYVTAINTVNTITND--GVNDGNA
540      550      560      570      580      590

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4090435 STSTKREVRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570

cry2ab2_820. PSNININNVVAKGSGVPLDINVTNSGQDFLNMIMLVPTNISPLY
600 610 620 630

4090435 FTS-SIGNVGRN-SGTATIDPEFTVTALE
580 590 600 610

cry2ab2_820.pep
NRAA:22770982

22770982 source="GENBANK_PROT" insect toxin CryIA(c) [synthetic construct]

SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 269.0 E(1): 1.1e-06
>NRAA:22770982
Initn: 128 Initl: 128 Opt: 237 z-score: 269.0 expect(1): 1.1e-06
Smith-Waterman score: 254; 23.6% identity in 598 aa overlap
(60-604:41-591)

cry2ab2_820. FOHKSLLTVQKEWTEKKNHSLYDPIVGTIVASFLKKVGSVGVKRLISELRNLIFFSG
30 40 50 60 70 80
22770982 IPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF--VFGAGFVLGLVDLWGIF
20 30 40 50 60

cry2ab2_820. STNLMQDLIRETEKFLNORLNTDILARVNAELTGL-----QANVEFNQVDNLFNPNNA
90 100 110 120 130 140
22770982 GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLIQIYAESFREWADPTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTVQQLFLNRLPQFOMQGYQLLLPLFAQAANHLHSIFRDVILNADWGIS
150 160 170 180 190 200
22770982 LREEMRIQFNDMNSALTTAIPLFAVQNYQFPPLSVYVQANHLHSVLRDVSFGGWRGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTYRDYLNKYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFTYFNLNVEFY
210 220 230 240 250
22770982 AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DMIRYNQFRELITLVLDI
190 200 210 220 230 240

cry2ab2_820. VSIWSLFKQSLVSSGANL---YAS-----GS--GPOQ-----TQSF
260 270 280
22770982 VSLFPNYSFTPIETVSQLTREIYTNFVLENFNGDFSGSQAQIEGSIKSPHLMIDVNSI
250 260 270 280 290 300

cry2ab2_820. T-----SDQWPFYLSLFQVNSYVNLGFGSARLSNFTPNVIGLPGSTITHALLAARVNSYG
300 310 320 330 340
22770982 TIYTDHARGEYVMSGHOIMASPV--GFSGPEF--TFP-LYGTMGNAAPQORIVAQLQG--
310 320 330 340 350

cry2ab2_820. GIS---SGDIGASPPNQNFNCSTFLPPLLTPFVRWLDGSDREGVATVNNQTESFTT
350 360 370 380 390 400
22770982 GYVTLTSLLYRRFPNIGINNQQQL-----SVLD-GTEF-AYGTSSNLSFSAVYRKS
360 370 380 390 400

cry2ab2_820. LGRSGAFTARGNSNYFPDY--FIRNISGVPLVVRNEDLRRLPHLYNEIRNIASP--SGTPG
410 420 430 440 450 460
22770982 GTLDSLEIDPEPPONNVPPROGFSRLSHVSM-----FRSGFSNTSVIIIRAPMFSWIHR
410 420 430 440 450

cry2ab2_820. GAAAYVSVVHREKKNITHAVH-----ENGSMIHLAPNDYTGFTISPIHATQVNNOTETISE
470 480 490 500 510
22770982 SAEFNIIASDSITQIPAVKGNFLNGSVIS--GPG--FIGGDVLRLNSSGNNIQNRGIEV
460 470 480 490 500 510

cry2ab2_820. KFGNQGDSLRPEQNNTIARTYTLRGNGSYN--LYLRVSSIGNSTIRVINGRVYATNVNT
520 530 540 550 560 570
22770982 P-----IHFPP--STSTRVRLRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDN
520 530 540 550 560

cry2ab2_820. TTNNND--GVNDNGARPSDINIGNOVASSNSDVPDLINVTLSNGTQDFLNMIMLVPTNISPL
580 590 600 610 620 630
22770982 LQSSDFGYFESANAFTS--SLGNTVGVRFNFGSTAGVIIDREFEIPVTVATLEAE
570 580 590 600 610

cry2ab2_820.pep
NRAA:22770982

2555147 source="GENBANK_PROT" CryIA(c) [synthetic construct]

SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 269.0 E(1): 1.1e-06
>NRAA:2555147
Initn: 128 Initl: 128 Opt: 237 z-score: 269.0 expect(1): 1.1e-06
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(60-604:42-592)

cry2ab2_820. FOHKSLLTVQKEWTEKKNHSLYDPIVGTIVASFLKKVGSVGVKRLISELRNLIFFSG
30 40 50 60 70 80
2555147 IPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEF--VFGAGFVLGLVDLWGIF
20 30 40 50 60

cry2ab2_820. STNLMQDLIRETEKFLNORLNTDILARVNAELTGL-----QANVEFNQVDNLFNPNNA
90 100 110 120 130 140
2555147 GPSQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNLIQIYAESFREWADPTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTVQQLFLNRLPQFOMQGYQLLLPLFAQAANHLHSIFRDVILNADWGIS
150 160 170 180 190 200
2555147 LREEMRIQFNDMNSALTTAIPLFAVQNYQFPPLSVYVQANHLHSVLRDVSFGGWRGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTYRDYLNKYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFTYFNLNVEFY
210 220 230 240 250
2555147 AATINSRYNDLTRLIGNYTDHAVRWYNTGLERVWGPDSR--DMIRYNQFRELITLVLDI
190 200 210 220 230 240

cry2ab2_820. VSIWSLF---KYOSLLVSS--GANLYASGSGPOQSTFTSQDWPFYLSLFQVNSYVNLNGF
260 270 280 290 300 310

```
2555147  VALFNYDSRYPIRTVUSQLTREIYNTPVLENFPGSGFRGAQGIERSIRSPHMLDLINSL
          250      260      270      280      290      300
cry2ab2_820.  SGARLSTNFPNIVGLPGSTTHALLAARVNYSGGSISS---GDIGASPFNQNCST---
          320      330      340      350      360
2555147  TI--YTDARHGYIWSG---HQIMASVPGSGPEFTFPFLYGTMGNAAPQQRIVAQLGQG
          310      320      330      340      350
cry2ab2_820.  FLPLLTFFVRSWLDGSDREGVATVNMQTESFETTLGLRSQAGTARGNSNYPDYFIR
          370      380      390      400      410      420
2555147  VYRTLSLILYRRPFNIGINNQQI--SVLDGTEFRAGTSSNLPSPAVYKSGTVDLSLEIPQ
          360      370      380      390      400      410
cry2ab2_820.  NISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS--VHNK--NNIHAVHE--
          430      440      450      460      470      480
2555147  N--NNVP--PROGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNNIIASDSIT
          420      430      440      450      460      470
cry2ab2_820.  -----NGSMIHLAPNDYGTFTISPIHATQVNNQTRFISEKFGNQGDSLRFEQN
          490      500      510      520      530
2555147  QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNIQNRGVIEVP-----IHFP--
          480      490      500      510      520
cry2ab2_820.  NISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS--VHNK--NNIHAVHE--
          600      610      620      630
2555147  FTS--SLGNTVGVNRNFSGTAGVIIDRFEPFIPVTATLEPP
          580      590      600      610
cry2ab2_820.  pep
NR000:2414156
2414156  source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
          600      610      620      630
SCORES  Init1: 128  Initn: 128  Opt: 237  z-score: 269.0 E(): 1.1e-06
>NR000:2414156
Initn: 128  Init1: 128  Opt: 237  z-score: 269.0 expect(): 1.1e-06
Smith-Waterman score: 257; 22.6% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820.  FQHSKSLDVTQKEWTEWKNHNSLYLDPVIGTVASFLKKVGSVLGKRIILSERNLIFPSG
          30      40      50      60      70      80
2414156  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLASEF--VPGAGFVLGLVDIIGWIF
          20      30      40      50      60
cry2ab2_820.  STNLMDILRETEKFLQRLNTDTTLARVNAELTGL---QANVEENRQVDFNPNR000
          90      100      110      120      130      140
2414156  GPSQWDAFLVQIEQLINQRIEFAFNQAIKSLRLEGLSNLYQIYAESFREWEADPINP--A
          70      80      90      100      110      120
```

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cry2ab2_820.  VPLSTSSVTNQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFTRDVILNADENGIS
          150      160      170      180      190      200
2414156  LREEMRIQNDMSALTALPFAVONTQVLLSVYVQAANLHLSVLRDVSFQGRWGF
          130      140      150      160      170      180
cry2ab2_820.  AATIRTYRDYLNKNTDRYNYCINTYQSAFK--GLNTRLHML---EFRTYMLNVEFY
          210      220      230      240      250
2414156  AATINSRYNDLRLIGNYTDHARVWNTGLERVWGPDSR--DWIRYNQFRRELTTLVLDI
          190      200      210      220      230      240
cry2ab2_820.  VSIMSLFYQILLVSSGANI-----YASGSGPQIQSTQDWPFFLYSLFQNSNYVINGF
          260      270      280      290      300      310
2414156  VSLFPNYSRTYPIRTVQSULTRITXNTPLENFDFGSRGSAQGIERSIRSPHMLDLINSL
          250      260      270      280      290      300
cry2ab2_820.  SGARLSTNFPNIVGLPGSTTHALLAARVNYSGGSISS---GDIGASPFNQNCST---
          320      330      340      350      360
2414156  T-----IYTDARHGYIWSG---HQIMASVPGSGPEFTFPFLYGTMGNAAPQQRIVAQLGQG
          310      320      330      340      350
cry2ab2_820.  FLPLLTFFVRSWLDGSDREGVATVNMQTESFETTLGLRSQAGTARGNSNYPDYFIR
          370      380      390      400      410      420
2414156  VYRTLSLILYRRPFNIGINNQQI--SVLDGTEFRAGTSSNLPSPAVYKSGTVDLSLEIPQ
          360      370      380      390      400      410
cry2ab2_820.  NISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS--VHNK--NNIHAVHE--
          430      440      450      460      470      480
2414156  N--NNVP--PROGFSHRLSHVSMFRSGFSNSSV--SIIRAPMFSWIHRSAEFNNIIASDSIT
          420      430      440      450      460      470
cry2ab2_820.  -----NGSMIHLAPNDYGTFTISPIHATQVNNQTRFISEKFGNQGDSLRFEQN
          490      500      510      520      530
2414156  QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNIQNRGVIEVP-----IHFP--
          480      490      500      510      520
cry2ab2_820.  NISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS--VHNK--NNIHAVHE--
          540      550      560      570      580      590
2414156  STSTRVVRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
          530      540      550      560      570
cry2ab2_820.  NTTPARTLFGNGSNYN--LYLRVSSIGNSTIRVTINGRVYATNVTNTTND--GYNDNGAR
          540      550      560      570      580      590
2414156  STSTRVVRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
          530      540      550      560      570
cry2ab2_820.  FSDINIGNVVASSNDVPLDINVLNLSGTQFDLMNIMLVETNISPLY
          600      610      620      630
2414156  FTS--SLGNTVGVNRNFSGTAGVIIDRFEPFIPVTATLEAYNL
          580      590      600      610
cry2ab2_820.  pep
NR000:22415751
22415751  source="GENBANK_PROT" insecticidal protein CryIaC1 [synthetic
construct]
          600      610      620      630
SCORES  Init1: 128  Initn: 128  Opt: 237  z-score: 269.0 E(): 1.1e-06
```

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cry2ab2_820. PSDINTGNVVVASSSDVPLDINTVLTSGTGQDFLMMIMLVPTNISPLY
::: :|||:|
FTS:SLGNTIVGYRNVFSGTAGVIIDRFEPVITALEAYNL
580 590 600 610

cry2ab2_820.pep
NRAA:37993013

37993013 source="GENBANK_PROT" hybrid CryIab-CryIca protein [synthetic
construct]

SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 268.7 E(): 1.1e-06
>>NRAA:37993013
Initn: 128 Initl: 128 Opt: 237 z-score: 268.7 expect(): 1.1e-06
Smith-Waterman score: 237; 25.2% identity in 230 aa overlap
(60-279:41-263)

cry2ab2_820. FQHSKSLDTVQKEWTWKNNHSLYLPVIGTVASFLKKVGSVLGKRILSENLNLPFSG
37993013 IPYNCLSNPEVELLGGRIETGYTPIDISLSLTQFLISEF--VFGAGFVLGVLDVIIMGIF
20 30 40 50 60 70 80 90 100 110 120 130 140
37993013
cry2ab2_820. STNLMDILRETEKEFLNORLNTDTLARVNAELTGL---QANVEENRQVDNFLNPNENA
37993013
cry2ab2_820. VPLPFASSVNTVQQLNRLPQFQMGQYQLLLPLPFAQAANLHLSFIRDVILNADMGIS
37993013 LREEMRIQFNDMNSALITKALIPAVQYQVPLLSVYVQAANLHLSVLRDVSVFQGMGDF
130 140 150 160 170 180 190 200
37993013
cry2ab2_820. AATLIRVRLKNTYNTQISNCTVTSQAFK--GLNTRLHDML---EPRTYFMVLNVEFY
190 200 210 220 230 240 250
37993013 AATINSRYNDLRELLGNVTDVMAVWATGLERWQFQSR--DMIRINQFRRELTITVLDI
190 200 210 220 230 240
cry2ab2_820. VSIWSPFKYQSLVSSGANLYAGSSRPOQTQFTQANPLFYLFQNSYNYLVNGFSGAR
260 270 280 290 300 310
37993013 VSLFPNVDSRTVPITRVSQLTRREYINLVNDFDSSGFGAGGIEGSSPSPLMDILNSI
250 260 270 280 290 300
cry2ab2_820.pep
NRAA:50539655

50539655 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]

SCORES Initl: 98 Initn: 130 Opt: 237 z-score: 268.3 E(): 1.2e-06
>>NRAA:50539655
Initn: 130 Initl: 98 Opt: 237 z-score: 268.3 expect(): 1.2e-06
Smith-Waterman score: 238; 23.5% identity in 260 aa overlap
(21-263:22-275)

```

```
cry2ab2_820. MQAMDSVNSGRITTCDAYNVAADHPSFQHSKSLDTQK--EWTWKNNHSLYDPI
10 20 30 40 50
50539655 MWPYQNKSEVFEYHNNQKIDPNRYPT---NNPNVAMKNGYKDWNECEGNSVPS
10 20 30 40 50
cry2ab2_820. -VGTVASFLKKVGSVVGKRLSELRLIPPS-G-----STNLMQDILRETEKFLNRL
60 70 80 90 100
50539655 PAAAVTSAIISIVLKTAKALVSSLVDAIKSSIGISEVITKNNYSQSLSMELYNOLINRI
60 70 80 90 100 110
110 120 130 140 150 160
cry2ab2_820. NTDILARVNAELTGLQANVEEFNRQVDNFLNPNRNVPL--SITSSVNTMQQLFLNRLPQ
120 130 140 150 160 170
50539655 QETIMDLGASASLNGLSIYKRYLNALEAM-DKDKSNITLQENVIEEFKYVESFENLKG
120 130 140 150 160 170
170 180 190 200 210 220
cry2ab2_820. -FOMGVQLLLPLPFAQANHLHSFIRDVILNADWEGISAATLRTYDYLKNTYRDSNY
180 190 200 210 220
50539655 IYRTSSQIILLPTPFAQANHLHSLWLRDAVMYQEGNQLSHL--DYKWLDELIALKDYNY
180 190 200 210 220 230
cry2ab2_820. CINTYQSAFKGL-NTRLHDMLEFRTY---MFLNVFEYVSIWSLFKYOSLLVSSGANLYAS
230 240 250 260 270 280
50539655 CVEVYNRGLNALRGSTALDWLEFNSFRDRMTLMVLDLVAIFPNYDPVQYPLPTKIGLSRK
240 250 260 270 280 290
cry2ab2_820. GSGPQQTGSTQDMWFLYSLFQVNSVNLGFSGARLSNTFPNIVGLPGSTITHALLAA
290 300 310 320 330 340
50539655 IYTDVGTTRDTDFGNWTLTDRTLANFNDLDRDVTDSPLVKNLVNNIYTGDAISYPIS
300 310 320 330 340 350
cry2ab2_820.pap
NRAA:40294
40294 source="GENBANK PROT" unnamed protein product [Bacillus
thuringiensis]gi|61252386|sp|P0A375|CRICA BACTE Pesticidal crystal protein
crylCa (insecticidal delta-endotoxin CryIC(a)) (Crystalline entomocidal protoxin)
(134 kDa crystal protein)
SCORES Initl: 200 Initn: 200 Opt: 239 z-score: 266.5 E(): 1.5e-06
>>NRAA:40294
initl: 200 initn: 200 opt: 239 z-score: 266.5 expect(): 1.5e-06
Smith-Waterman score: 239; 24.8% identity in 202 aa overlap
(70-263:54-246)
```

```
cry2ab2_820. TMQQLFLNRLPQFOMGVQOLLPLPFAQANHLHSFIRDVILNADWEGISAATLRTYDY
160 170 180 190 200 210
40294 ILDGLERDIPSPRISGFEVPLSVYAQAANHLHLALRDSVIFGERWGLTTINVNENYR
140 150 160 170 180 190
cry2ab2_820. LKNYTRDSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNLNVFEYVSIWSLFKYQSL
220 230 240 250 260 270
40294 LIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDLTLTLVDIAAFFPNVDNRY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQQTGSTQDMWFLYSLFQVNSVNLGFSGARLSNTFPNIVGLP
280 290 300 310 320 330
40294 PIQPVGQLTREVTYDPLNFPNQLQSVQALPTFNVMESSRIRNPHLFDILNNLTIFTDMF
260 270 280 290 300 310
cry2ab2_820.pap
SW:61252386
61252386 description="Pesticidal crystal protein crylCa (Insecticidal
delta-endotoxin cryIC(a)) (Crystalline entomocidal protoxin) (134 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar entomocidus"
source="swissprot_prot" version="NA type="PRT
SCORES Initl: 200 Initn: 200 Opt: 239 z-score: 266.5 E(): 1.5e-06
>>SW:61252386
initl: 200 initn: 200 opt: 239 z-score: 266.5 expect(): 1.5e-06
Smith-Waterman score: 239; 24.8% identity in 202 aa overlap
(70-263:54-246)
```

```
cry2ab2_820. KENTWKKNNHSLYLDPIVGTVASFLKKVGSVVGKRLSELRLIPPSGNTLMQDILR
40 50 60 70 80 90
61252386 DGERISTGNSSIDISLSLVQFLVSNFVPGGGFLVG--LIDFVWGIVGFSQWDAFLVQI--
30 40 50 60 70
cry2ab2_820. ETEKFLNRLPQFOMGVQOLLPLPFAQANHLHSFIRDVILNADWEGISAATLRTYDY
100 110 120 130 140 150
61252386 --EQLINERIAE--FAR-NAAIANLEGLGNFNIVYEAKEWEEDPNNPETRTVIDRFR
80 90 100 110 120 130
cry2ab2_820. TMQQLFLNRLPQFOMGVQOLLPLPFAQANHLHSFIRDVILNADWEGISAATLRTYDY
160 170 180 190 200 210
61252386 ILDGLERDIPSPRISGFEVPLSVYAQAANHLHLALRDSVIFGERWGLTTINVNENYR
140 150 160 170 180 190
cry2ab2_820. LKNYTRDSNYCINTYQSAFKGL-NTRLHDMLEF--RTYMFNLNVFEYVSIWSLFKYQSL
220 230 240 250 260 270
61252386 LIRHIDEYADHCANTYNRGLNLPKSTYQDWITYNRLRDLTLTLVDIAAFFPNVDNRY
200 210 220 230 240 250
cry2ab2_820. LVSSGANLYASGSGPQQTGSTQDMWFLYSLFQVNSVNLGFSGARLSNTFPNIVGLP
280 290 300 310 320 330
61252386 PIQPVGQLTREVTYDPLNFPNQLQSVQALPTFNVMESSRIRNPHLFDILNNLTIFTDMF
260 270 280 290 300 310
```

[illegible]

```
cry2ab2_820. 150 160 170 180 190 200
>NRAA:2584729 VPLSITSSVNTWQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWNGIS
23344760 LREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAANLHLSVLRDVSVEGQWGF
130 140 150 160 170 180
cry2ab2_820. 210 220 230 240 250
AATLRTYRDYLNKYTRDYSNYCINTYQSAPK---GLNTRLHDM---EFTYMFNLVFEY
23344760 AATINSRYNDLRLIGNYTDYAVRWYNTGLERVMGPDSE--DWRYNQPRRELTITLVDI
190 200 210 220 230 240
cry2ab2_820. 260 270 280 290 300 310
>NRAA:2584729 VSIWLSLF---KYQSLVSS--CANLYASGSGPQQTOSTSQDWPFYLSLQVNSNVLNGF
23344760 VALFPNYDSRRYPPIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHMDILNSI
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350 360
>NRAA:2584729 SGARLSNTFPNIVGLPGSTTTTHALLAARVNSYSGISS---GDIGASPFNQFNCGST---
23344760 TI--YTDHAGYYWWSG---HQIMASPVGFSGPEFTFPLYGTMGNAAPOQRIVAQLGQ
310 320 330 340 350
cry2ab2_820. 370 380 390 400 410 420
>NRAA:2584729 FLPLLPLFPVRSWLDGSDREGVATVNTMQTESFETTLGLRSAGFTARGNSYFPDYFIR
23344760 VYRTLSSTFYRRPFNIGINNOQL--SVLDGTEFAYGTSSNLPSAVYRKSQGVSDLEIPPO
360 370 380 390 400 410
cry2ab2_820. 430 440 450 460 470 480
>NRAA:2584729 NISGVPLVVDNEDLRPLHYNEIRNIASPSGTPGARGAYMVS--VHNK--NNIHAVHE--
23344760 N--NVP--PRQGSFHRSLSHVSMFRSGFSNV--IRAPMFSWIHRSAPFNILASDSIT
420 430 440 450 460 470
cry2ab2_820. 490 500 510 520 530
>NRAA:2584729 NGSMIHLAPNDYGTFTISPIHATOVNQTRTFISEKFGNQDGLRFEQN
23344760 QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNGNIRGYIEVP-----IHFP--
480 490 500 510 520
cry2ab2_820. 540 550 560 570 580 590
>NRAA:2584729 NTYRTYLRNGNSYN--LYLRVSSIGNSTIRVTINGRVITATVNTITNND--GVNDNGAR
23344760 STSTRYRVRYASVTPHLMVN--WGNSSIFS--NTVPATATSLDNLQSSDFGESANA
530 540 550 560 570
cry2ab2_820. 600 610 620 630
>NRAA:2584729 PSDINIGNVAVSSNDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
23344760 FTS--SLGNIYGVNFPSTAGVILDRFEFIPVTATLEAVENLERAKAVNALFTSTNQLGL
580 590 600 610 620 630
cry2ab2_820.pep
NRAA:2584729
2584729 source:"GENBANK PROT" insecticidal crystal protein [Bacillus
thuringiensis]gi|2993657|gb|AA072077.1| CryIaC [Bacillus
thuringiensis]gi|11547|sp|P05068|CIRAC_BACTK Pesticidal crystal protein cryIaC
(insecticidal delta-endotoxin CryIa(C)) (Crystalline entomocidal protoxin) (133
kDa crystal protein)gi|1842095|gb|AAC44841.1| crystal protein [Bacillus
thuringiensis serovar kurstaki]gi|1889559|gb|AAB49768.1| CryIaC delta-endotoxin
```

```
SCORES Initl: 128 Initn: 128 Opt: 237 z-score: 264.3 E(): 2e-06
>NRAA:2584729
Initn: 128 Initl: 128 Opt: 237 z-score: 264.3 expect(): 2e-06
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(160-604:41-591)
cry2ab2_820. 30 40 50 60 70 80
FOHKSLLDTYKQEWTEWKNHNSLYLDPVIGTVASFLKKVGSVGVKRIILSELNRLIPPSG
2584729 IPNCLSNPEVEVLGGERIETGTPDIDISLITQFLLSSEF--VPGAGFVLGLVDIIGIF
20 30 40 50 60
cry2ab2_820. 90 100 110 120 130 140
STNIMQDILRETEKEFLNORLNTDTLARVNAELTGL---QANVEEFNRQVDNLFNPNRNA
2584729 GPSQWDAFLVQIEQLINRIEIEFARNQAIISRLGLESLNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
cry2ab2_820. 150 160 170 180 190 200
VPLSITSSVNTWQQLFLNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWNGIS
2584729 LREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYQAAANLHLSVLRDVSVEGQWGF
130 140 150 160 170 180
cry2ab2_820. 210 220 230 240 250
AATLRTYRDYLNKYTRDYSNYCINTYQSAPK---GLNTRLHDM---EFTYMFNLVFEY
2584729 AATINSRYNDLRLIGNYTDYAVRWYNTGLERVMGPDSE--DWRYNQPRRELTITLVDI
190 200 210 220 230 240
cry2ab2_820. 260 270 280 290 300 310
>NRAA:2584729 VSIWLSLF---KYQSLVSS--CANLYASGSGPQQTOSTSQDWPFYLSLQVNSNVLNGF
2584729 VALFPNYDSRRYPPIRTVSQLTREIYTNVLENFDFGSRGSAQGIERSIRSPHMDILNSI
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350 360
>NRAA:2584729 SGARLSNTFPNIVGLPGSTTTTHALLAARVNSYSGISS---GDIGASPFNQFNCGST---
2584729 TI--YTDHAGYYWWSG---HQIMASPVGFSGPEFTFPLYGTMGNAAPOQRIVAQLGQ
310 320 330 340 350
cry2ab2_820. 370 380 390 400 410 420
>NRAA:2584729 FLPLLPLFPVRSWLDGSDREGVATVNTMQTESFETTLGLRSAGFTARGNSYFPDYFIR
2584729 VYRTLSSTFYRRPFNIGINNOQL--SVLDGTEFAYGTSSNLPSAVYRKSQGVSDLEIPPO
360 370 380 390 400 410
cry2ab2_820. 430 440 450 460 470 480
>NRAA:2584729 NISGVPLVVDNEDLRPLHYNEIRNIASPSGTPGARGAYMVS--VHNK--NNIHAVHE--
2584729 N--NVP--PRQGSFHRSLSHVSMFRSGFSNV--SIIRAPMFSWIHRSAPFNILASDSIT
420 430 440 450 460 470
cry2ab2_820. 490 500 510 520 530
>NRAA:2584729 NGSMIHLAPNDYGTFTISPIHATOVNQTRTFISEKFGNQDGLRFEQN
2584729 QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNGNIRGYIEVP-----IHFP--
480 490 500 510 520
cry2ab2_820. 540 550 560 570 580 590
>NRAA:2584729 NTYRTYLRNGNSYN--LYLRVSSIGNSTIRVTINGRVITATVNTITNND--GVNDNGAR
2584729 STSTRYRVRYASVTPHLMVN--WGNSSIFS--NTVPATATSLDNLQSSDFGESANA
530 540 550 560 570
cry2ab2_820. 600 610 620 630
>NRAA:2584729 PSDINIGNVAVSSNDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
2584729 FTS--SLGNIYGVNFPSTAGVILDRFEFIPVTATLEAVENLERAKAVNALFTSTNQLGL
580 590 600 610 620 630
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cry2ab2_820. NTAATYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRYVTATNVTNTTND-GVNDNGAR
2584729 STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
cry2ab2_820. FSDINTGNVASSNDVPLDNLVNLSTGTQFLDNLMLVPTNISPLY
2584729 FIS-SLGNIVGVNFSGTAGVIIDRFEPFIPVTATLEAYNLERAQKAVNALFTSTNQLGL
cry2ab2_820.pdp
NRAA:52783575
52783575 source="GENBANK_PROT" CryIac [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 128 Opt: 237 Z-score: 264.3 E(): 2e-06
>NRAA:52783575
Initn: 128 Initl: 128 Opt: 237 Z-score: 264.3 expect(): 2e-06
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820. FQHSKSLTVQKWEKTEWKKNNHSLYLDPIVGTVASFLKKVGLVKRILSELRLNLIFFSG
52783575 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VEGAGFVLGLVDIINGIF
cry2ab2_820. STNLMQDILRETEKFLNRLNLTDTLARVNSLGL----QANVEFNQVDFNLPNNA
52783575 GPQWDALVQIEQLINQRIEFAFNQASRLQGLSNLYQIYAESFEWEADPTNP--A
cry2ab2_820. VPLSITSSVNTMQLFLNRLPQOMOGYQLLLPLFAQAANLHLSFIRDVILNADWGIS
52783575 LREMRIOFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQWGF
cry2ab2_820. VSIWLSF--KYQSLLVSS--CANLYASGSPQOTOSTSDWPLFLSLFQVNSVNLNGF
52783575 VALPNYDSERPIETVSQLTREIYNVLENFDSFGSGAQGISRSRPLMDILNSI
cry2ab2_820. SGARLSNTFPNIVGLPGSTITTHALLAARNVYSGISS----GDIGASPNQNFNCST---
52783575 TI--YTDHRGYVYWSG---HQMSPVGFSGPEFTPLPYGTWGNAAPOQRIVAQLQGG
cry2ab2_820. FLPLLLTPFVRSMDSGSDREGVATVNNWQTESFETTLGLRSGAFTARGNSVFPDYFIR
52783575 VYRTLSLTLYRRFPFNIGINNQL--SVLDCGTEFAYGTISNLSFSAVYKSGTVDLDEIPPO

360 370 380 390 400 410
cry2ab2_820. NISGVPLVNRNEDLRPHYNEIRNTIASPSGTPGARGAYVVS-VHNRK--NNIHAVE--
52783575 N-NNVP--PQGFSLHLSHVSMPFSGFSNSSV-SIIRAPFMSWHSRAEFNNIATSDSIT
cry2ab2_820. NGSMIHLAPNDYGTFTIPIHATQVNNQTRTFISEKFGNQGSLSRFEQN
52783575 QIPAVKGNFLFNGVIS-GPG-FTGGDLVRLNSSGNNTQNRGYIEVP-----IHFP--
cry2ab2_820. NTAATYTLRGNGNSYN-LYLRVSSIGNSTIRVTINGRYVTATNVTNTTND-GVNDNGAR
52783575 STSTRYRVRVRYASVTPIHLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
cry2ab2_820. FSDINTGNVASSNDVPLDNLVNLSTGTQFLDNLMLVPTNISPLY
52783575 FIS-SLGNIVGVNFSGTAGVIIDRFEPFIPVTATLEAYNLERAQKAVNALFTSTNQLGL
cry2ab2_820.pdp
SN:117547
117547 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAC (INSECTICIDIAL
DELTA-EMENDOXIN CRYIAC) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (133 KDA CRYSTAL
PROTEIN) [Library=na Species="Bacillus thuringiensis serovar kurstaki"]
Source="sw,spirot prot, version=na type=prt"
SCORES Initl: 128 Initn: 128 Opt: 237 Z-score: 264.3 E(): 2e-06
>SW:117547
Initn: 128 Initl: 128 Opt: 237 Z-score: 264.3 expect(): 2e-06
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820. FQHSKSLTVQKWEKTEWKKNNHSLYLDPIVGTVASFLKKVGLVKRILSELRLNLIFFSG
117547 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VEGAGFVLGLVDIINGIF
cry2ab2_820. STNLMQDILRETEKFLNRLNLTDTLARVNSLGL----QANVEFNQVDFNLPNNA
117547 GPQWDALVQIEQLINQRIEFAFNQASRLQGLSNLYQIYAESFEWEADPTNP--A
cry2ab2_820. VPLSITSSVNTMQLFLNRLPQOMOGYQLLLPLFAQAANLHLSFIRDVILNADWGIS
117547 LREMRIOFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSVFGQWGF
cry2ab2_820. AATLRTYRDLKNTYRDYSNYCINTYQSAFK--GLNTRLHML---EFTYMFNLNVEFY
117547 AATINSRYNDLRLIGNYTDYAVRWYNTGLERVWGPDSR--DWRYNQFRRLTLTVIDI

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```
cry2ab2_820. 190 200 210 220 230 240
260 270 280 290 300 310
cry2ab2_820. VSIWSELF--KYQSLVSS--GANLYASGSGPQQTQSTQDWPFLYSLFQVNSNYVNGF
117547 VALFPNYSRRYPRTVTSQTLREIYTNVLENFDGSGFRGSAQGIERSIRSHPLMDLINSI
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350 360
370 380 390 400 410 420
cry2ab2_820. SGARLSTNFPNIVGLPGSTTHALLAARNVYSGGISS---GDIGASFPNCFNCST---
117547 TI--YTDARHGYIWSG---HQIMASPVGSGPEFTFPLGYGTMGNAAPQQRIVQAQLGQG
310 320 330 340 350
cry2ab2_820. 370 380 390 400 410 420
390 400 410 420 430 440
cry2ab2_820. NISGVLVVRNEDLRPLHYNEIRNIASPGTGGARAYMS--VHNRK--NNIHAVE--
117547 N--NNVP--PROGFSRHLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNNIADSIIT
420 430 440 450 460 470
cry2ab2_820. 490 500 510 520 530
540 550 560 570 580
cry2ab2_820. NGSMIHLAPNDYTGFTTSPHATOVNNQTRTFISEKFGNQGDSLRPEQN
117547 QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP--
580 590 600 610 620 630
cry2ab2_820. 600 610 620 630
640 650 660 670 680
cry2ab2_820. FSDINIGNVVASSNSDVPDLINVTLSGTFQDLMNIMLVPTNISPLY
117547 FTS--SLGNIVGVRRNFSGTAGVIIDREFIPTVATLEAEYNLERAQKAVNALFTSTNQLGL
580 590 600 610 620 630
cry2ab2_820.pcp
NRAA:1171235
1171235 source="GENBANK_PROT" CryIA(c)

SCORES Init1: 128 Initn: 128 Opt: 231 z-score: 262.3 E(): 2.6e-06
>NRAA:1171235
Initn: 128 Init1: 128 Opt: 231 z-score: 262.3 expect(): 2.6e-06
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. 30 40 50 60 70 80
90 100 110 120 130 140
1171235 IPYNCLSNPEVEVLGGERIETGTPIDISLITQFLLSEF--VPGAGFVLGLVDIIMGIF
20 30 40 50 60
40275 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]
```

```
cry2ab2_820. STNLMDILRETEKFLNQRNTDITLARVNAELTGL----QANVEEFNRQVDNFLNPRNA
1171235 GFSQWDAFLVQIEQLINQRIEFARNOAISRLGLEGLSNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVTMQQLFNLFKPFQMGQVQLLLPLFAQAANLHLSFIRDVILNADWEGIS
1171235 LREEMRIQFNDMSALTATPILAVONYQVPLSVYVQAANLHLSVLDRDSVFGQWGED
130 140 150 160 170 180
cry2ab2_820. 210 220 230 240 250
260 270 280 290 300 310
cry2ab2_820. VSIWSELF--KYQSLVSS--GANLYASGSGPQQTQSTQDWPFLYSLFQVNSNYVNGF
1171235 VALFPNYSRRYPRTVTSQTLREIYTNVLENFDGSGFRGSAQGIERSIRSHPLMDLINSI
250 260 270 280 290 300
cry2ab2_820. 320 330 340 350 360
370 380 390 400 410 420
cry2ab2_820. SGARLSTNFPNIVGLPGSTTHALLAARNVYSGGISS---GDIGASFPNCFNCST---
1171235 TI--YTDARHGYIWSG---HQIMASPVGSGPEFTFPLGYGTMGNAAPQQRIVQAQLGQG
310 320 330 340 350
cry2ab2_820. 370 380 390 400 410 420
390 400 410 420 430 440
cry2ab2_820. NISGVLVVRNEDLRPLHYNEIRNIASPGTGGARAYMS--VHNRK--NNIHAVE--
1171235 N--NNVP--PROGFSRHLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNNIADSIIT
420 430 440 450 460 470
cry2ab2_820. 490 500 510 520 530
540 550 560 570 580
cry2ab2_820. NGSMIHLAPNDYTGFTTSPHATOVNNQTRTFISEKFGNQGDSLRPEQN
1171235 QIPAVKGNFLNGSVIS--GPG--FTGGDLVRLNSSGNNIQRGYIEVP-----IHFP--
580 590 600 610 620 630
cry2ab2_820. 600 610 620 630
640 650 660 670 680
cry2ab2_820. FSDINIGNVVASSNSDVPDLINVTLSGTFQDLMNIMLVPTNISPLY
1171235 FTS--SLGNIVGVRRNFSGTAGVIIDREFIPTVATLEAEYNLERAQKAVNALFTSTNQLGL
580 590 600 610 620 630
cry2ab2_820.pcp
NRAA:40275
40275 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]
```

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SCORES Initl: 128 Initn: 128 Opt: 231 z-score: 262.2 E(): 2.6e-06
>NRAA:40275 (618 aa)
Initn: 128 Initl: 128 Opt: 231 z-score: 262.2 expect(): 2.6e-06
Smith-Waterman score: 261; 23.1% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FQKSLDTVQKTEWKNHSLVLDPIVGTVASFLKVGSLVKRILSELNLIIPPSG
40275 IFYNCLSNFEVEVLGGNETSTPTDLSLTQFLLSEF--VAGAGFVLGLVDIINGIF

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 GPSQWDAFLVQIEQLINQRIEFPARQAISSRLGSLNLYQIYAESFREWADPTNP--A

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 VPSILSSVNTWQOGLRFPQMGQYQLLLPLFAQAANLHLSFIRVDILNADWGIS

cry2ab2_820. STNLMODILRETEKFLNRLPQFQOMQGYQLLLPLFAQAANLHLSFIRVDILNADWGIS
40275 LREEMRIQFNDMSALITTAIPLAQVNYQVPLLSVYVQAANLHLSVLRVSVFGQMGFD

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8469152  -----TLSSPL---YRRIILGSGPNNQEL-FVLDGTFESFASLTITNLPSTIYRQRTGTVDS
360 370 380 390 400 410
cry2ab2_820.  PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHAV
430 440 450 460 470 480
8469152  L-DVIPPQNSVP--PRAGFSHRLSH---VPMLSQAAGAVYTLRASLFLLL-----VLLI
420 430 440 450
cry2ab2_820.  HENGSMIHLAPNDYTGFTISPIHATQVNNQRTFISEKFGNQSDIRFPQNNITARTLR
490 500 510 520 530 540
8469152  HARSIFNNIIPSSQITQSFK-----KIISWTSVVKPGFTG-GDILRRSPGLIS--TLR
460 470 480 490 500 510
cry2ab2_820.  GN-----GMSYNLYLRVSSIGNSTIRVTINGRVTATNVTNTTNDGVNDGARFSDINI
550 560 570 580 590
8469152  VNITAPLSQRVRYRIRYAFNTNLQFLTSIDGRPINQGNFYATMSS-GSNLQSGSFRIVGF
520 530 540 550 560 570
cry2ab2_820.  GNVVASSNSDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630
8469152  TTPFNFGSSSVFTLSAHVFNSGNEVYIDRIEFVPAEYTFEAEYDLERAQNGVNLFTSS
580 590 600 610 620 630
8469152  NQIGLKTGDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDERNLLQDPNFRG
640 650 660 670 680 690
cry2ab2_820.ppep
SW:8469152
8469152 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAG (INSECTICIDAL
DELTA-ENDOTOXIN CRYIA(G)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type=PRT
SCORES  Init1: 128  Initn: 157  Opt: 235  Z-score: 262.0 E(): 2.7e-06
>>SW:8469152
Initn: 157 Init1: 128 opt: 235 Z-score: 262.0 expect(): 2.7e-06
Smith-Waterman score: 261; 22.5% identity in 609 aa overlap
(60-634:41-609)
cry2ab2_820.  FOHKSLOTQKWEWKNNHSLYLDPIVGTVASFLKKVGLSVGLKILSELRLNLIFFSG
30 40 50 60 70 80
8469152  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIGIF
20 30 40 50 60
cry2ab2_820.  SINLMQDILRETEKFLNQRLNIDTLARVNAELTGL-----QNVVEFNQVDNPLRNENA
90 100 110 120 130 140
8469152  GPSQWDAFLVQIEQLINQRIEFAFNQAIISLEGLSNLYQIYAESFREWEADFTNP---A
70 80 90 100 110 120
cry2ab2_820.  VPLSTSSVNTMQQLFLNPLFOFMQGVQLLLPLFAQAANHLHSFTIRDLINADWNGIS
150 160 170 180 190 200
8469152  LREEMRIQFNDMNSALTITAPLLAVNQIYVPLLSVVQVQANHLHSVRDYSVFGQWGF
130 140 150 160 170 180
```

```
cry2ab2_820.  AATLRITYDKLKNYTRDYSNYCINTYQSAFK---GLNLRHDML---EFRITMFLNVFEY
210 220 230 240 250
8469152  ARIINSRYNDLRILGNTYDIYAVRWNTGLSRVWGPDSR--DWVYNQFRRELTTLVLDI
190 200 210 220 230 240
cry2ab2_820.  VSIWSLFF--KYQSLVSS--GANLYAS-----GSGFOQTQSF--SQ--DWPFYLSLFQVN
260 270 280 290 300
8469152  VALFSYNDSSRRYPRITVYSQLTRITVFNPLENFDGSGFRGMAQRIEPEYRQPHLMDILNSI
250 260 270 280 290 300
cry2ab2_820.  SNY--VLNGF---SCARLSNTFPNIYGLPGSTTTTHALLAARVNYSGISSGDI GASPFNQ
310 320 330 340 350 360
8469152  SIYDVRHGFNYSWGHQITIS-P--VFGSGPEFTFPLYGYGNAAPPQELIAQTGLGIFR-
310 320 330 340 350
cry2ab2_820.  NFNGSTFLPPLTPFVRSMWLDGSDREGVATVNMOTESFET-TLGLRSGAFTARGNSNY
370 380 390 400 410 420
8469152  ----TLSSPL---YRRIILGSGPNNQEL-FVLDGTFESFASLTITNLPSTIYRQRTGTVDS
360 370 380 390 400 410
cry2ab2_820.  PDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHAV
430 440 450 460 470 480
8469152  L-DVIPPQNSVP--PRAGFSHRLSH---VPMLSQAAGAVYTLRASLFLLL-----VLLI
420 430 440 450
cry2ab2_820.  HENGSMIHLAPNDYTGFTISPIHATQVNNQRTFISEKFGNQSDIRFPQNNITARTLR
490 500 510 520 530 540
8469152  HARSIFNNIIPSSQITQSFK-----KIISWTSVVKPGFTG-GDILRRSPGLIS--TLR
460 470 480 490 500 510
cry2ab2_820.  GN-----GMSYNLYLRVSSIGNSTIRVTINGRVTATNVTNTTNDGVNDGARFSDINI
550 560 570 580 590
8469152  VNITAPLSQRVRYRIRYAFNTNLQFLTSIDGRPINQGNFYATMSS-GSNLQSGSFRIVGF
520 530 540 550 560 570
cry2ab2_820.  GNVVASSNSDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630
8469152  TTPFNFGSSSVFTLSAHVFNSGNEVYIDRIEFVPAEYTFEAEYDLERAQNGVNLFTSS
580 590 600 610 620 630
8469152  NQIGLKTGDYHIDQVSNLVECLSDFECLDEKQELSEKVKHAKRLSDERNLLQDPNFRG
640 650 660 670 680 690
cry2ab2_820.ppep
NRAA:1797979
1797979 source="GENBANK_PROT" Cry29Aa protein [Bacillus thuringiensis serovar
medellin]
```

SCORES Init1: 66 Initn: 66 Opt: 231 Z-score: 261.8 E(): 2.7e-06
>>NRAA:1797979
Initn: 66 Init1: 66 opt: 231 Z-score: 261.8 expect(): 2.7e-06
Smith-Waterman score: 238; 21.4% identity in 519 aa overlap

~~(94-524:52-543)~~

[illegible]

NRAA: 5052774

5052774 source="GENBANK_PROT" insecticidal protein CryIac [Bacillus thuringiensis]

SCORES Initl: 128 Initn: 128 Opt: 231 z-score: 261.0 E(): 3e-06
>>NRAA:5052774
initn: 128 opt: 231 z-score: 261.0 expect(): 3e-06
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604;41-590)

30 40 50 60 70 80
cry2ab2_820. FQKSLDITVQKEWTWKNNHNSLYLDPVIGTVASFLKKVGSVGVKRIISLSENLNLPSPG
5052774 IPYNCLSNPEVEVLGGRIETGYTPIDISLSLTGLSEF--VFGAGFVGLGVLIDWIGIF
20 30 40 50 60
cry2ab2_820. STNLMDILRETEKFLNQRINTDTLARVNAETLGL---QANVEEENRQVNFNLNPNRNa
5052774 GPSOWDAFLVQLEQLINQRIIEEFAARNQALSRLEGLSNLYQIYAESFREWEADPNP--A-A
70 80 90 100 110 120 130 140
215 220 230 240 250
cry2ab2_820. AATRLTRDYLNKYTRDYSNYCINTYQSAFK--GLNTRLHML--EPTYMFYMLNVEFY
5052774 AATINSRYNQLRLGNGYTDVAVRWYNTGLERVMGPDSE--DWRYNQFRRELTTLVLDI
150 160 170 180 190 200
215 220 230 240 250
cry2ab2_820. VPSITSSVNTWQQLFNRPLPQFMQCYQLLLPLPFAQANLHLSFIRDVILNADENGWIS
5052774 LREMRIRQFNMDNSALITPLPLAVQNYQVPLSVVYVQAAANLHLSVLRDVSVFGRGWGF
130 140 150 160 170 180
215 220 230 240 250
cry2ab2_820. VSHWSL--KYQSLVSS--GALYASGGPQQTOSTSQDWFLVLSLFOVNSNVLVNFG
5052774 VALDPNWSRRYV--SOLTRFNTNVLNFDGSPRGSQAQIERSIRSPLHMDLINSI
250 260 270 280 290 300
320 330 340 350 360
cry2ab2_820. SGARLSNTEFNIGLPLPETHHPLA--RYNYSQSSS--GDIGASPNQNFNCST--
5052774 TI--YTDAHGGYYNSG--POLMASQ--EFTFPPLNGWENAAPOQRIIVAAQLQGG
310 320 330 340 350
370 380 390 400 410 420
cry2ab2_820. FLPLPLTFVRSWLDGSDREGVAIVNTQTSFETTLLESGAFTARGSNVPEYDFIR
5052774 VYRTLSFTFVRFPFNGINNOQL--SVLDDGTEFAFATSNLPSAVYFKSGVDSLEIFP
360 370 380 390 400 410
430 440 450 460 470 480
cry2ab2_820. NISGVPLVVRNEDRLPLHYNEIRNTASPSGTPGCGARVWYS--VNRK--NNI--
5052774 N--NVP--PQGFSEHRLSHVSNFMSGSSSVSI--IRAPMFWHSRSENNYLNADSTI
420 430 440 450 460 470
490 500 510 520
cry2ab2_820. -----NGSMTHLAPNDYTFPTISPIAHQVNNQTRTFSEKFGNQGDGSRFQEN
5052774 QIPAVKGNFLFNGSVIS--GPG--FTGGDGLVRLMSNGNINQRGYIEV-----IHFP--

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400354 LSKTEFTREIYALVESPSPSKSIAALEALRDVHLFTWMLKRVDFWNTIYQDLRFLSAN
290 300 310 320 330 340

crly2ab2_820.pep
SW:8488969

8488969 description="PESTICIDIAL CRYSTAL PROTEIN CRY4BA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIVB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (128 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar israelensis"
source="swisprot_prot" version=NA type=PR1

SCORES Initl: 142 Inltn: 166 Opt: 233 z-score: 260.0 E(): 3.5e-06
>>SW:8488969
Initl: 166 inltn: 142 opt: 233 z-score: 260.0 expect(): 3.5e-06
Smith-Waterman score: 244; 22.8% identity in 254 aa overlap
(30-266:11-264)

crly2ab2_820. MQAMDSVLNSGRTTICDAYNVAADHPTFSQHKSLDTQKTEWKNKHNLSLYLDP1---
10 20 30 40 50
: : : : :
: : : : :
: : : : :
MNSGYPLANDLQSGMKNTNYKDWLAMCENNOQYGVNPAAIN
10 20 30 40

8488969

crly2ab2_820. ---VGT---VASFLKKVGSVLGK--RIILSELRLNLIIPSGSTN---LMODILRETEKFLN
60 70 80 90 100
: : : : :
: : : : :
: : : : :
SSSVSTALKVAGAILKFNVPAGTIVLTLSAVSLFILPMTIPTPERVWNDFMTNTGNLID
50 60 70 80 90 100
: : : : :
: : : : :
: : : : :
QRLNTDTLARVNAELTGLQANVEFNQVDNFL-NPNRNNAVPLSITSSVNTWQOLFNLRL
110 120 130 140 150 160
: : : : :
: : : : :
: : : : :
QTVAVRTDANAKMTVVKYLDQYTKENTWKREPNNOQSVRYTAVITQFNLTSAKILRETA
110 120 130 140 150 160
: : : : :
: : : : :
: : : : :
VYFSLNWKGLVLLPIYQAQVANFLNLLIRDLGNAQGSWLSARSAGDQLTWTWVQVYKEYI
170 180 190 200 210 220
: : : : :
: : : : :
: : : : :
NYCINTYQSAFGKGLNTRLHDM--LEFRTYFLNVPYEVSIWMSLYQSLVSSGANLYASG
230 240 250 260 270 280
: : : : :
: : : : :
: : : : :
AHSITWYKGLDVLNKSGWITFNDYKREMTIQVLDLLALFASVDPYRYPADKIDNTK
230 240 250 260 270 280
: : : : :
: : : : :
: : : : :
SGPOQTQSFTSQDWPFYLSLQVNSNVYLVNGFSGARLSNTEFPNIVGLPGSTTHALLAAR
290 300 310 320 330 340
: : : : :
: : : : :
: : : : :
LSKTEFTREIYALVESPSPSKSIAALEALRDVHLFTWMLKRVDFWNTIYQDLRFLSAN
290 300 310 320 330 340
: : : : :
: : : : :
: : : : :
crly2ab2_820.pep
NRAA:11493827

11493827 source="GENBANK_PROT" crystal protein (Paenibacillus popilliae)

SCORES Initl: 193 Inltn: 193 Opt: 220 z-score: 259.6 E(): 3.6e-06
>>NRAA:11493827

1693 init1: 193 opt: 320 z-score: 259.6 expect(): 3.6e-06
Smith-Waterman score: 220; 20.2% identity in 90 aa overlap
(5-94:94-157)

cry2ab2_820. LDTVQKTEWKNHSHSLDVGTVASFLKKVGSVGRILSELRLNLIFFSGSTNLM
11493827 ICCLAPVNSDNNNDATCOEGLTPNNPNCSDYTPF----NVMRTDFP--RKKS
10 20 30
110 120 130 140 150
160 170 180 190 200
11493827 MAMDNSVLNSGRITICDAYNVAADHDPFSFOHKS
10 20 30
110 120 130 140 150
160 170 180 190 200
11493827 LDTVQKTEWKNHSHSLDVGTVASFLKKVGSVGRILSELRLNLIFFSGSTNLM
100 110 120 130 140 150
160 170 180 190 200
11493827 TOELIREWTEWKNKSPSLPTPANGVTSFLDCAANVTIGALLRLNLIFFPGSTLTM
100 110 120 130 140 150
160 170 180 190 200
11493827 QDILRETEKFLNQRLNTDILARVNAELTGLQANVEENRQVDNLFNPNNAVPLSTSSV
100 110 120 130 140 150
160 170 180 190 200
11493827 cry2ab2_820. QDILRETEKFLNQRLNTDILARVNAELTGLQANVEENRQVDNLFNPNNAVPLSTSSV
100 110 120 130 140 150
160 170 180 190 200
11493827 cry2ab2_820. pep
NRAA: 40310
40310 source="GENBANK_PROT" unnamed protein product (Bacillus thuringiensis)

SCORES Init1: 141 Initn: 165 Opt: 232 z-score: 258.9 E(): 4e-06
>>NRAA: 40310
initn: 165 init1: 141 opt: 232 z-score: 258.9 expect(): 4e-06
Smith-Waterman score: 243; 22.8% identity in 254 aa overlap
(30-266:11-264)

cry2ab2_820. MAMDNSVLNSGRITICDAYNVAADHDPFSFOHKS LDTVQKTEWKNHSHSLDPI--
40310 MNSGYPLANDLOGSMKNTNYKQWLAMCENNOCQYGVNPAIN
10 20 30 40 50
110 120 130 140 150
160 170 180 190 200
40310 cry2ab2_820. ---VGT---VASFLKKVGSVGRILSELRLNLIFFSGSTN---LMQDILRETEKFLN
60 70 80 90 100
110 120 130 140 150
160 170 180 190 200
40310 SSSVSTALKVAGAILKFNPPAGTVLTLSAVLPFLMPTNTPTPERVWDFMTWGLID
50 60 70 80 90 100
110 120 130 140 150
160 170 180 190 200
40310 QRLNTDILARVNAELTGLQANVEENRQVDNLFNPNNAVPLSTSSVNTMQQLFLNRL
110 120 130 140 150 160
170 180 190 200 210 220
40310 QTAVAVRTDANAKMTVVDQYTKENTMKREPNNQSYRTAVITQFNLTSAKLRETA
110 120 130 140 150 160
170 180 190 200 210 220
40310 POTQ-MCGVQLLLPLFQAQANHLSTFIRDVILNADENGISAALTRVDRYKNTDRYS
170 180 190 200 210 220
40310 VYFSNLVGYELLPLPIYAQVANFNLLIRDLGLNAQWLSARSGDQLYNTMWQYKEYI
170 180 190 200 210 220
40310 AHSITWNGLDVLRNKSNGWITFNDYKREMTIQVLDLIALPASVDPRPAKIDNTK
230 240 250 260 270 280
40310 cry2ab2_820. NYCINTYQSAFGKGLNTRLDHM-LEFRTYMLNVPYVSWLSFKYQSLVSSGANLYASG
230 240 250 260 270 280
40310 AHSITWNGLDVLRNKSNGWITFNDYKREMTIQVLDLIALPASVDPRPAKIDNTK
230 240 250 260 270 280
40310 cry2ab2_820. SGPOQTQSFTSDMPFLYSLFQVNSVNLNFGSGARLSNTFPNIVGLPGSTITTHALLAAR
290 300 310 320 330 340

40310 LSKTEFTREIYALVESPSKSIALLAALTRDVHFLFTWLKRVDFWNTIYQDLRFLSAN
290 300 310 320 330 340
cry2ab2_820. pep
NRAA: 1669651
1669651 source="GENBANK_PROT" delta-endotoxin (Bacillus thuringiensis)

SCORES Init1: 147 Initn: 171 Opt: 232 z-score: 258.6 E(): 4.1e-06
>>NRAA: 1669651
initn: 171 init1: 147 opt: 232 z-score: 258.6 expect(): 4.1e-06
Smith-Waterman score: 232; 20.9% identity in 234 aa overlap
(32-264:12-242)

cry2ab2_820. QAMDNSVLNSGRITICDAYNVAADHDPFSFOHKS LDTVQKTEWKNHSHSLDPIVGT
1669651 MEISDQOYIPIPCNNPSEIENFNAENSNFGL-VSQVSSGL
10 20 30 40
110 120 130 140 150
160 170 180 190 200
1669651 cry2ab2_820. ASFLKKVGSVGRILSELRLNLIFFSGSTNLMQDILRETEKFLNQRLNTDILARVNAEL
70 80 90 100 110 120
130 140 150 160 170 180
1669651 TRFLLERAAVPEAGFAL--GLFDLIWALGVGDVNSLFLRQIOLRQIETELERNRATAIL
50 60 70 80 90
100 110 120 130 140 150
1669651 IGLSSQNDLVEALREWENDPNNPASQERVTRFRUTDDAIVTGLTLAIRNLEVNLSV
100 110 120 130 140 150
1669651 cry2ab2_820. FAQANHLSTFIRDVILNADENGISAALTRVDRYKNTDRYSNYCINTYQSAFGKGLNT
160 170 180 190 200 210
1669651 VYFSNLVGYELLPLPIYAQVANFNLLIRDLGLNAQWLSARSGDQLYNTMWQYKEYI
160 170 180 190 200 210
1669651 cry2ab2_820. RLHDMLEFRTYMLNVPYVSWLSFKYQSLVSSGANLYASGSGPOQTQSFTSQDWPFLL
220 230 240 250 260 270
1669651 ISRRYLDQFQRLTISLTDIIVAPFSAVPIYPIPTSSQDREIYTSVPVAGNINFGLSI
220 230 240 250 260 270
1669651 cry2ab2_820. pep
SW: 8469137

8469137 description="PESTICIDIAL CRYSTAL PROTEIN CRIB (INSECTICIDAL
DELTA-ENDOTOXIN CRIB (B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN (1174 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar delta-endotoxin"
source="swissprot_prot" version="NA type="PRT

SCORES Init1: 134 Initn: 134 Opt: 232 z-score: 258.6 E(): 4.1e-06
>>SW: 8469137
initn: 134 init1: 134 opt: 232 z-score: 258.6 expect(): 4.1e-06
Smith-Waterman score: 266; 22.4% identity in 589 aa overlap
(73-634:50-601)

```
cry2ab2_820.  TENKKNHSLYLDPIVGTVASFLKKVGLVGRKILSELNRLIFFSGSTNLMQDILRETE
8469137      VEILGTERSNSVAAEIGLGLSLLVSRIPGLGFIILG-LFDVIMGAIGPSQWDIFLEQIE
                20      30      40      50      60      70

cry2ab2_820.  KFLNQRLNTDILARVNAELTGLQANVEEFNRQVDF-LNPNRNNAVPLSITSSVNTMOQLF
8469137      LLIGQRIEFARNOAISRLQGLSLLVSRIPGLGFIILG-LFDVIMGAIGPSQWDIFLEQIE
                80      90      100     110     120     130

cry2ab2_820.  LNRLPQFQMGQYQLLLPLFAQANLHLSFIRDVILNADWEGISAAATLRTYRDYLNKNTYR
8469137      TTAIFLFSVQGVYEIPLLSVYVQAANLHLSVLRDVSFGQWGFVDATINSRYNDLTRLIG
                140     150     160     170     180     190

cry2ab2_820.  DYSNYCINTYQSAPKGLNTRLDHMLEFRITMFLANVFEYVSIWLSFKYQSLVSSGANLYA
8469137      EYTDYAVRWYNT---GLN-RLPNRNEGVRGWARFNRRFRELITISVLDIISFFQNDYDSLXP
                200     210     220     230     240     250

cry2ab2_820.  SGSGPQQTQSFTSQDWPFL-YSLFQVNSNY--VLNG-FSGARLSNTFPNIV-GLPGSTTT
8469137      IPTIYQLTREVYTD--PVINITDYRVTSPFSIESAIRSPHLMDFLNLIIDTDLIRGV
                260     270     280     290     300     310

cry2ab2_820.  HALLAARV--NYSGG---ISSGIG---ASPFQNFQNCSTFLPPLTFFVRSWLDGSGD
8469137      HYWAGHRVTSHTFTGSSQVSSPOYGITANAEP-SRTIAPSTF--PGLNLFYRTILSDPFFR
                320     330     340     350     360

cry2ab2_820.  LRLPLHNEIRNIASPSGTGGARAYMVSVHNRKNNIHAVHE---NGSMIHLAPNDYTG
8469137      LTRSLYNTNITSLPTFWTHSATDRNIIPDVITQIPLVKSFSLTSGTSVVRGP---G
                370     380     390     400     410     420

cry2ab2_820.  FTISPFIATQVNNQTRTFISEKFGNQDLSLFEQNNNTIARTYLRGN-GNSNMLYLRVSSI
8469137      FTGGDIIRTNVNGNVLMS-----SLNF-SNTSLQRYRVRVRYAASQTMVRVN-V
                430     440     450     460     470     480

cry2ab2_820.  GNSITRVINGRVYATNATNTTNDGVNDGARSFSDINTGVNASSNDYPLDINLTN
8469137      GGST-----FTDQGFPTMSANGSLTSQSFRFAEPFVG--ISTSGSQTQ-GISISNN
                490     500     510     520     530     540

cry2ab2_820.  SGITQ-FDLNIMLVPTNISPLY
8469137      PGRQTFLDRIEFIPVDATFEAEYDLERAQKAVNSLFTSSNQIELKTDVTDYHIDQVSNL
                550     560     570     580     590     600
```

```
cry2ab2_820.pdp
NPAA:8469137

8469137 source="GENBANK_PROT" Pesticidal crystal protein cryIEb (Insecticidal
delta-endotoxin CryIE(b)) (Crystalline entomocidal protoxin) (134 kDa crystal
protein)gi|142754|gb|AAA22346.1| cryIE(b)

SCORES   Init1: 134   Initn: 134   Opt: 232   z-score: 258.6 E(): 4.1e-06
>>NRAA:8469137
initn: 134 init1: 134 opt: 232 z-score: 258.6 expect(): 4.1e-06
Smith-Waterman score: 266; 22.4% identity in 589 aa overlap
(73-634:50-601)

cry2ab2_820.  TEWKKNHSLYLDPIVGTVASFLKKVGLVGRKILSELNRLIFFSGSTNLMQDILRETE
8469137      VEILGTERSNSVAAEIGLGLSLLVSRIPGLGFIILG-LFDVIMGAIGPSQWDIFLEQIE
                20      30      40      50      60      70

cry2ab2_820.  KFLNQRLNTDILARVNAELTGLQANVEEFNRQVDF-LNPNRNNAVPLSITSSVNTMOQLF
8469137      LLIGQRIEFARNOAISRLQGLSLLVSRIPGLGFIILG-LFDVIMGAIGPSQWDIFLEQIE
                80      90      100     110     120     130

cry2ab2_820.  LNRLPQFQMGQYQLLLPLFAQANLHLSFIRDVILNADWEGISAAATLRTYRDYLNKNTYR
8469137      TTAIFLFSVQGVYEIPLLSVYVQAANLHLSVLRDVSFGQWGFVDATINSRYNDLTRLIG
                140     150     160     170     180     190

cry2ab2_820.  DYSNYCINTYQSAPKGLNTRLDHMLEFRITMFLANVFEYVSIWLSFKYQSLVSSGANLYA
8469137      EYTDYAVRWYNT---GLN-RLPNRNEGVRGWARFNRRFRELITISVLDIISFFQNDYDSLXP
                200     210     220     230     240     250

cry2ab2_820.  SGSGPQQTQSFTSQDWPFL-YSLFQVNSNY--VLNG-FSGARLSNTFPNIV-GLPGSTTT
8469137      IPTIYQLTREVYTD--PVINITDYRVTSPFSIESAIRSPHLMDFLNLIIDTDLIRGV
                260     270     280     290     300     310

cry2ab2_820.  HALLAARV--NYSGG---ISSGIG---ASPFQNFQNCSTFLPPLTFFVRSWLDGSGD
8469137      HYWAGHRVTSHTFTGSSQVSSPOYGITANAEP-SRTIAPSTF--PGLNLFYRTILSDPFFR
                320     330     340     350     360

cry2ab2_820.  R-EGVATVNWQTESFETTLGLRSGA--FTARGSNVFPDYFI---RNISGVPLVWNEED
8469137      RSDNIMPTLGINVVGQVGFQPNNGEVLYRRRGTVDSLDELFDGNSLVGYSRHLSHVT
                370     380     390     400     410     420

cry2ab2_820.  LRLPLHNEIRNIASPSGTGGARAYMVSVHNRKNNIHAVHE---NGSMIHLAPNDYTG
8469137      LTRSLYNTNITSLPTFWTHSATDRNIIPDVITQIPLVKSFSLTSGTSVVRGP---G
                430     440     450     460     470     480
```


001
cry2ab2_820. FTISLIDVATVNNQRTNISEKFGNQDSLRFEQNNITARTLRGNSYNLYLRVSSI 500 510 520 530 540 550
8469137 FTGSDILATVNNVLSM-----SLNF-SNTSLQRYRVVRVYAAQITMVRVN-V 490 500 510 520 530
cry2ab2_820. GNSTIRVINSRYTATNNTVITWDGVNNGARFSDNIGNVYASSNSDVLDINVTLN 560 570 580 590 600 610
8469137 GGST-----FTDQGFSTNNGASTSQSPRAREVVG--ISTSGQTA-GISISNN 540 550 560 570 580
cry2ab2_820. SGTQ-FDLMMIMLVPTNISPXY 620 630
8469137 PGRQTFHLDRIEFIPVDATFEAEYDLERAGQAVNSLSTSSKQELKTDVADYNDQVSNL 590 600 610 620 630 640
cry2ab2_820.pep
NRAA:4574730

4574730 sources="GENBANK PROT" Cry28Aa1 delta-endotoxin [Bacillus thuringiensis serovar finitimus]gi|8928040|sp|Q9X682|C28AA_BACTF_Pesticidal_Crystal_Protein Cry28Aa (Insecticidal delta-endotoxin CryXXVIIIA(a)) (Crystalline entomocidal protoxin) (126 kDa crystal protein)

SCORES Initl: 98 Initn: 152 Opt: 231 Z-score: 257.9 E(): 4.5e-06
>>NRAA:4574730
Initn: 152 Initl: 98 opt: 231 Z-score: 257.9 expect(): 4.5e-06
Smith-Waterman score: 240; 22.8% identity in 413 aa overlap
(57-447:41-440)

cry2ab2_820. PFSFHKSLTVQCKEWTWKNNHSLYLDPIVGTVASFLKKKGVSLGKRIISELRNLIF 30 40 50 60 70 80
4574730 QSTEWNSESIFFNPVDSSDTVAVVSAGIVVVGITLTAFASFVNPVGVLISFGTLAPVLW 20 30 40 50 60 70

cry2ab2_820. PSGSTN---LMQDILRETEKFLNQRLNTDILARVNAELTGLQANVEEFNRQVDNLF-NPN 90 100 110 120 130 140
4574730 PDPEEDPKKWSQFMKHGEDLLNQTISTAVKETALAHNGFKDVLTYIERAFNDKRNPS 80 90 100 110 120 130

cry2ab2_820. RNAVPLSITSSVNTMQQLFNRLPFQFMQGYQLLLPLFAQAANLHLSFTRDVLNADWE 150 160 170 180 190 200
4574730 ANTARL-VSORFENAHFVSNMPLQQLPTDYLTLSCVTEARNLHNLHLCQVQFADQW 140 150 160 170 180

cry2ab2_820. GIS---AATLR---TYRDLYKNYTRDYSNYCINTYOSAFKGLNTRLH---DMLE-FRTYM 210 220 230 240 250
4574730 NADQPHSPMLKSSGTYDELLVYIEKYINCYTKTVHKLHKLSEKSEKITWDANTYRREM 190 200 210 220 230 240

cry2ab2_820. FLNVEYVWSLWLFKYQSLVSSGANLYASGSPQQTQSFTSQDWPLY-SLPQVNSYV 260 270 280 290 300 310
4574730 TLIVLDLVATFPFDIRF--PRGVELELTVREYVTSLDHLRPPGLFTWLSDIELYTSV 250 260 270 280 290 300

cry2ab2_820. LNG--FSGARLS-----NTTFNIVGPGSTTTTHALLAARVNYSGGSSGDIGASPPNQNF 320 330 340 350 360
4574730 AEGDYLSGIRSEKYYTGNQFTMKNIYGNTRLNSKQLITLLPGEFMTLSIN-RPF-QTI 310 320 330 340 350 360
cry2ab2_820. NCSTFLPPLTTFVRSWLDSSDREGVAVTWTWQTESFEITLGLRSGAFTARGNSYFPD 370 380 390 400 410 420
4574730 AGINKLYSLIQKIVFTTFKNDQNEQKQNFVNN-ONEPOEIT-----NYFNDYGGSN--SQ 370 380 390 400 410
cry2ab2_820. YFIRNIGVPLVVRNEDLRRPLHYNEIRNIASPSGTPGGAAYVSVVHNRKNNIHAVHEN 430 440 450 460 470 480
4574730 KFKENLSHFLLIHKLEFAEYFHSIFALGWTNSVNSQNLISSESVSTQIPLVKAVEVTNN 420 430 440 450 460 470

8928040 descriptions="PESTICIDIAL CRYSTAL PROTEIN CRY28AA (INSECTICIDAL DELTA-ENDOTOXIN CRYXXVIIIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (126 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar finitimus" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 98 Initn: 152 Opt: 231 Z-score: 257.9 E(): 4.5e-06
>>NRAA:8928040
Initn: 152 Initl: 98 opt: 231 Z-score: 257.9 expect(): 4.5e-06
Smith-Waterman score: 240; 22.8% identity in 413 aa overlap
(57-447:41-440)

cry2ab2_820. PFSFHKSLTVQCKEWTWKNNHSLYLDPIVGTVASFLKKKGVSLGKRIISELRNLIF 30 40 50 60 70 80
8928040 QSTEWNSESIFFNPVDSSDTVAVVSAGIVVVGITLTAFASFVNPVGVLISFGTLAPVLW 20 30 40 50 60 70

cry2ab2_820. PSGSTN---LMQDILRETEKFLNQRLNTDILARVNAELTGLQANVEEFNRQVDNLF-NPN 90 100 110 120 130 140
8928040 PDPEEDPKKWSQFMKHGEDLLNQTISTAVKETALAHNGFKDVLTYIERAFNDKRNPS 80 90 100 110 120 130

cry2ab2_820. RNAVPLSITSSVNTMQQLFNRLPFQFMQGYQLLLPLFAQAANLHLSFTRDVLNADWE 150 160 170 180 190 200
8928040 ANTARL-VSORFENAHFVSNMPLQQLPTDYLTLSCVTEARNLHNLHLCQVQFADQW 140 150 160 170 180

cry2ab2_820. GIS---AATLR---TYRDLYKNYTRDYSNYCINTYOSAFKGLNTRLH---DMLE-FRTYM 210 220 230 240 250
8928040 NADQPHSPMLKSSGTYDELLVYIEKYINCYTKTVHKLHKLSEKSEKITWDANTYRREM 190 200 210 220 230 240

cry2ab2_820. FLNVEYVWSLWLFKYQSLVSSGANLYASGSPQQTQSFTSQDWPLY-SLPQVNSYV 260 270 280 290 300 310
8928040 TLIVLDLVATFPFDIRF--PRGVELELTVREYVTSLDHLRPPGLFTWLSDIELYTSV 250 260 270 280 290 300

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NF5A..67089175

67089175 source="GENBANK_PROT" CryIac [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 231 z-score: 257.5 E(:): 4.7e-06
>>NRAA:67089175
initn: 128 init1: 128 opt: 231 z-score: 257.5 expect(:): 4.7e-06
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:34-583)

30 40 50 60 70 80
cry2ab2_820. FQKSLDTVQKWEWKKNNHSLYLDPVIGTVASFLKKKSLVGRKILSELNLIFFSG
67089175 IPYNCLSNPEVEVLGGRIETGTPIDISLSTQPLSEF--VPGAGFVLGVLVDIIGWIF
10 20 30 40 50 60
30 100 110 120 130 140
cry2ab2_820. STNLMDILRETEKFLNRLNTDTLARVNAELTGL---QANVEENRQVDNLFNPNRA
67089175 GPSONDAFLVQLIEQLINRIEERPARNOALSRLEGLSNLYQIYAESFREWEADPTNP---A
70 80 90 100 110 120
150 160 170 180 190 200
cry2ab2_820. VPSITSSVNTWQQLFNLRLPQCMQGYQLLLPLPFAQANLHLSIRVDVILNADWGIS
67089175 LREEMRIQFDNWSALTITPLLAQVNYQVPLSVQOANLHLSIRVDVFGQRWGFD
120 130 140 150 160 170
210 220 230 240 250
cry2ab2_820. AATLRTYRDYLNKTRDYSNYCTIYOSAFK--GLNTRLHDML---ERTYMFNLNVEY
67089175 AATINSRYNDLRLIGNVTDYAVRWYNTGLERVMGPDNR--DWRYNQFRRELTITLVDI
180 190 200 210 220 230
260 270 280 290 300 310
cry2ab2_820. VSIWSLF---KYOSLLVSS--GAMLIASGSGPQOTQSTSQDWPELYSLFQVNSNVNLGFP
67089175 VALFPNYDRSRYPITVSQUTREITPNVLEINFDGSGFSGAQGERSIRSPHMLDILANSI
240 250 260 270 280 290
320 330 340 350 360
cry2ab2_820. SGARLSNTPFNIVGLPGSTTHALAARVNYSGGTSS---GDIGASPFNQNFNGST---
67089175 TI--YTDAHRGYVWSG---HQIMASPVGFSGPEFTPLPYGTWGNAAPOQRIVAQLGOG
300 310 320 330 340 350
370 380 390 400 410 420
cry2ab2_820. FLPLPLTPFVRSLWDSGDRGAVTVNMQTESFTTILGLKSGAFTARGNSNVPDYDIR
67089175 VYRTLSTSYRRFPFNGINNQOL--SVLDGTGEYATGTSNLPASVAVYKSGFVDSLOEIPPO
360 370 380 390 400
430 440 450 460 470 480
cry2ab2_820. NISGVLVWRNEDLRPLHYNEIRNTASPSGTPGGARMYVVS--VHNFK--NNHVAHVE--
67089175 N-NNVP--PQGFSHRLSHVSMFSGSSSSSVIS--IRAPMFSWLRSAEFNNILASDTSIT
410 420 430 440 450 460
490 500 510 520 530
cry2ab2_820. -----NGSMHILAPNDYTGFTTSPHATQVNNQMTTFTISEKFGNQGDSURFQEN
67089175 QIPAKVGNFLFNGSVIS--GPG--FTGGDVLRLNSNGNNTQNGRYTEVP-----THFP--
470 480 490 500 510

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cry2ab2_820. NTATYTLRGNGNSYN-LYLRYSSIGNSTIRVTINGRVYATNVTNTIND-GVNDNGAR
67089175 STSRVRVRPRASVTPIHLNN-WGNSSIFS--NTVPATATSLDNLOSSDGFYFESANA
cry2ab2_820. FSDINIGNVVASSNDVPLDINVLSNGTQFDLMNIMLVPTNISPLY
67089175 FTS-SIGNIVGVVRNFSCTAGVIIDREF--PTATLEAEYNLERAQKAVNALFTSTNOLGL
cry2ab2_820.pcp
NEAA:142742
142742 source="GENBANK_PROT" cryIA(c)3
SCORES Init1: 128 Inith: 128 Opt: 231 z-score: 257.5 E(): 4.8e-06
>>NR2A:142742
inith: 128 inith: 128 opt: 231 z-score: 257.5 expect(): 4.8e-06
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)
cry2ab2_820. FOHKSLDTVQKTEWEMKNNHSLYLDPIVGTWASFLKVKVSLGKRLSELRLIFPSG
142742 IPYNCLSNPEVEVLGGERIETGTPIDISLITQFLSEF--VPGAGFVLGLVDIIWGIF
cry2ab2_820. STNLMODILRETEKFLNQRINTDTLARNVAELTGL---QANVEEFNQQVNFVLPNPRNA
142742 GPSQWDAFLVOIEQLINQRIEFAFNQAIISLEGLSLQYQVAVSFRWEADPTNP---A
cry2ab2_820. VPLSITSSVNTMQQLFLNLPQFOMQGYQLLLPLFAQAANHLSDVLRDVLNADWGLS
142742 LREEMRIQFNDMNSALTTPILAVONYQVPLLSVYVQAANHLSDVLRDVSFQORWGF
cry2ab2_820. AATLRTYRDYLNKTYRDSNYCINTYQSAFK---GLNTRLDHML---EFRTYMLNVEFY
142742 AATINSRYNDLTRIGNYTDYAVRWNTGLERVMGPDSP--DWVRYNQFRRELTTLVLDI
cry2ab2_820. VSIWLSF--KYQSLVSS--GANLVASGSGPQQTQSODWPFYLSYLFQVNSYVINGF
142742 VALFNVDSDRYPIRTVSQTLREITVNFLENFDGSPRGSAGQIERSTRSPLMDILNSI
cry2ab2_820. SGARLNTFFNIVGLPGSITTHALLAARVNSYSGGIS---GDIGASPFNQFNCSF---
142742 TI--VTDARHGYVWSG---HOINASPVGSGPFEFFPLYGTMGNAAPQORIVAQLGGG
cry2ab2_820. FUPPLLTFFVRSWLDGSDREGVATVNWQTESPETTLGLRSAGTARGNSFPDFYIR
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142742 VYTLSSIFYRRPFNIGINNQQ--SVLDGTEFAYGTSSNLPASVYRKSGTVDSDLEIPQ
cry2ab2_820. NISGVPLVVRNEDLRRLHLYNEIRNIASPGTGGAFAYMVS-VHNRK--NNTHAVHE--
142742 N-NWVP--PROGFHRLSHVSWFRSGSSSVSI--IPAPMFWIHRSAEFNIIASDSIT
cry2ab2_820. -----NGSMIHLAFNDYGTFTSPIHATQVNNQTRTFISEKEFGNQSGLAFEQN
142742 QIPAVKGNFLFGSVIS-GPG-FTGGDLVRLNSSGNNIQRGVIEVP-----IHFP--
cry2ab2_820. 540 550 560 570 580 590
NTATYTLRGNGNSYN-LYLRYSSIGNSTIRVTINGRVYATNVTNTIND-GVNDNGAR
142742 STSRVRVRPRASVTPIHLNN-WGNSSIFS--NTVPATATSLDNLOSSDGFYFESANA
cry2ab2_820. FSDINIGNVVASSNDVPLDINVLSNGTQFDLMNIMLVPTNISPLY
142742 FTS-SIGNIVGVVRNFSCTAGVIIDREF--PTATLEAEYNLERAQKAVNALFTSTNOLGL
cry2ab2_820.pcp
NEAA:142742
142742 source="GENBANK_PROT" CryIac [Bacillus thuringiensis]
SCORES Init1: 128 Inith: 128 Opt: 231 z-score: 257.5 E(): 4.8e-06
>>NR2A:142742
inith: 128 inith: 128 opt: 231 z-score: 257.5 expect(): 4.8e-06
Smith-Waterman score: 263; 23.1% identity in 584 aa overlap
(60-604:41-590)
cry2ab2_820. FOHKSLDTVQKTEWEMKNNHSLYLDPIVGTWASFLKVKVSLGKRLSELRLIFPSG
33321716 IPYNCLSNPEVEVLGGERIETGTPIDISLITQFLSEF--VPGAGFVLGLVDIIWGIF
cry2ab2_820. STNLMODILRETEKFLNQRINTDTLARNVAELTGL---QANVEEFNQQVNFVLPNPRNA
33321716 GPSQWDAFLVOIEQLINQRIEFAFNQAIISLEGLSLQYQVAVSFRWEADPTNP---A
cry2ab2_820. VPLSITSSVNTMQQLFLNLPQFOMQGYQLLLPLFAQAANHLSDVLRDVLNADWGLS
33321716 LREEMRIQFNDMNSALTTPILAVONYQVPLLSVYVQAANHLSDVLRDVSFQORWGF
cry2ab2_820. AATLRTYRDYLNKTYRDSNYCINTYQSAFK---GLNTRLDHML---EFRTYMLNVEFY
33321716 AATINSRYNDLTRIGNYTDYAVRWNTGLERVMGPDSP--DWVRYNQFRRELTTLVLDI
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260      270      280      290      300      310
cry2ab2_820. VSIWLSF--KYQSLVSS-GANLYASGSPQQTOSTQDMFPLYSLFQVNSNVLNGF
33321716 VALPNYDSRRYPPIRTVSQLTREIYNPVLENFDSFRGSAQGIERSIRSHPLMDILNSI
250      260      270      280      290      300
cry2ab2_820. SGARLNTFPNIVGLPGSTTHALLAARNYSGGISS-----GDIGASPNQNFNCST---
33321716 TI--YTDARHGYIYWSG-----HQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLCQG
370      380      390      400      410      420
cry2ab2_820. FLPPLLTFVVRSLDSDREGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYFIR
33321716 VYRTLSSTFYRRFPFNIGINNQL--SVLDGTEFAYGTSSNLPASVAYRKSGTVDLSDEIPPO
360      370      380      390      400      410
cry2ab2_820. NISGVPLVVRNEDLRPLHYNEIRNTASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
33321716 N--NNVP--PRQGFSHRLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNNITASDSIT
420      430      440      450      460      470
cry2ab2_820. -----NGSMIHLAPNDYGTFTISPIHATQVNNQRTFISEKFGNQGDSLRFEQN
33321716 QIPAVKGNFLFNGSVIS-GPG-FITGGDLVRLNSSGNNIQNGYIEVP-----IHFP--
480      490      500      510      520      530
cry2ab2_820. NNTARYTLRNGNSYN-LYLRVSSIGNSTIRVTINGRVYATVNTNITND--GVNDNGAR
33321716 STSTRYRVRVYASVTPHNLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530      540      550      560      570      580
cry2ab2_820. FSDINIGNVVASNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
33321716 FTS-SLGNIVGVNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
580      590      600      610      620      630
cry2ab2_820.pgp
NRAA:42717976

42717976 source="GENBANK_PROT" cryIacAT modified toxin [synthetic construct]

SCORES   Initl: 119   Initn: 119   Opt: 227   Z-score: 257.0 E(): 5.1e-06
>NRAA:42717976
initn: 119 initl: 119 opt: 227 Z-score: 257.0 expect(): 5.1e-06
Smith-Waterman score: 240; 22.8% identity in 584 aa overlap
(60-604:41-591)

cry2ab2_820. 30      40      50      60      70      80
FOHKSLOTQKQKNTKWKNNHSLYLDPIVGTVASFLKKKVGSLVKFKILSELNLIFFSG
42717976  IPYCNLSNPEVILGGERIETGYTPIDISLSLQFLLEF--VFGAGFVLGLVDIIGIF
20      30      40      50      60
cry2ab2_820. 90      100      110      120      130      140
STNLMQDILRETEKFLNQLNSTDTLIARVNAELTGL-----QANVEEFNRQVDNLFNPNRNA
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70      80      90      100      110      120
42717976 GPGQWDAFLVQIEQLINQRIEERFARNOAISRLGLSNLYQIYAESFREWEADPTNP--A
150      160      170      180      190      200
cry2ab2_820. VPLSITSSVNTMQQLFLNRLPQOMQYQLLLFLPFAAANHLHSFIRDVLNADWGIS
250      260      270      280      290      300
42717976 LRREMIQFNDMNSALITTAIPFQVQYQVPLSVYVQAANHLHSVLDRDVSFQGRGFD
130      140      150      160      170      180
cry2ab2_820. AAILRIYRDLYKNYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFITYMELNVFEY
210      220      230      240      250
42717976 AATINSRYNDLTRLIGNYTDYARWYNTGLERVWGPDSR--DWRYNQPRRELTLTVIDI
190      200      210      220      230      240
cry2ab2_820. VSIWLSF--KYQSLVSS-GANLYASGSPQQTOSTQDMFPLYSLFQVNSNVLNGF
260      270      280      290      300      310
42717976 VALPNYDSRRYPPIRTVSQLTREIYNPVLENFDSFRGSAQGIERSIRSHPLMDILNSI
250      260      270      280      290      300
cry2ab2_820. SGARLNTFPNIVGLPGSTTHALLAARNYSGGISS-----GDIGASPNQNFNCST---
320      330      340      350      360
42717976 TI--YTDARHGYIYWSG-----HQIMASPVGFSGPEFTFPLYGTMGNAAPQRIVAQLCQG
310      320      330      340      350
cry2ab2_820. FLPPLLTFVVRSLDSDREGVATVNMQTESFETTLGLRSGAFTARGNSNYFPDYFIR
370      380      390      400      410      420
42717976 VYRTLSSTFYRRFPFNIGINNQL--SVLDGTEFAYGTSSNLPASVAYRKSGTVDLSDEIPPO
360      370      380      390      400      410
cry2ab2_820. NISGVPLVVRNEDLRPLHYNEIRNTASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
430      440      450      460      470      480
42717976 N--NNVP--PRQGFSHRLSHVSMFRSGSSSVSI--IRAPMFSWIHRSAEFNNITASDSIT
420      430      440      450      460      470
cry2ab2_820. -----NGSMIHLAPNDYGTFTISPIHATQVNNQRTFISEKFGNQGDSLRFEQN
490      500      510      520      530
42717976 QIPAVKGNFLFNGSVIS-GPG-FITGGDLVRLNSSGNNIQNGYIEVP-----IHFP--
480      490      500      510      520      530
cry2ab2_820. NNTARYTLRNGNSYN-LYLRVSSIGNSTIRVTINGRVYATVNTNITND--GVNDNGAR
540      550      560      570      580      590
42717976 STSTRYRVRVYASVTPHNLNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530      540      550      560      570
cry2ab2_820. FSDINIGNVVASNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
600      610      620      630
42717976 FTS-SLGNIVGVNFSGTAGVIIDRFEFIPVTATLEAEYNLERAQKAVNALFTSTNQLGL
580      590      600      610      620      630
cry2ab2_820.pgp
NRAA:3979717

3979717 source="GENBANK_PROT" crystal toxin protein [Bacillus thuringiensis]
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3979717 STSTRVVRVRYASVTPIHLNVN--WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
530 540 550 560 570
>NRAA:143126
600 610 620 630
cry2ab2_820. FSDINIGNVASSNSDVLINVTLSGTQFDLNMIMLVPTNISPLY
1178 aa
3979717 FTS-SLGNIVGVNPSGTAGVIIDREFPIVATLEAEYNLEAQAQVNAALFTSTNQLGL
580 590 600 610 620 630
cry2ab2_820.pep
NRAA:143126

143126 source="GENBANK_PROT" [Bacillus thuringiensis gene, complete cds]., gene
product
SCORES Initi: 128 Initn: 128 Opt: 230 z-score: 256.3 E(): 5.5e-06
>NRAA:143126
Initn: 128 Initn: 128 Opt: 230 z-score: 256.3 expect(): 5.5e-06
Smith-Waterman score: 254; 22.9% identity in 584 aa overlap
(60-604:41-591)

3979717 cry2ab2_820. FOHKSLLTVQKTEWTKNNHSLVLDPIVGTVASFLKKVSLGVKRIILSELRLNIPFSG
30 40 50 60 70 80
143126 IPYNCLSNPEVEVLGQRIETGTYPTDNLISLTQFLLSEF--VPGAGFVLGLVDIINGIF
20 30 40 50 60
cry2ab2_820. STNLMQDILRETEKFLNORLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPNRRA
90 100 110 120 130 140
3979717 GFSQWDALFLVQIEQLINRIIEEFARNOAISREKSGSNXKXVTAESFREWEADPTNP--A
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVNTWOOLFARLQFQMOGYQLLLPLFAQAANHLHSFIRVDVILNADENGIS
150 160 170 180 190 200
3979717 LREEMRIQFNDMNSALITAIPLLAQVQYVPLLSVYVQAANHLHSVLRDVSFGQRMGFD
130 140 150 160 170 180
cry2ab2_820. AATLRTYRDYLNATYSDYSNNTYVTSYSAFK--GINTRLHDM---EFTYMFANVFEY
210 220 230 240 250
3979717 AATINSYNDLTRLIGNVTDYAVRWYNTGLERVMGPDSE--DWVRVNOFRRELTITVLDI
190 200 210 220 230 240
cry2ab2_820. VSIWLSF---KQSLVSS--GANLYASCSGQOOSTSTSWPFLYSFNONNSVNLNGF
260 270 280 290 300 310
3979717 TI--YTDHAGYYVWSG---HQIMASPVGFSGPETFPFLYGTWGNAAPOQRIVAQLQGG
310 320 330 340 350
cry2ab2_820. FLPLLLTPFVRWLDSDREGVATVNMQTESFETTLGLRSAGFTARGNSNYFPDYFIR
370 380 390 400 410 420
3979717 VYRTLSSTFFVRPEFNIGNQOL--SVLDGTEFAYGTSSNLPASVYKRSKGTVDLSLEIPPO
360 370 380 390 400 410
cry2ab2_820. MISGVLVWNEDLRPLHYNEIRNIASPGTPGAGAYMVS--VHNK--NNIHAVHE--
430 440 450 460 470 480
3979717 N--NVP--PRQGFHRLSHVSMFSGSSNSV--SIIRAPMFSMIHRSAEFNNIIASDSIT
420 430 440 450 460 470
cry2ab2_820. -----NGSMHLAPNDYTGFTISPIHATQNNQOTFISEKFGNQSGLRFEQN
490 500 510 520 530
3979717 QIPAVKGNFLNGSVIS--GPG--FTGGDLVFLNSSGNNIGNGYIEP-----IHPF--
480 490 500 510 520
cry2ab2_820. NTATRYTLRNGNSYN--LYLRVSSIGNSTIRVTINGRVYATVNTVNTND--GVNDNGAR
540 550 560 570 580 590
3979717 VYRTLSSTLVRPFPFNIGNQOL--SVLDGTEFAYGTSSNLPASVYKRSKGTVDLSLEIPPO
360 370 380 390 400 410

001 Proprietary Information

Monsanto Company

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430      440      450      460      470      480
cry2ab2_820. NISGVPLVWNEDELRLPLHYNEIRNIASPGCTPGGARAYMVS-VNHEK--NNIHAVEH--
143126      N-NVVP--PRQGHSHLVSMFRSGFSNSV-SIIRAPMFSWTHRSAEFNIIASDSIT
420      430      440      450      460      470
cry2ab2_820. -----NGSMIHLAPNDYTGFTISPIHATOVNQTRTFSEKFGNQGSRLRFEQN
143126      QIPAVKGNFLNGSVIS-GPG-FTGGDLVRLNSSGNNTQNRGYIEVP-----IHPF--
480      490      500      510      520
cry2ab2_820. NTAARYTLRGNNSYN-LYLRVSSIGNSITRVINGRVYATNVTNNITND-GVNDNGAR
143126      STSTRYRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYESANA
530      540      550      560      570
cry2ab2_820. FSDINIGNVASSNSDVPDLINVINSCTQFDLMNIMLVPTNISPLY
143126      FTS-SLGNIVGVNFGNFGTAGVIIDRFEPVPTATLEAEYNLERAKKAVNALFTSTNQGL
580      590      600      610      620      630
cry2ab2_820.ppep
NRAA:45387401
45387401 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis setovar
kurstaki]

SCORES      Initl: 103      Initn: 135      Opt: 229      z-score: 255.2 E(): 6.4e-06
>>NRAA:45387401
Initn: 135 Initl: 103 opt: 229 Z-score: 255.2 expect(): 6.4e-06
Smith-Waterman score: 229; 21.6% identity in 222 aa overlap
(64-279:47-260)

cry2ab2_820. SLDTVQKEWTEWKNNHSLYLDPIVGTVASFLKKV--GSLVKGKRIISELNLIIPFSGT
45387401      NNPESEIILDIEGLSTRSREQVAEISGLTRFLENLFPGATFGCLDIIGWIFGPDQWS
20      30      40      50      60      70

cry2ab2_820. NMQDILRETEKFLANQLNTDLARVNAELTGLQ----ANVEEFNRQVDNFLNPNRNVAP
45387401      MFLEGI-----EQLIDQRIETVERNRAITQTLIGLSNYDVNIEAL-KEWEN--NPDNSASQ
80      90      100      110      120      130      140

cry2ab2_820. LSITSVNTMQFLNRLPQFOMQGYQLLLPLFAQANLHLSFTIROVLNARDWCISAA
45387401      ERVNRRTDDALISIELLAIENFEIATLSVYQANLHLSLRLVAVFGERGELTQI
130      140      150      160      170      180

cry2ab2_820. TLRTYRDYLNKRYTRDYSNYCINTYQSAFKGLNTRLHDMLEFFRYMFLNVEYVSWLSFK
45387401      NVDDLRYRLTNIRKYSHDCAWYNEGLDNISG-LSRSINFOREVTSVLDIVALFPNDY
190      200      210      220      230      240      250      260

cry2ab2_820. ARGSNYPDYFFIRNISGVPLVWNEDELRLPLHYNEIRNIASPGCTPGGARAYMVSVHNR
1946622      RRSE-NTITFLGINVQGVGFQIPNNA---EVLDRSRGIVDSLNELFDIGENSLVGYSHR
420      430      440      450      460      470

cry2ab2_820. QSLVSSGANLYVASGSGPQCTQSTQSDWPFYLSLQVNSVYVNLGFGSARLSNTFPNI
45387401      IRTPIITTSQTLREIFTSPVWPNDFSAVAGCVRRAPHLFDFLEKLVITYTGRSGIRHM
250      260      270      280      290      300

cry2ab2_820.ppep
NRAA:1946622
1946622 source="GENBANK_PROT" CryIEa4 [Bacillus thuringiensis]

SCORES      Initl: 117      Initn: 117      Opt: 227      z-score: 253.0 E(): 8.5e-06
>>NRAA:1946622
Initn: 117 Initl: 117 opt: 227 Z-score: 253.0 expect(): 8.5e-06
Smith-Waterman score: 234; 22.0% identity in 605 aa overlap
(32-607:13-576)

cry2ab2_820. QAMDNSVLNSGRITTCIDANVAADHPFSGHKSJLDTVQKEWTEWKNNHSLYLDPIVGT
1946622      MEIVNNQOCVPCYNLANNPENELDIERSNSTVATN--IALE
10      20      30      40

cry2ab2_820. ASFLKKVGLVGRILSELNLIIPFSGSTNLMQDILRETEKFLNQLNLTDLARVNAEL
1946622      ISRLLAGATPIGG--ILLGLFDALWGSIGPSQWDLFLEQIELLIDQKI--EFAFAR-NOAI
50      60      70      80      90

cry2ab2_820. TGLQANVEEFNRQVDNF----LNPNRNVAPLSITSSVNTMQFLNRLPQFOMQGYQLLL
1946622      SRLGEISLGIITTEAFREWADATNPALKEEMRTQFNDMNSILVTAIPLFSVQNYQVFF
100      110      120      130      140      150

cry2ab2_820. LPLFAQANLHLSFIRDVILNADEWGISAAATLRTYRDYLNKRYTRDYSNYCINTYQSAFKG
1946622      LSVYVQANLHLSVLDRDVSVPQAGFDIATINSRVNDLTRLIPIYTDYAVRWYNT---G
160      170      180      190      200      210

cry2ab2_820. LNTRLHDMLEFFRYMFLNVEYVSWLSLQVNSVYVNLGFGSARLSNTFPNIVGLPGSTTHALLAARVNYSGG--ISSGDI
1946622      LD-RLRPTGTGLRNWAFNPOFRRELTISVLDIISFFPNYDSRLYPIPTSSQLTREVT-DP
220      230      240      250      260      270

cry2ab2_820. PFLYSLFQVNSVYVNLGFGSARLSNTFPNIVGLPGSTTHALLAARVNYSGG--ISSGDI
1946622      VINITDVRVGSFENIENSARS----PHLMDFLANLITDILARGVHYWAGHRYTSHT
280      290      300      310      320      330

cry2ab2_820. GASPFQNFNCSTFLPPLTLP-FVRSWLDGSDREGVATVNTWQTESFETTLGRSGAPT
1946622      GSSQV-----ITTPQYGN--QNAEPRRTIAPFPFGLNLFYRTL---SNPFF
330      340      350      360

cry2ab2_820. ARGSNYPDYFFIRNISGVPLVWNEDELRLPLHYNEIRNIASPGCTPGGARAYMVSVHNR
1946622      RRSE-NTITFLGINVQGVGFQIPNNA---EVLDRSRGIVDSLNELFDIGENSLVGYSHR
420      430      440      450      460      470
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cry2ab2_820. LNTRLHMLFRFYMFNVFVSIWLSFKYQSLVSSGANLVASGSGPOQTOSTSDW
1946622 LSWTDLTSLVYNNLTPPTFWTTHSANTNTINDDIITQIPVKGFRGGTGVKGP
cry2ab2_820. KGNQDGLRPFQNTNRIITLNGNS---YNILNSIGNSTIRVTINGRYTAT
1946622 GTTG-GDILR--RNTIGETVSNVINSPIQYRLRFYSSARITVAIGGQIRVDM
cry2ab2_820. NVNTITNDGVNDGARGFSDINIGNVA--SSNDVPLSNVLTSGTQFDLMMLVPTN
1946622 TLEKTMET-GESLTSRTFSYTNFSNPFSPRANFELIRASLPFGGELSDKIELLAD
cry2ab2_820. ISPLY
1946622 ATFEEDYDLERAOKAVNALFTSTNQLGLKTDVTDYHIDQVSNLVECLSDKFCDEKREL
cry2ab2_820. pep
NRAA:17979619
17979619 source="GENBANK PROT" Cry032 [Bacillus
thuringiensis]gi|58397442|gb|AAW72936.1| insecticidal delta endotoxin CryIEa
[Bacillus thuringiensis]gi|142752|gb|AAA22345.1| cryIE(a)
SCORES Initl: 117 Initn: 117 Opt: 227 z-score: 253.0 E(): 8.5e-06
>>NRAA:17979619
initn: 117 initl: 117 opt: 227 z-score: 253.0 expect(): 8.5e-06
Smith-Waterman score: 234; 21.9% identity in 604 aa overlap
(32-607:13-576)
cry2ab2_820. QAMDSVLNSGRITICDAYNVAADHPFQHSKSLDTVQKEWTWKXNHSLYLDPIVTV
17979619 MEIVNNQNCVPYCNLNNPENELDIERSNSTVATN--IALE
cry2ab2_820. ASFLKKVGLVGRKILSLRLNLIFFPSGSTNLMDILRETEKFLNORLNTDILARNEL
17979619 ISRLASATPIGG--ILLGLFDAWGSIGPSQWDLFLQIELLDQKI--EFAFAR-NOAI
cry2ab2_820. TGLQANVEENRQVDNF----LNFNRNAVLSITSSVNTMQOLFNLRLPQFMQGYQLLL
17979619 SRLEGISLLYGVITEAFREWEADPTNPALKEEMRTQFNDMSILVTAIPLFVSQNVQVPF
cry2ab2_820. LPLFAQANLHLSFRDVLNADENWGISAAILRTYRDVLYKNYTRDYSNICYNTYQAPKG
17979619 LSVYVQAANLHLSVLRDVSFVGQAGFDIATINSRYNDLTLPIYTDYAVRWYNT--G
```

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cry2ab2_820. LNTRLHMLFRFYMFNVFVSIWLSFKYQSLVSSGANLVASGSGPOQTOSTSDW
17979619 LD-RLPRTGRLGNARWAFNQFRRELTISVLDIISFFRNVDLSLYPIPTSSQLTREVYT-DP
cry2ab2_820. PFLYSLVQVNSVLNGSFGARLNTFPNVGLPGSTTHALLAARVNVYSGG--ISSGDI
17979619 VINITDRVQSPFENISAIRS----PHLMDFLANLITDILIRGVHVMAGHRTVSHFT
cry2ab2_820. GASPFNQNFNCSTFLPPLLTPTPVSMLDSCSOREGVATVTNWQTESFETTLGLRSGAFTA
17979619 GSSQV-----ITTP-QYGITANAPRRTIAFSTPGLNLFYRL---SNPFR
cry2ab2_820. RGNNSYFPDFIENISGVPLVVRNEDLRRLPHYNEIRNIAFSPGTPGGARAYMVSVHNRK
17979619 RSE-NITPTLGINVQGVGFQPNNA---EVLVRSRGVTVDLSNELPIDGENSLVGVSHRL
cry2ab2_820. NNIIHAVHE--NGSMHILAPNDYTCF-----ILSIHATQV-----NNQTRIFISEK
17979619 SHVLTIRSLYNTNITSLPTFVWTHHSATNTINDDIITQIPVKGFRGGTGVKGPFG
cry2ab2_820. FQNGODLRSPQNTTARTYLRNGNS-----YNLYLRVSSIGNSTIRVTINGRYTATN
17979619 FTG-GDILR--RNTIGETVSNVINSPIQYRLRFYSSARITVAIGGQIRVDMT
cry2ab2_820. VNTITNDGVNDGARGFSDINIGNVA--SSNDVPLSNVLTSGTQFDLMMLVPTNI
17979619 LEKTMET-GESLTSRTFSYTNFSNPFSPRANFELIRASLPFGGELSDKIELLADA
cry2ab2_820. SPLY
17979619 TFEEDYDLERAOKAVNALFTSTNQLGLKTDVTDYHIDQVSNLVECLSDKFCDEKRELSE
cry2ab2_820. pep
NRAA:40282
40282 source="GENBANK PROT" crystal protein [Bacillus
thuringiensis]gi|40257|emb|CAA37933.1| crystal protein [Bacillus
thuringiensis]gi|8469151|sp|Q57458|CRIEA BACTX Pesticidal crystal protein
cryIEa (Insecticidal delta-endotoxin CryIE(a)) (Crystalline entomocidal protein)
(133 kDa crystal protein)
SCORES Initl: 117 Initn: 117 Opt: 227 z-score: 253.0 E(): 8.5e-06
>>NRAA:40282
initn: 117 initl: 117 opt: 227 z-score: 253.0 expect(): 8.5e-06
Smith-Waterman score: 234; 21.9% identity in 604 aa overlap
```

(32-607:13-576)	
cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADHPPFSQHKSLDVTQKRWTEWKKHSLYLDPIVGV	10 20 30 40 50 60
40282	LEKTMEL-GEGLSRTFSVTNPSFRANPDIIIRAEELPIRGELYIDKIELILADA 550 560 570 580 590 600
cry2ab2_820. SPLY	TFEEYDLERAQAVNALFTSTNQLGKTDVTDYHDQVSNLVECLSEDFCLDEKRELSE 610 620 630 640 650 660
40282	SW:8469151
cry2ab2_820. pep	8469151 description="PESTICIDIAL CRYSTAL PROTEIN CRY1EA (INSECTICIDAL DELTA-ENDOTOXIN CRYIE(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar kenya" source="swissprot_prot" version="NA type="PRT
40282	SCORES Init1: 117 Initn: 117 Opt: 227 z-score: 253.0 E(): 8.5e-06 >>SW:8469151 initn: 117 init1: 117 opt: 227 z-score: 253.0 expect(): 8.5e-06 Smith-Waterman score: 234; 21.9% identity in 604 aa overlap (32-607:13-576)
cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADHPPFSQHKSLDVTQKRWTEWKKHSLYLDPIVGV	10 20 30 40 50 60
8469151	MEIVNNQNCVPCVNCNPNPENEILDIERSNSTVATN--IALE 10 20 30 40
cry2ab2_820. ASFLKKGSLVGRILSELRLNLIFFSGSNLMQDLIRETEKFLNQRLNTDILARVNAEL	70 80 90 100 110 120
8469151	ISRLASATPIGG--ILLGLFDALWGSIGPSQWDLFLEQIELLDQKI--EEFAR-NQAI 50 60 70 80 90
cry2ab2_820. TGLQANVEEFNRQVDNF---LNPNRNAVPLSITSVNTMQQLFLNRLPQFMQGYQLLL	130 140 150 160 170
8469151	SRLEGISSLYGIYTEAFREWEADPTNPALKEEMRTQFNDMSILVTAIPLFVSQYQVFF 100 110 120 130 140 150
cry2ab2_820. LPLFQAANLHLSFIRDVILNADWGISAAITLRYDYLNKNTYRDYNSYNTYQSAFKG	180 190 200 210 220 230
8469151	LSVYVQAANLHLSVLRDVSVFGQAWGFDIATINSRYNDLTRLIPIYTDYAVRWYNT--G 160 170 180 190 200 210
cry2ab2_820. LNLRLHMDLEFRTYMFNLVFEYVSWLSFKYQSLVSSGANLYASGSGPOQTOSFTSQDM	240 250 260 270 280 290
8469151	LD-RLPRTGGLRWARFNQFRRELTISVLDIISFFRNYSRLYPIPTSSQLTREVT-DP 220 230 240 250 260 270
cry2ab2_820. PFLYSLFQVNSYVNLGFGSARLSNTFFNIVGLPGSTTHALLAARVNSGG--ISSGDI	300 310 320 330 340 350
8469151	VINITDYVGVSPFENIENSAIRS---PHLMDFLNNLTIDTLIRGVHWAGHRVTSHT 280 290 300 310 320
cry2ab2_820. GASPNQNFNCSTPLPPLTPFVRSWLDGSDREGVATVNNQTESFETTLGLRSAGFTA	360 370 380 390 400 410

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8469151 GSSGVV... 330 340 350 360 370
cry2ab2_820. RGNKNEPDYF... 380 390 400 410 420
8469151 RSE-NITILSLN... 380 390 400 410 420
cry2ab2_820. NNIHAVHE--NGSMIHLENDITGF-- 480 490 500 510
8469151 SHVTLTRSLYNTNITSLPTFVMTNLSANTNT... 430 440 450 460 470 480
cry2ab2_820. FGNQGSLSRPFQNNITARTILRGNS-- 520 530 540 550 560 570
8469151 FTG-GDILK--RNTIGFVSLQNVNISPITORYELRFA-- 490 500 510 520 530 540
cry2ab2_820. VNTITNDGVNDGARFSDINIGNVA--SSNSDVPDINVTLSGTFSLMMLVPTNI 580 590 600 610 620 630
8469151 LKTEWEI--GESLTSRTSYNTESNPFSFRANPDIIRTADELPIRGELYIDKILILADA 550 560 570 580 590 600
cry2ab2_820. SPLV 580 590 600 610 620 630
8469151 TPEEYVDLERAQKAVNALFTSTNQLGLKTDVYHDVDSNVLECLDEFCDEKRELSE 610 620 630 640 650 660
cry2ab2_820.pcp
NRAA:142740
142740 source="GENBANK_PROT" delta-endotoxin
SCORES Initl: 128 Initn: 128 Opt: 225 z-score: 250.6 E(): 1.1e-05
>>NRAA:142740
initn: 128 initl: 128 opt: 225 z-score: 250.6 expect(): 1.1e-05
Smith-Waterman score: 257; 22.9% identity in 584 aa overlap
(60-604:41-590)
cry2ab2_820. FQHSLSIDIVQKEWTEWKKNNLSLYLDPVIGTVASFLIKKVGSLGKRLSLRLNLIFFPSG 30 40 50 60 70 80
142740 IPFNCLSNPEVEVLGGERTIETGYTIDISLSLTQFLLEP--VPGAGFVLGLVDIILWIF 20 30 40 50 60
cry2ab2_820. STNLMDILRETEKFLNQLRINTDILARVNAELTGL----QANVEFNQVDNFTLNFRNA 90 100 110 120 130 140
142740 GPSQWDAFLVQIEQLINQRIEFAFNQALSLRGLSNLYQIVAESFREWEADPTNP--A 70 80 90 100 110 120
cry2ab2_820. VPLSITSSVNTMQGLFNRLPQFMQGYQLLLPLFAQANLHLFIIRDVILNADENGIS 150 160 170 180 190 200
142740 LREEMRIQFNDMSALTTAIFLLAVQNYQVLLSVYQVQANLHLFLDRDVSFQGMGFD 130 140 150 160 170 180

cry2ab2_820. AATLTATYRDYLNKYTDYNSCINTYSAFK--GLNTRLHDMLE--EFRTYMLNVEY 210 220 230 240 250
142740 ATINSRYNDLTGLIGNYTDHAYRYNTGLERVWGPDSR--DWRYNQFRRELTJVLDI 190 200 210 220 230 240
cry2ab2_820. VIMSLF--KYOSLIVSS--GANLYASGSPQOTQFTSQDMPFLYSLFQVNSYVINGF 260 270 280 290 300 310
142740 VALFNYOSRRYPIRTVTSQUTREIYTNFVLENFDGSRGSAQGIERSIRSPHMLDILNSI 250 260 270 280 290 300
cry2ab2_820. SGARLSNTFPNIVGLPGSTTTTHALLARVNSVGGISS--GDIGASPPNFQNFCSST-- 320 330 340 350 360
142740 TI--YTDARHGYYYWGS--HQAIVASVGFSGPEFTFFLIGTMGNAAPQORIVAOLOGG 310 320 330 340 350
cry2ab2_820. FLPPLLTFFVRSWLDGSDRGVATVNMWOTESFETTLGLRSGAFTARGNSYFPDYFIR 370 380 390 400 410 420
142740 VVRLTSSTFYRRPFENIGINNQL--SVLDGTEFAYGTSSNLPSPAVYKSGVGLDLEIPPQ 360 370 380 390 400 410
cry2ab2_820. NISGVPLAVRNEDLRPLHYNEIRNIASPSTPGGARAYMVS--VHNK--NNIHAVHE-- 430 440 450 460 470 480
142740 N--NNVP--PROGFSHRLSHVSNFRSGSSSVSI--IRAPMFSWIHRSAEFNNIIASDSIT 420 430 440 450 460 470
cry2ab2_820. NGSMIHLPNDYTGFTTSPHATQVNNQTRTFISEKFGNQGLRFEON 490 500 510 520 530
142740 QIPAMKGNFLPNSVNS--GPG--FTGGDLVRLNSSGNNIGNRGYIEVP-----IHFP-- 480 490 500 510 520
cry2ab2_820. NTPATYTLRGNSVY--LYLRSSSSTIRVTINGRVYTAINVNTNND--GVNDNGAR 540 550 560 570 580 590
142740 SYSTIRTRRYASVY--TNDYWN--WGNSSLS--NTVPATATSLDNLQSSDFGYFESANA 530 540 550 560 570
cry2ab2_820. FSDINIGNVASSNSDPNINVTNLTOTDLMNIMVFNISPLY 600 610 620
142740 FTS--SLGNIVGVNFSGTAGVLDNREFIPATDPAFVNLERSAQVNALFTSTNQLGL 580 590 600 610 620 630
cry2ab2_820.pcp
NRAA:11493829
11493829 source="GENBANK_PROT" crystal protein [Paenibacillus tentoriobus]
SCORES Initl: 187 Initn: 187 Opt: 212 z-score: 250.1 E(): 1.2e-05
>>NRAA:11493829
initn: 187 initl: 187 opt: 212 z-score: 250.4 expect(): 1.2e-05
Smith-Waterman score: 212; 41.4% identity in 87 aa overlap
(5-91:78-158)
cry2ab2_820. MQAMDNSVLNSGRITTCDAYNVAADHPPFSFQHS 10 20 30

```
11493829  ICCLPIYNNDDNNNDNDAICDELGLTIPDNNITCSDTYPI---NWMTDFP--REKS
          50 60 70 80 90 100
cry2ab2_820.  LDIVOKEWTEKKNHSLYLDPIVGTVASFLKKVGLSVGKRLSELNRLFFSGSTNLM
          40 50 60 70 80 90
11493829  TQBELIREWTEKENSPLFTPAIVGIVTSYLLKQIAKVITGALLKPLTNLLFFPGSTLT
          110 120 130 140 150 160
cry2ab2_820.  QDLIRETEKFLNQRNLDTDLARVNAELTGLQANVEEPNQVDFLNPRNAVPLSTISSV
          100 110 120 130 140 150
cry2ab2_820.pcp
NRAA:60308967
60308967 source="GENBANK_PROT" truncated CryIac (Bacillus thuringiensis serovar
kenyae)
SCORES Init1: 128 Initn: 128 Opt: 219 z-score: 248.1 E(): 1.6e-05
>>NRAA:60308967
initn: 128 init1: 128 opt: 219 z-score: 248.1 expect(): 1.6e-05
Smith-Waterman score: 245; 21.5% identity in 578 aa overlap
(160-604:41-590)
cry2ab2_820.  FOHKSLLDTVQKEWTEKKNHSLYLDPIVGTVASFLKKVGLSVGKRLSELNRLFFSG
          30 40 50 60 70 80
60308967  IPYNCLSNPEVEVLGGERIETGTPIDISLSLTHFLSEF--VPGAGFVLGLDIWGIF
          20 30 40 50 60
cry2ab2_820.  STNLMODILRETEKFLNQRNLDTDLARVNAELTGL---QANVEEPNQVDFLNPRNRA
          90 100 110 120 130 140
60308967  GPSQWDAFLVQIEQLINQRIEFAFNQALISLEGLSLNYQIYAESFREWEDPTNP--A
          70 80 90 100 110 120
cry2ab2_820.  VPLSITSSVNTMOQLFLNLPQFOMQGYQLLLPLFAQAANLHLSFIRDVLINADENGIS
          150 160 170 180 190 200
60308967  LREEMRIQFNDMSNALTATPILAVQYQVPLLSVYVQAANLHLSVLRDVSFVGORWGF
          130 140 150 160 170 180
cry2ab2_820.  AALIRTYRDLKNTYRDSNYCINTYQSAFK---GLNTRLHML---EFRTYMFNLNVEY
          210 220 230 240 250
60308967  AATINSRYNDLTRIGNYTDNAVRYNTGLERVMGPDNR--DWRYNQFRRLTLTVLDI
          190 200 210 220 230 240
cry2ab2_820.  VSLTWSLTF---KYQSLVSS--GANLYASGSGPQQTQSOTSDWPFLSYFOVNSYLVNGF
          260 270 280 290 300 310
60308967  VALFPNDSRRPIRTISQLTREIYNVLENFVDFGSPFGSAQGIERSIRSPHLMWILNSI
          250 260 270 280 290 300
cry2ab2_820.  SGARLNTFPNIVLPGSTTHALLAARVNVSSGGISS---GDIGASPPNQNFNCST---
          320 330 340 350 360
60308967  TI--YTDAHRGYYVWSG---HOIMASPVGFSGPFTFPLYGTMGNAAPQQRIVAQLGQG
          310 320 330 340 350 360
          370 380 390 400 410 420
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cry2ab2_820.  FLPLLELTPFVRSMLDSGREGVATVNWQTESFETTLGLRSAGTARGNSNYFPDYFIR
          360 370 380 390 400 410
60308967  VYRTLSSTFRRFPENGINNQQL-SVLDTGTEPAYGTSSNLPSAVYKRSVGTVDLSLDEIPQ
          360 370 380 390 400 410
cry2ab2_820.  NTS-----GVPLVVRNEDLRRPLHYNEIRNIASP--SGTPGGARAYMVSVHNNKNIHAV
          430 440 450 460 470 480
60308967  NNSVPRQGFHSRLSHVSMFRSGSGSVSIIRAPMFESIYWGSAEFNNIIASDSITQIPAV
          420 430 440 450 460 470
cry2ab2_820.  H-----ENGSMHLAPNDYTGFIISPIHATQVNNQTRTFISEKFGNQGDSLRFQNNNTTAR
          490 500 510 520 530
60308967  KGNFLFNGSVIS-GPG-FTGGDLVRLYSSGNNINRGYIEVP-----IHPFSTSIITYR
          480 490 500 510 520
cry2ab2_820.  YTLRNGNSYNYLYRVSSIGNSTI-RVTINGRVVATVNTTINNDGVNONGARFSDINI
          540 550 560 570 580 590
60308967  VVRYVASVT-PIHLNVN-WGNSIFSNTVPAKGASLDNLQSS--DFGYFESANAFTS-SL
          530 540 550 560 570 580
cry2ab2_820.  GNVVASSNSDVPDLINVTNLNSGTQFDLMNIMLVPTNISPLY
          600 610 620 630
60308967  GNMVGVNRFSGTAGVIIDRFEPFIVTATLEAYNLERAQKAVNALFTSTNPLGLKTNVTD
          590 600 610 620 630 640
cry2ab2_820.pcp
NRAA:66360322
66360322 source="GENBANK_PROT" Chain A, Mosquito-Larvicidal Toxin Cry4ba From
Bacillus thuringiensis Ssp. israelensis
SCORES Init1: 142 Initn: 142 Opt: 208 z-score: 236.7 E(): 6.8e-05
>>NRAA:66360322
initn: 142 init1: 142 opt: 208 z-score: 236.7 expect(): 6.8e-05
Smith-Waterman score: 208; 23.0% identity in 174 aa overlap
(96-266:8-181)
cry2ab2_820.  LKKVGLVGVKRLSELNRLFFSGSTNLMQDILRETEKFLNQRNLDTDLARVNAELTGLQ
          70 80 90 100 110 120
66360322  TPERVWDFMTNTGLNLDIQVTAVYRTDANAKMTVK
          10 20 30
cry2ab2_820.  ANVEEENRQVNF--NPNRNAVPLSITSSVNTMOQLFLNRLPQFQ-MQGYQLLLPLFAQ
          130 140 150 160 170 180
66360322  DYLDQYTKFNTKREPNQSVRTAVITQFNLTSAKLRETAVYFNSLVGYELLPLPIYQ
          40 50 60 70 80 90
cry2ab2_820.  AANLHLSFTRDVLINADENGISAAITLRYRDLKNTYRDSNYCINTYQSAFKGINTLH
          190 200 210 220 230 240
66360322  VAVFNLLIRDLGRLNAQENSLARSGDQLYNTVMQYTKYEIAHSITWYKNGLDVLRKNS
          100 110 120 130 140 150
cry2ab2_820.  DM-LEPRTYMFNLNVEYVSLWSLKYQSLVSSGANLYASGSGPQQTQSOTSFSTQDWPFLYS
          250 260 270 280 290 300
```

470

RVSSGN
|: :|
RLCYASN

610
D-VPLDI

DELYLEF

SECTICIDAL
="Clostridium

RETEKFL
:: | :
EDGETIT
70

160
NTMQQLF
|:::
NSICE--
130

YLKNYTR
: | ::
SPNHL

KY2SLLV
 11:~
 -YDPAV

FFNINUGL
|
SGNKF-L

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cry2ab2_820. 340 350 360 370 380 390
PGSTITTHALLAARVNSGGISGIGASFPNQFNCFPLPLTPFVRSLDSSGDRG
10719937 NCHVNRH--VGTDLYNG-LRETHYG--YGSNVESENAFDKAYSNNYFNQNNP
310 320 330 340 350 360

cry2ab2_820. 400 410 420 430 440
VATVNWQTSFETTLGLRSGAFTARGNSYFPDYFIRNISGVPLVRNEDLRPL----
10719937 ----TSVKSIKFLITKNDEWIYGEPPSSNI--D-FTRNIQIYLSNLNSESYTHLSDMI
370 380 390 400 410

cry2ab2_820. 450 460 470 480 490
--HYNEIR-NIASP-----SGTPGGRAYMVSVHNRKNNIHAVHENGSMHLAPNDYTG
10719937 LANNDKIQINIDTPHSYSYMIYKGIEDTNYISDKLINOIPLVKE-----VKLSRHYSEI
420 430 440 450 460 470

cry2ab2_820. 500 510 520 530 540 550
TISPIHATQNNQTRTFISEKFGQGSLSRFEQNNNTARYTLRNGNSYNLYLRVSSIGN
10719937 SVIKPGFTGGLILSKV-HKPAHQIPA-QYMKNKITIPIKTKFPAGSQDPKVRCLYASN
480 490 500 510 520

cry2ab2_820. 560 570 580 590 600 610
STIRV--TINGRYVYATNV---NTTNDGVNDGASFPDINIGNVASSNSD-VPLDI
10719937 HDIGLRLIAGSKYIITNIQOTENTENNPSLIYDDFKYFNFTLISSGIDELYLF
530 540 550 560 570 580

cry2ab2_820. 620 630
NVTLSNGTQDLMNMLVPTNISPLY
10719937 YYSYTDGN-FEDFPKLSIPYTRNYS
590 600 610

cry2ab2_820.pap
NRAA:8928008

8928008 source="GENBANK_PROT" Pesticidal crystal protein cry20Aa (Insecticidal
delta-endotoxin CryXXA(a)) (Crystalline entomocidal protoxin) (86 kDa crystal
protein)/gi|2228580|gb|AAB93476.1| mosquitoicidal toxin [Bacillus thuringiensis]

SCORES Init1: 101 Initn: 126 Opt: 207 z-score: 233.4 E(): 0.0001
>NRAA:8928008
Initn: 126 Init1: 101 Opt: 207 Z-score: 233.4 expect(): 0.0001
Smith-Waterman score: 210; 21.1% identity in 653 aa overlap
(24-632;27-631)

cry2ab2_820. 10 20 30 40 50
MQAMDSVLSNGRTTICDAYNVAAHDP-FSFOHSLDTPQKEMTEWKKNNHSLYLD
8928008 MNPYQNDEIVDPENIDNNLRYFYANDPNVAMQ-----NTNYKDWNGVEYENPSSITA
10 20 30 40 50

cry2ab2_820. 60 70 80 90 100 110
IVGTVASFLKKVGSVLG-----KRILSELNR-LIFPGSGTNLMQDLRETEKFLNQRNL
8928008 ILASIG--ILNRVIALTVLNGTOEVISIQDALGFIRNGTG--NELLIRHVEQLQQTFLA
60 70 80 90 100 110
```

```
cry2ab2_820. 120 130 140 150 160
TDTLARVNAELTGLQANVEE---FNROVDNFINNRNNAVPLSITSSVNTMOOLFNRLL-P
8928008 TOYRSATGAIYGISRSYDNYLMFFROMER--NRTRFN-CQOVESAFITNITCINALAP
120 130 140 150 160

cry2ab2_820. 170 180 190 200 210 220
QFQW--QGYQLLLLPFAQAANHLSPFIRVILNADW--GISATLRTYRDYKKNYTRDY
8928008 QASLSRSGPFTLLPNYMAAANFLLLRDAVLYRNQWLSNISISTANVNLILRAAINEY
170 180 190 200 210 220

cry2ab2_820. 230 240 250 260 270
SNYCINTYQSAFKGLN-TLHDMLPEPTY-----MFLNVEYUYSIWSLFKYQSLLVSSG
8928008 ITHCTRYQDGLNRPDRSRANMWERFRNAYRDMTSLVDLFAIVFPT--XDPVLFPAA
230 240 250 260 270

cry2ab2_820. 280 290 300 310 320
ANLYASG--SGPQQTQSTQDWPFFLYSLFQVNSYVNLNGFSGARLSNTF---P-NIVG
8928008 INVELTRVYVTDPIVMAGRTAIPGFTRMENLVNSASRVSLNQMNIIYTSFYFRPHNIPR
290 300 310 320 330 340

cry2ab2_820. 350 360 370 380 390 400
YFWGNGNQLNSGTSNLGYRSDGR---TTFNVS-NIDIFRVNMTTHIGGAFTDDYRGLH
8928008 YWNGNQLNSGTSNLGYRSDGR---TTFNVS-NIDIFRVNMTTHIGGAFTDDYRGLH
350 360 370 380 390 400

cry2ab2_820. 410 420 430 440 450
RAEFIGANTQNTQRTSLLYSVEIPSSHFRFENHTVLEPGE-----SGLEPNERNYTHL
8928008 RAEFIGANTQNTQRTSLLYSVEIPSSHFRFENHTVLEPGE-----SGLEPNERNYTHL
410 420 430 440 450

cry2ab2_820. 460 470 480 490 500
LHYNEIRNTASGTPGGRAYMVSVHNRKNNIHAVHENGSMHLAPNDYTGFTISPIHA
8928008 OMNNEVS--VNPNR---GRVFLHAWTHRSRLR---RTNG---LRSDQILQI---PAVK
460 470 480 490 500

cry2ab2_820. 510 520 530 540 550
TOVNNQTRTFISEKFGNOGDS-LFFEQNNNTARYTL-----RNGNSYNLYLRVSSIGN
8928008 TISNGGDRAVL---NYGENIMKLDNLITGLSYKLTAVDSEASNTFRFVRVRYASMNN
510 520 530 540 550

cry2ab2_820. 560 570 580 590 600 610
TIRVTINGRYVYATNVTTINDGVNDGASFPDINIGNVASSNSDVPDLINVLN--
8928008 KNLIVLNGAQIALSNVEITVOR-----GGSITDLQYGNFKYATFAGNFKMGQSILGIF
560 570 580 590 600 610

cry2ab2_820. 620 630
---SGTQFDLMNMLVPTNISPLY
8928008 KEINIDFVLDKIELIPLSPNSSLSEOTQNTYNTYNODTIYTHNOGYDTYDQNSSGMYHOSY
620 630 640 650 660 670

cry2ab2_820.pap
SW:8928008
```

8928008 description="PESTICIDIAL CRYSTAL PROTEIN CRY20AA (INSECTICIDAL DELTA-ENDOROXIN CRY20A(A)) CRYSTALLINE ENTOMOCIDAL PROTOXIN (86 KDA CRYSTAL PROTEIN) "Bacillus thuringiensis serovar fukuokaensis" source="swissprot.pdb" version="1.1" type="PRT"

SCORES Initl: 101 Initl: 106 Opt: 207 z-score: 233.4 E(): 0.0001
>SW:8928008
Initl: 126 Initl: 101 Opt: 207 z-score: 233.4 expect(): 0.0001
Smith-Waterman score: 210 21.1% identity in 655 aa overlap
(24-632:27-631)

CRY2AB2_820. MQAMDSVLNSGRITTCDAANVNDHP-PFCHKSLDTVOKNTWKNNHSLYLDP
8928008 MNPYQNDDEIVDPENYDNNLNRPVANDPNAHQ--NFKDMMNGNEELNPSSITA

CRY2AB2_820. IGVTVASFLLKVGSLNG-----KRILSELN-LIFPGSINLMQDNLKFLNORLN
8928008 ILASIG--ILNRVIALTGNTQEVISIIODALGFRNGTG--NELTHVEQVFOOTLA

CRY2AB2_820. TDTLARNALGTGLQANVEE---FNQVDNFLNPNRNAPVLSITSSVNTMOOLKLNLP
8928008 TOYRSAATGAIYGISRSYDNLVLMFFQWER--NRTREN-GQVESAFITNLTCLINADP

CRY2AB2_820. QFQW--QGVQLLLPLFAQANLHLSFIRVDVILNADEW-GISATLRTYRDYLNKTYRDY
8928008 QASLSRGFTLLLPNAMAANFHLLLLDVLYRNQWLNSISTANVNLRAAINEY

CRY2AB2_820. SNYCINTYOSAFKGLN-TRLHDMLEPTY-----MFLNVFEVSVIWSLFKYQSILVSSG
8928008 ITHCTRWYDGLNRFDRSSSEANNEWNRNAYRDMTSLVDLPATVFT--YDPLFPAA

CRY2AB2_820. ANLYASG---SQPQOTQSTSDQWPEFLYSLFQVNSKVLNFGSGARLSNTP---P-NIVG
8928008 TNVELTRVVTVDPIVMAGGRTAIPGFTRMENLVNSAKRSVFLNOMNIYTSFVFRPHNIPR

CRY2AB2_820. LPGSTITHALLAARVNYSGISSGDIQSPNQFNQFNSTFLPLLTFFVRSWLDS--GSD
8928008 YYWSGNQLNSGNTSLNYGYSRGR---TFNVIS-NIDIFRVNMTHTGGFTDYYGLH

CRY2AB2_820. R-EGV-ATVNMQTESFETTLGLRSGAFTARGNSNPPDYFIRNIGSVPLVVRNEDLRPP
8928008 RAEFICANTQNNQRTSLYSVEIPSPSHFFENHTVFLGE-----SGLEPHERNYTHLP

CRY2AB2_820. LHYNEIRNTASPGFGGARAYMVSVHNRKNNIHAVHENGSMTHLPNDYTGFTISPIHA
8928008 QMNEVYS--VNPNAF---GRVFLHAWTHSLR---RTNG---LRSQILQI---PAVK

CRY2AB2_820. TQVNNOTRFTISEKFGNQDS--LRPEONNITARTYL-----RNGNSNLYLVRVSSIGNS
8928008 TISNGDRAVL---NYGENIMKLDNLTGLSYKLTAVDSEASNTRFIVRVRVYASNNNN

CRY2AB2_820. TIRVTINGRVYATNNTTNDGNDGARFSIDINIGNV-VASSNSDVPLDINVTLN--
8928008 KMLNLVNGAQIASLNVEHTVQR-----GSLTDLQYGNFKVATFAGNFKMGQSILGIF

CRY2AB2_820. ---SGTQDFLNNIMLVPTNISPLY
8928008 KEIPNIDFVLDKIELIFSNFMSLSLQOTQNYNTYNQDTIYTHNGQYDTYDQNSSGMHYQSY

CRY2AB2_820.pdp
NRAA:66800187

66800187 source="GENBANK PROT" hypothetical protein DB0192018 [Dictyostellium discoideum]gi|60462380|gb|EAL60601.1| hypothetical protein DB0192018 [Dictyostellium discoideum]

SCORES Initl: 79 Initl: 127 Opt: 205 z-score: 232.1 E(): 0.00012
>SW:66800187
Initl: 127 Initl: 79 Opt: 205 z-score: 232.1 expect(): 0.00012
Smith-Waterman score: 305 24.3% identity in 226 aa overlap
(52-266:53-274)

CRY2AB2_820. VAAHDFSPKSLDYNKATWEMKNNHSLYLDPIVGTVASFLKKGVSIVGKRLSEL
66800187 VTRNLISDQFTNSVDYDYTEIKNYVGGSLSMPTIGNPLSLV---SAVAHIITNT

CRY2AB2_820. RNLIFFSGSTIMQILIRETFEFGNORLNTDANNAELTGLQANVEEFNRQVDNF-LN
66800187 NETTYEV--YNSYREKKS---IDVDYDASTIATVSKLNALVIDYTKAKKNYLT

CRY2AB2_820. PNRNAVPISTTSVNTMQ-QLFNLRP--SQMGGQLLPLFAQANLHLSFIRVDIL
66800187 PNOAPVKDLVDANLHLLYIELRGSLLPLSDIKESYEAQEGAFALMTLHLLNREGST

CRY2AB2_820. NADWEGISAATLRTYRDYLNKTYRDSNYC-INTYOSAFK---LN--LWVWVFEFT
66800187 NGKINGISEKIEIFEQEFNKWVEYAOCHKLAYYKGVAKIAGLGVNFKVNFVRS

CRY2AB2_820. YMFNLNVFEVSIWSLFKYQSILVSSGANLYASGSGPQOTQSTSDQWPEFLYSFQVNSN
66800187 FCARYVDFVNLWSGFGNETIYPNGCYTENVRIFYESDVIGRPIDPSQTAKPNKPYVPSCD

cry2ab2_820.pep
NRAA:17385650

17385650 source="GENBANK_PROT" crystal protein CryE6s [Bacillus thuringiensis]

SCORES Init1: 89 Initn: 115 Opt: 202 z-score: 223.9 E(): 0.00036
(1280 aa)
>NRAA:17385650
initn: 115 init1: 89 opt: 202 z-score: 223.9 expect(): 0.00036
Smith-Waterman score: 223; 17.7% identity in 631 aa overlap
(40-634:48-653)

cry2ab2_820. LKVGSLVKGKILSELNLIKPSGSLNLMQDILRETEKELNORLNTDL-ARVNAELTGL
10 20 30 40 50 60 70 80 90 100 110 120
17385650 GQSRYPILTNAPSAEALQDMNYIELNDNCTLKEQVELFRDTSTTVRDALATTAGIITALLS
20 30 40 50 60 70

cry2ab2_820. LKVGSLVKGKILSELNLIKPSGSLNLMQDILRETEKELNORLNTDL-ARVNAELTGL
70 80 90 100 110 120
17385650 VSNPAAATAGIITILIPQWFGSDGDEVTEKFWAAAEILIQKITEARVNAELTGL
80 90 100 110 120 130

cry2ab2_820. QANVEEFNRQVDFNLFNRRN--AVPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFA
130 140 150 160 170 180
17385650 YRTIRLYGLAAERW-NQKNDPQAESIRTOFRATNITIEFAPMSFRVAGFEVPLNLYA
140 150 160 170 180 190

cry2ab2_820. QANLHLSEFIRDVILNADENGISAATLT-YRDLKKNYTRDYSNCTIYSAF---KGL
190 200 210 220 230
17385650 EAAQLQALLDAVKFGDMGDPQDEVDIYSEQLLPRAEHTDCHVYFNRGLAEKLL
200 210 220 230 240 250

cry2ab2_820. NTRLHDMLEFRYTMFLN--VFYVSIWSLF---KYQSLVSSGANLYASGSGPQQTQSF
240 250 260 270 280 290
17385650 KANLNDYARYPWAQYINHSKIQIENWNLFNDRYNNITLVLVDLVALWPTVDPRYSMT
250 260 270 280 290 300 310

cry2ab2_820. TSQDWPFLLYS-----LFQVNSNIVLNGFSGARLSNFPNIVGLPGSTTH-----A
300 310 320 330
17385650 KSELTRLYTSVRGAFYGHNDYDQNFBEIERNIISPPHLVTPNFTVYTQNDYYYPWA
320 330 340 350 360 370

cry2ab2_820. LLAAARNVSGGISGIDGASPFNFQNGSTFLPPLLPFVRSLDSDGSDREGVATVNWQ
340 350 360 370 380 390
17385650 GLOHKNFTESIVLSLESPVTGVTGTSNLNFEVTA--DPFLAVTIIGFGLQGLTSLGI---
380 390 400 410 420 430

cry2ab2_820. TESFETTLGLASGAFARGNSNFFDYTRNIGSVPLVVRNEDLRPLHYEIRNIASPS
400 410 420 430 440 450
17385650 ---YAMSFGRKSGSISHVGDIETGDDYLDVDRIPV---GDSFNPKLSWMS-----AAPT
440 450 460 470 480

cry2ab2_820. GTPGGARVWVSVHNKKNHVAHENGSMIHLAPNDYTGTFISPHATQVNNQRTFISE
460 470 480 490 500 510

17385650 TLGSTTFLQVSVYAWHPHSVD-----SNRISIDKIT--QIPAVKAFIFIDNHNKVIK
490 500 510 520 530

cry2ab2_820. KFGNQSLRPEQNNTTARYTLRGNS-----YNLYLVSSIGNSTIRVTINGRYV-TAT
520 530 540 550 560 570
17385650 PGSTGGDLVAFSREGYSGISVIFPGSDLVSYFYRIRYVASSQAKVTMGFGGGVEESES
540 550 560 570 580 590

cry2ab2_820. NVNTTNNNGVNDGARFSDINIGNVASSNSDVLIDINVTLSGTQFDLMNIMLVPTNI
580 590 600 610 620 630
17385650 KNFPATYSGNLTYSFGYINTL-AIASQSTAQTIENVFYRQYEEAEFIVDKLEFIPMEM
600 610 620 630 640 650

cry2ab2_820. SPFY
560 570 580 590 600 610 620 630 640 650
17385650 SLEEQADQDLKARKANVALFTSDAKSELKNVITDYAVDQAANLVECVSEDFHAQEKRI
660 670 680 690 700 710

cry2ab2_820.pep
NRAA:62548293
62548293 source="GENBANK_PROT" CryIA toxin [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 128 Opt: 185 z-score: 221.1 E(): 0.00051
>NRAA:62548293
initn: 128 init1: 128 opt: 185 z-score: 221.1 expect(): 0.00051
Smith-Waterman score: 185; 29.9% identity in 97 aa overlap
(140-236:30-126)

cry2ab2_820. NTDTLARNVNAELTGLQANVEEFNRQVDFNLPNPNVAPLSITSSVNTMQQLFNRLPQFQ
110 120 130 140 150 160
62548293 FARNAQISRLRGLSNLYOIYAESFREWEADPTNPALREEMFIQFNDMNSALTTPILLA
10 20 30 40 50

cry2ab2_820. MQGYQLLLPLFAQANLHLSFIRDVILNADENGISAATLTIRYRDLKKNYTRDYSNCTIN
170 180 190 200 210 220
62548293 VQNYQVPLLSYVQAANLHLSVLRDYSVFGQWGFDAATINSRYNDLTRLIGNYTDHAVR
60 70 80 90 100 110

cry2ab2_820. TYQSAFKGLNTRLHDMLEFRYTMFLNVEFYVSIWSLFKYQSLVSSGANLYASGSGPQQT
230 240 250 260 270 280
62548293 WYNTGLERVWGFDP
120 130

cry2ab2_820.pep
NRAA:8927990
8927990 source="GENBANK_PROT" Pesticidal crystal protein cry5Ab (Insecticidal
delta-endotoxin CryVAb) (Crystalline entomocidal protoxin) (142 kDa crystal
protein)/gi|142770|gb|AAA67693.1| delta-endotoxin

SCORES Init1: 95 Initn: 157 Opt: 196 z-score: 217.0 E(): 0.00086
>NRAA:8927990
(1289 aa)

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[illegible]

```
8927991  LPSNRAGQYGGLLQPYLWAEVQDSVETRLYGQLPAVDPOAGPNYSIDSSN---PIIQ
380      390      400      410      420      430

cry2ab2_820.  PFVRSWLDGSDREGVATVNMQTSFETTL-GL- ---RSGAFTARGNSNYFPD-----
380      390      400      410      420      430
8927991  INMDTW---KTPPGA---SGWNTNMRGVSGLSFLQDGTSLAGMGSGFADTIYSLP
440      450      460      470      480      490

cry2ab2_820.  --VFIRNIGSVPLVRNEDLRRLHYNEIRNIASP--SGTPG--GARAYMYSVHNRKNNI
430      440      450      460      470      480
8927991  ATHLSYLGTPYQTSN---YSGHVGLVGVSTPQEAFLNIIGOPDEQGNVSTMGFFP
490      500      510      520      530      540

cry2ab2_820.  HAVHENGSMHILAPNDVTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQNNTIARY
480      490      500      510      520      530
8927991  EKASYGTVKWEKWLNGANAMKLSFGOSIGIPITNVTG---GEYQIRCRYASNDNTNVF
540      550      560      570      580      590      600

cry2ab2_820.  TLRGNSYNLYLRV---SSIGNSTIRVTINGRVYATVNTNITNDGVNNGARFSDIN
540      550      560      570      580      590
8927991  FNVDTGCANPFIQQINFASVDNNTGVQANG-VYVVKSIATIDNS--FTEIPAKTINVH
600      610      620      630      640      650

cry2ab2_820.  p.p
SW:8927991

8927991  description="PESTICIDIAL CRYSTAL PROTEIN CRY5AA (INSECTICIDAL
DELTA-ENDOTOXIN CRYVA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (152 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar darmstadtensis"
source="swissprot_prot" version="NA type="prt

SCORES  Initl: 95  Initn: 128  Opt: 196  Z-score: 216.5 E(): 0.00092
>>SW:8927991
initn: 128 initl: 95 opt: 196 Z-score: 216.5 expect(): 0.00092
Smith-Waterman score: 201; 19.0% identity in 585 aa overlap
(87-610:114-669)

cry2ab2_820.  IVGTVASFLKKVGLVKRLSELNLIFFPSGNTNLMQDILRETEKFLNQLFNTDLAR
60      70      80      90      100      110
8927991  LITLAVPEIGITTPFIFGLFPAALNKDADPPPNKADIFEAQKPAIGEMIDRLIADQETP
90      100      110      120      130      140

cry2ab2_820.  VNAELTGLQANVEENROVDNF-----LNPENNAVPLSITSSVNTMQQLFLNLPQF---
120      130      140      150      160
8927991  LNGEISGLQWLAARYQSTMDDIQSHGKFNKVDSGLIKKFTDEVLSNYSFTYRLPVTID
150      160      170      180      190      200

cry2ab2_820.  QMOQSYQLLLPLPFAQANLHLSFTRVILNADEW-----GISATLRYDYLNKTRIDYS
170      180      190      200      210      220
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8927991  NTADRTLLGLPYVAILASMHMLLRDILITKGTWDSKINFTPDALIDSKTDIKNNIKLYS
210      220      230      240      250      260

cry2ab2_820.  NYCINTYQSAFKGNTRLMDLEFRYVFLNVEFYVSIWSL--FKYQSLVSSGAILYAS
230      240      250      260      270      280
8927991  KTIYVFOKGLASGTP-SDLESFAKQ-----KYIEIMTHCLDFARLFTDFDPLPYT
270      280      290      300      310      320

cry2ab2_820.  GSCP---QOTQSQTSDWPFLYS--LFQVNSVYLVNGFSGARLSN-TFPNI-----
290      300      310      320      330      340
8927991  GSGDISLQKTRILSPFIRIADGLINLTISDTSNWPENYENGGAFFPNKPKERILKQFK
320      330      340      350      360      370

cry2ab2_820.  -----VGLPGSTITTHALLAARVNS-----GGISGGDIGASFPNQNFNCSTFLPPLLT
330      340      350      360      370      380
8927991  LYPNRAGQYGGLLQPYLWAEVQDSVETRLYGQLPAVDPOAGPNYSIDSSN---PIIQ
380      390      400      410      420      430

cry2ab2_820.  PFVRSWLDGSDREGVATVNMQTSFETTL-GL- ---RSGAFTARGNSNYFPD-----
380      390      400      410      420      430
8927991  INMDTW---KTPPGA---SGWNTNMRGVSGLSFLQDGTSLAGMGSGFADTIYSLP
440      450      460      470      480      490

cry2ab2_820.  --VFIRNIGSVPLVRNEDLRRLHYNEIRNIASP--SGTPG--GARAYMYSVHNRKNNI
430      440      450      460      470      480
8927991  ATHLSYLGTPYQTSN---YSGHVGLVGVSTPQEAFLNIIGOPDEQGNVSTMGFFP
490      500      510      520      530      540

cry2ab2_820.  HAVHENGSMHILAPNDVTGFTISPIHATQVNNQTRTFISEKFGNQDGLRFEQNNTIARY
480      490      500      510      520      530
8927991  EKASYGTVKWEKWLNGANAMKLSFGOSIGIPITNVTG---GEYQIRCRYASNDNTNVF
540      550      560      570      580      590      600

cry2ab2_820.  TLRGNSYNLYLRV---SSIGNSTIRVTINGRVYATVNTNITNDGVNNGARFSDIN
540      550      560      570      580      590
8927991  FNVDTGCANPFIQQINFASVDNNTGVQANG-VYVVKSIATIDNS--FTEIPAKTINVH
600      610      620      630      640      650

cry2ab2_820.  p.p
NRAA:8927987

8927987  source="GENBANK_PROT" Pesticidal crystal protein cry5Ac (Insecticidal
delta-endotoxin CryVA(c)) (Crystalline entomocidal protoxin) (135 kDa crystal
protein)

SCORES  Initl: 95  Initn: 153  Opt: 194  Z-score: 215.1 E(): 0.0011
>>NRAA:8927987
initn: 153 initl: 95 opt: 194 Z-score: 215.1 expect(): 0.0011
Smith-Waterman score: 194; 20.6% identity in 228 aa overlap
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897-300:114-335)
cry2ab2_820. IVGVASFLKVKGLVGRILSELRLNLFPSGSLNLMODILRETEKFLNQLNTDLAR 110
8927987 LNLAVPEIGITFTPIGLFFAALNKHDPNPNKADIFPAKFAIOEMIDRLTADQTF 140
120 130 140 150 160 170 180 190 200
cry2ab2_820. VNAELTGLQANVEENROVDNF-----LNPNNVPLSITSSVNTWQQLFNRLPQF--- 160
8927987 LNGEISGLQNLAAQYQSMDIQSHGNTNFTDGLIKKFDDEVLSNFSYDRLVPEVITD 200
120 130 140 150 160 170 180 190 200
cry2ab2_820. QMOGYQLLLPLFAQAANLHLSFIRDVYLNSEW---GISATLTLYRNLVYTRDYS 220
8927987 NTADRTLLGLPYVAILASWMLMLRDIITKGFWDKSNIPDPAIDSFYDKNNIKLYS 260
210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. NYCINTYQSAFKGLNTRLHDMLEFRTYMLNVFVYSIWSL--FKYQSLVSSGANLYAS 270
8927987 KTIYDVFOKGLASVGTGTP--SDLESFAKKK-----KYIEIMTTHCLDFARLFPDPLXPT 310
270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. GSGPQQTQSFQDWPFYLSLQVNSYVNLNFGSGARLSNTFPNIVGLPGSTTHALLAA 340
8927987 GSGDISLQKTRILSPFPIRTADGLTLNNTSIDTSNWPYENGNGAFNPKERILKQFK 370
290 300 310 320 330 340 350 360 370
cry2ab2_820. pep
SW:8927987
8927987 description="PESTICIDIAL CRYSTAL PROTEIN CRY5AC (INSECTICIDAL
DELTA-ENDOTOXIN CRVA(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (135 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT
SCORES Initl: 95 Initn: 153 Opt: 194 z-score: 215.1 E(): 0.0011
>>SW:8927987
Initn: 153 initl: 95 opt: 194 z-score: 215.1 expect(): 0.0011
Smith-Waterman score: 194; 20.6% identity in 228 aa overlap
(87-300:114-335)
cry2ab2_820. IVGVASFLKVKGLVGRILSELRLNLFPSGSLNLMODILRETEKFLNQLNTDLAR 110
8927987 LNLAVPEIGITFTPIGLFFAALNKHDPNPNKADIFPAKFAIOEMIDRLTADQTF 140
120 130 140 150 160 170 180 190 200
cry2ab2_820. VNAELTGLQANVEENROVDNF-----LNPNNVPLSITSSVNTWQQLFNRLPQF--- 160
8927987 LNGEISGLQNLAAQYQSMDIQSHGNTNFTDGLIKKFDDEVLSNFSYDRLVPEVITD 200
120 130 140 150 160 170 180 190 200
cry2ab2_820. QMOGYQLLLPLFAQAANLHLSFIRDVYLNSEW---GISATLTLYRNLVYTRDYS 220
8927987 NTADRTLLGLPYVAILASWMLMLRDIITKGFWDKSNIPDPAIDSFYDKNNIKLYS 260
210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. NYCINTYQSAFKGLNTRLHDMLEFRTYMLNVFVYSIWSL--FKYQSLVSSGANLYAS 270
8927987 KTIYDVFOKGLASVGTGTP--SDLESFAKKK-----KYIEIMTTHCLDFARLFPDPLXPT 310
270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. pep
SW:8927987
8927987 description="PESTICIDIAL CRYSTAL PROTEIN CRY5AC (INSECTICIDAL
DELTA-ENDOTOXIN CRVA(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (135 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT

210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. NYCINTYQSAFKGLNTRLHDMLEFRTYMLNVFVYSIWSL--FKYQSLVSSGANLYAS 280
8927987 KTIYDVFOKGLASVGTGTP--SDLESFAKKK-----KYIEIMTTHCLDFARLFPDPLXPT 310
270 280 290 300 310 320 330 340 350 360 370
cry2ab2_820. GSGPQQTQSFQDWPFYLSLQVNSYVNLNFGSGARLSNTFPNIVGLPGSTTHALLAA 340
8927987 GSGDISLQKTRILSPFPIRTADGLTLNNTSIDTSNWPYENGNGAFNPKERILKQFK 370
320 330 340 350 360 370
cry2ab2_820. pep
SW:8928024
8928024 description="PESTICIDIAL CRYSTAL PROTEIN CRY12BA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (142 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT
SCORES Initl: 87 Initn: 87 Opt: 187 z-score: 206.9 E(): 0.0031
>>SW:8928024
Initn: 87 initl: 87 opt: 187 z-score: 206.9 expect(): 0.0031
Smith-Waterman score: 228; 19.8% identity in 602 aa overlap
(52-632:8-818)
cry2ab2_820. VAAVDPFSPQHKSLDTVQKEWTEWKNHNSLYLDPVIGTVASFLKVKVGLVGRILSEL 80
8928024 GKGDLLDAVNTYITGTEIDPLNVKGLSVLTLLPEVGTVAS--AASTIVSFIMPKIFGDK 100
50 60 70 80 90 100
cry2ab2_820. PHLIFPSSTNLMODILRETEKFLNQLNTDLARVNAELTGLQANVEENROVDNFLNP 140
8928024 PN-----AKNIFPQIEALNODINQYQDAINOKKFDLSLOKTIPLYVAIDN--ND 150
110 120 130 140 150
cry2ab2_820. NRNAVPLSITSSVNTWQQLFNRLPQF--MOGYQSLVSSGANLYASFAQAANLHLSFIRDVILNADE 200
8928024 YVTA-----KTQLENLNSLTISQISIFCEVYKGGGLPYVANNVNAHILLRLDAIVNAEX 210
160 170 180 190 200 210
cry2ab2_820. WGISATLTLYRNLVYTRDYNKYCNVQSA---EAGATLTLYRNLVYTRDYS 250
8928024 LGSDKEVDTHKKYIKMTIHNHTHEAVIKAFNLGSGRPLSDVNSYVNLNFGSGARLSNTFPNIVGLPGSTTHALLAA 270
220 230 240 250 260 270
cry2ab2_820. EYVSIWSL--FKYQSLVSSGANLYAS---GSGPQQTQSFQDWPFYLSLQVNSYVNLNFGSGARLSNTFPNIVGLPGSTTHALLAA 310
8928024 DLVALMPTDPDHYQKEVEIEFTRTISSPYQPKMONTSSSIYP--GLDNLVYSGDNL 330
280 290 300 310 320 330
cry2ab2_820. LNFSGAR----LSNTPFNIVGL-----PGS-TTHALLAARVNYSGISSGDIAGSPNG 350
8928024 KLEFSTRINDGLAKIFTGIRNTFYKSPNTHETHYVDFSVNTQSSGNISRGSSNPIDIL 360
320 330 340 350 360

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[illegible]

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SCORES Initl: 103 Initn: 127 Opt: 181 Z-score: 200.9 E(): 0.0068
>SW:117538
Initn: 127 Initl: 103 Opt: 181 Z-score: 200.9 expect(): 0.0068
Smith-Waterman score: 194 20.9% identity in 254 aa overlap
(30-266:11-263)

cry2ab2_820. MQAMDNSVLNSGRITICDAYNVAADHPFQHKSLDVTQKEWTEWKKNNHSLYLDP--IV
117538 MNSGYPLANDLQGSMTNTYKDWLACENNOQGVNPAIN

cry2ab2_820. GTVASFLKKVGSV-----GK--RIILSELNLIFFSGSTN--LMODILRETEKFLN
117538 SSSVSTALDKAGAILKFNPPAGSVLTLSAVLPIFMPTNTPTPERVWDFMTWNTGNLID

cry2ab2_820. QRLNTDLARVNAELTGLQANVEEFNRQVDNLF--NPNNAVPLSITSSVNTWMOOLFNLRL
117538 QTVTAVRTDANAKMTVKDYLOQYTTKENTWKREPNQSYRTAVITQFNLTSAKLRETA

cry2ab2_820. PQFQ-MOGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKNTDYS
117538 VYFSNLVGYELLPLPIYAQVANFNLLLRDGHKCTRM-VYARSCDQLYNTWVQYTKEYI

cry2ab2_820. NYCINTYQSAFGLNTRLHDM--LEFRTYMFNLFVYSIWSLFKYQSLVSSGANLYASG
117538 AHSITWYNGDLVLRKNSGOWITFNDYKREMTIQVLDLILALFASYPDRPYADKIDNTK

cry2ab2_820. SGPOQTQSFTSQDMPFLYSLFQVNSYVNLGFGSARLSNTFFNIVGLPGSTTHALLAAR
117538 LSKTEFTREIYALVESPSKSIATALEAALTRDVHLFTLKLKRVDFWNTIYQDLRFILSAN

cry2ab2_820.pap
NRAA:142738
142738 source="GENBANK_PROT" mosquitoicidal protein

SCORES Initl: 103 Initn: 127 Opt: 181 Z-score: 200.9 E(): 0.0068
>NRAA:142738
Initn: 127 Initl: 103 Opt: 181 Z-score: 200.9 expect(): 0.0068
Smith-Waterman score: 194 20.9% identity in 254 aa overlap
(30-266:11-263)

cry2ab2_820. MQAMDNSVLNSGRITICDAYNVAADHPFQHKSLDVTQKEWTEWKKNNHSLYLDP--IV
142738 MNSGYPLANDLQGSMTNTYKDWLACENNOQGVNPAIN

cry2ab2_820. GTVASFLKKVGSV-----GK--RIILSELNLIFFSGSTN--LMODILRETEKFLN
117538 SSSVSTALDKAGAILKFNPPAGSVLTLSAVLPIFMPTNTPTPERVWDFMTWNTGNLID

142738 SSSVSTALDKAGAILKFNPPAGSVLTLSAVLPIFMPTNTPTPERVWDFMTWNTGNLID
cry2ab2_820. QRLNTDLARVNAELTGLQANVEEFNRQVDNLF--NPNNAVPLSITSSVNTWMOOLFNLRL

142738 QTVTAVRTDANAKMTVKDYLOQYTTKENTWKREPNQSYRTAVITQFNLTSAKLRETA
cry2ab2_820. PQFQ-MOGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKNTDYS

142738 VYFSNLVGYELLPLPIYAQVANFNLLLRDGHKCTRM-VYARSCDQLYNTWVQYTKEYI
cry2ab2_820. NYCINTYQSAFGLNTRLHDM--LEFRTYMFNLFVYSIWSLFKYQSLVSSGANLYASG

142738 AHSITWYNGDLVLRKNSGOWITFNDYKREMTIQVLDLILALFASYPDRPYADKIDNTK
cry2ab2_820. SGPOQTQSFTSQDMPFLYSLFQVNSYVNLGFGSARLSNTFFNIVGLPGSTTHALLAAR

142738 LSKTEFTREIYALVESPSKSIATALEAALTRDVHLFTLKLKRVDFWNTIYQDLRFILSAN
cry2ab2_820.pap
NRAA:117329

117329 source="GENBANK_PROT" Pesticidial crystal protein cry10Aa (Insecticidal
delta-Endotoxin Cry10Aa) (Crystalline entomocidal protoxin) (78 kDa crystal
protein) [G143229] [GB|AAA3614.1] insecticidal endotoxin (put.); putative

SCORES Initl: 69 Initn: 101 Opt: 173 Z-score: 195.6 E(): 0.013
>NRAA:117329
Initn: 101 Initl: 69 Opt: 173 Z-score: 195.6 expect(): 0.013
Smith-Waterman score: 179 22.8% identity in 232 aa overlap
(55-263:68-296)

cry2ab2_820. HDPFQHKSLDVTQKEWTEWKKNNHSLYLDPVTQSAFLKKVGSVGVKRR-----
117329 PLKNTYKDWLNVCDNQOQGVNAGNFSSITVGVSAQIV-VGTMLGAFAPVLAAG

cry2ab2_820. ILSELNLI-IPFSGS--TNLMODILRETEKFLNTRLFTLQVNAELTGLQANVEEFNR
117329 IISFGTLPIFWQSDPANWODLNLIGRPT-SEIDNTIINVLTSVTVTKNQDRIQOE

cry2ab2_820. QVDFNLPNRRNAVPLSITSSVNTWMOOLFNLRLPOFOMOG-YQLNLLPLFAQAANLHLSF
117329 FFDKWEFARTHANAKVHDLFTTLEPIDDKOLDLWKNSASRYRPTPLPAGQNTWNTGNLID

cry2ab2_820. RDVILNADWEGISAATLRT---YRDYLNKNTDYSNYCINTYQSAFGLNTRLH
117329 KHAATYNIWLQNGINPSTFNSNYQYGLKRIQIEYTDYCIQTYNAGLTWIRTNTAT

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initn: 101 initl: 69 opt: 173 Z-score: 195.6 expect(): 0.013
Smith-Waterman score: 179; 22.8% identity in 232 aa overlap
(55-263:68-296)

cry2ab2_820. HDPSPQHSLOTVQKQEWTEWKKNNHSVLDPIVGTVASFLKKVGSIVGKR-----
21685444 PLKNTNYKDWLVNQCDNOQVGGNAGNFASSETIVGVSAGIIV-VGTMLGAPAAPVLAAG
40 50 60 70 80 90

cry2ab2_820. ILSELRLN-IPFSGS--TNLMQDILRETEKFLNQRINTDTLARVNAELTGLQANVEFNRR
21685444 IISFGTLLPIFWQSDSPANWQDLNIGRPI-DEIDKNIINVLTSIVTIKQKLDPKQOE
100 110 120 130 140 150

cry2ab2_820. QVDNFLNPNRNNAVPLQISTSSVTMOQLNRLNLPQFMQG-YOLLLLPLFLQARANLHLSFI
21685444 PFDKWEPTHANAKAVHDFTILSEPIDKOLDMLKKNASYRIFLPAIYAGIAIWHNLL
160 170 180 190 200 210

cry2ab2_820. RDVILNADEW---GISAAITRT---YRDYLNKTYTRDYSNYCINTYSAFKGLNTRLH--
21685444 KHAATYNIWLOQSDNPSTFNSSNYGYGLYKRIQDEYDTCIOFYAGLTMTIRTNAT
220 230 240 250 260 270

cry2ab2_820. -DMLE-FRTYMLNPNVFEVVSILFKYQSLVSSGANLVASGGSPQQTQSTQDWPFLY
21685444 WNNYNYRLEMTLVLDLIAIFENDVPEKYPIGVKSELREIVYTNNSDTRFRIELENL
280 290 300 310 320 330

cry2ab2_820.pcp
NRAA:17385648

17385648 source="GENBANK_PROT" crystal protein CryE6Q (Bacillus thuringiensis)

SCORES Initl: 75 Initn: 159 Opt: 172 Z-score: 189.9 E(): 0.028
>>NRAA:17385648
Initn: 159 initl: 75 opt: 172 Z-score: 189.9 expect(): 0.028
Smith-Waterman score: 178; 21.1% identity in 190 aa overlap
(93-266:111-296)

cry2ab2_820. SFLKKVGSVGGKILSELNLIFFSGTNLMQDILRETEKFLNQRINTDTLARVNAELT
17385648 RAAVQVINTVIKLLMPDPEKPEPAYDIDFTWKEILGRVEILIEEKIDREAYNAAIGRLS
90 100 110 120 130 140

cry2ab2_820. GLOANV---EFNRQVDNPLNPN-RNAVPLSITSSVTMOQLNRLNLPQFMQGVOLL
17385648 GLKRALSLVQESFTWIDNDEPQEDVRNRTSILFEL-----VTTIETFKYSGQELNL
150 160 170 180 190

cry2ab2_820. LPFLQAANLHLSFIRDVILNADEWGISAAITLYR-----DLYNKNTDRYSNCINTYQ
17385648 LTFVQAADFHMLLQGVQMYGVRRGQFQRTVDSFYQDRGEGKLLPKYSDYCTYWD
200 210 220 230 240 250

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cry2ab2_820. SAF--KGLNTRLHMDLRF--RTYMLNVFEYVSIMSFKYQSLLVSSGANLYASGSGP
17385648 GGLNRAKNDKAYSTVRYFWANLNNMSVLEQEDWNLNDYRRDRTILVLDLVAWVPT
cry2ab2_820. QQTQSFTSQDNPFLSLFQWNSYV LMGFSGAN--SNFPNIVGLPGSTTHALLAARVNY
17385648 YDLHYDNGNYGVQSETRISYIYQAVEN--KGVFTKEQEVSVFRPHLVLTWLEWFIQI
cry2ab2_820.pap
NRAA:17385646

17385646 source="GENBANK_PROT" crystal protein cry2ab2 [Bacillus thuringiensis]

SCORES Initl: 110 Initn: 163 Opt: 170 z-score: 187.5 expect(): 0.838
>NRAA:17385646
Initn: 163 initl: 110 opt: 170 z-score: 187.5 expect(): 0.838
Smith-Waterman score: 189; 20.7% identity in 256 aa overlap
(41-266:63-315)

cry2ab2_820. SGRITTCDAVVAANDPESFOHKS LDTVQKEMTKKNNHSLYLD---PIVGTVASFL
17385646 KLQNMKGKWRDWCDFDAKRLQLKQIGISPFEPDEWTKVQGSLLISAGLVAATAGVASVAF
cry2ab2_820. KKVGSLVGK--RIISLRLNLIFFPGSGTN----LMODILRETEKFLNQRINTDLARVNAE
17385646 PPLAIVAGAFATISMFDFVLWPESENNTNSQVVMADFAAAAEEMDEKIAEIKAEAVLQ

cry2ab2_820. LTGLQANVFEENQVDNLF--NPENNAVPLSITSSVNTMQQDFLNRLPQOMQYQLLLLP
17385646 LRIVQSKRLDYQQAACNFQSDPNNESYKALLRDADFDDADALKEVMILFSREGYEQLLLF

cry2ab2_820. LFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYTRD-----YSNVCINTY
17385646 DYVQAANLHLLKLDKQVFGVGFPGRVEQYYSNPTNLGNPCMVQLLAKYNTYVSL-

cry2ab2_820. QSAFKGLNTRL-----HDMLEFRTYMLNVFEYVSIMSFKYQSLLVSSGANLY
17385646 --CWKGIEERKWWVESEYRNNEEYAYRSNMTMMVLDMALWFTYDVPKYFYATAVELT

cry2ab2_820. ASGSGFQQTQSITSDQWPFYLSLQVNSYVLNGFSGARLSNTFPNIVGLPGSTTHALL
17385646 REIYSLIAGFRDYGKMPYQIYTWKFKGSLVNLNLERFTIYTNKKNFEYFFPACVETTYQTI

cry2ab2_820.pap

NRAA:54695305

54695305 source="GENBANK_PROT" Cry30-like [Bacillus thuringiensis]

SCORES Initl: 57 Initn: 91 Opt: 164 z-score: 185.2 expect(): 0.051
>NRAA:54695305
Initn: 91 initl: 57 opt: 164 z-score: 185.2 expect(): 0.051
Smith-Waterman score: 191; 18.5% identity in 626 aa overlap
(5-578:9-611)

cry2ab2_820. MOAMDSVMSNGRTTICDAVVAADHP--FSFOHKS LDTVQK--EMTEWKKNNHSL--
54695305 MNLVGNKNDSEILNASS---NNSNMSTTYPKYPLAHSRODSMNNYKEMINOCETINT

cry2ab2_820. YLDPI-----VGTVASF--LLKKVGLVGVKRLSELRLNI---FPGSTNLMQDI
54695305 FCTPIDTINSVAATIGAVGAILLIPGPGAIG--FVLSTFTSLPIYLPWSDTKKIGDF

cry2ab2_820. LRETEKFLNQRINTDLA---RVNAELTGLQANVFEENQVDNFPNRAVPLSISS
54695305 TKQGLQLPFPELGNDAIEIIGNVOSEYNSLKTQMFQFSDFTDMKKYENRATAVAVTND

cry2ab2_820. VNMGSFLNRLPQOMQY--QLLLPLFAQAANLHLSFIRDVILNADW-----GISAAAT
54695305 PSSVRDQVIRK--KDFRLNPNKPKAFILYAQTANFANFDLILYQRCALYADWENDINRSISP

cry2ab2_820. LRTVYK--LKNYTRNSVNTYQSAFKGLNTRLH---DMLFRTYMLNVFEYVS
54695305 LKSGDYVLSLAAKI--EYTNVCAETKNSNLILKKNKTNISWGTYNKYRREVTILGALLAA

cry2ab2_820. IWSLFYQSLLVSSGANL---FAGSGFQQTQSITSDQW-----PFLYS-LFQVNS
54695305 LFPNYDICIYPIQTKTSLTAVYMPSE--LQSNVYFQSLREGNALTHTPPSLFTWLNELNL

cry2ab2_820. NYVLNGFSGARLSNTFPNIVGLPGSTTHALLAARVKSQSSGSDISFSPNFCNST
54695305 YTRENFNFPALLVSLSGLOAISRXTQNPENRS--NPAQSWKNGIPTQIGLNLFPYKLL

cry2ab2_820. FLPLPLTPFVRSMIDSGSDREGVATVNTWQTESPETILGRSAPFARGNS--PFAFIR
54695305 SLQYHHP-----NECVSIAGISDMTFYKSDYNGNAPTQT--YQAESENNTNFM--

cry2ab2_820. NISCVPLVVRNEDLRRPLHY--NEIRNIASPSG--TPGGAARYWVS--VHNKKNHAYEN
54695305 NGPQEAASSNNISIKQTNHILSDIKMIYRSRTGTGTGYPDFGYSFAWHTTSVNPONLIVPN

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490 500 510 520 530 540
cry2ab2_820. GSMHLAPNDYTGFTISPIHATQVNNQTRTFISEXFGNQDSURFEONNTIARYTLRNG
54695305 --RITQIPAVKADYLTSPAKVIAGPGHTGDLVALINAATQAGRMQIOCKTGSFT---G
530 540 550 560 570
cry2ab2_820. NSYNYLVRVSSIGNSTIRVTINGRVYATINVTNTINDGVNDGARSDINIGNVASSN
54695305 ASRYGIRIRYAANNALTVSUSYVOGNTMSTIFERTFLRNNTIPTDLKIEEFYK
580 590 600 610 620 630
cry2ab2_820. SDVPLDINVLNSGTQFDLMNIMLVPTNISPLY
54695305 EYNOIITWAPONTIVTIAIQOLNAPFNDOLIIDRIEFYPMQGVPCVTN
640 650 660 670 680
cry2ab2_820.pcp
NRAA:48880
48880 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis]
SCORES Init1: 97 Initn: 127 Opt: 167 z-score: 184.8 E(): 0.053
>>NRAA:48880
Initn: 127 Init1: 97 Opt: 167 Z-score: 184.8 expect(): 0.053
Smith-Waterman score: 206; 24.1% identity in 444 aa overlap
(171-578:184-602)
cry2ab2_820. PNRNAVPLSITSSVNTMQQLFLNLPQFGYQVOLLPLPFAQANLHLSFIRDLINAD
54695305 ELRTFRIDSEFDRLITRGSITNGGSLARQNAQIILLPSPASAFHLLLDATRYGT
160 170 180 190 200 210
cry2ab2_820. EWGISAAT-LRTYRDYLNKTYRDSNYCINTYOSAFKGLNTRLHD---MLEFRTY---MF
54695305 NWGLYNATPFINTYOSKLVLELYDYCVHWYNGRNELRQGTSAWLEFHYREMT
220 230 240 250 260 270
cry2ab2_820. LNVFEYVSIWLSFKYQSLVSSGANL---YASGSPQQTQFTSQDWPFYLSFQVNSN
54695305 LNVLDIVASFSSLDITNYPIETDFOLSRVYTFPIGVRHSSLRGESW-FSP-VNEANFS
280 290 300 310 320 330
cry2ab2_820. YVINGFSGARLSNTPFNIVGLPGSTT---THALLAARVNYSGISGSDIGASPNQNFNC
54695305 DLENAIPNRPSPWFLNNMIISTGSLTLEVPSPSTDRARVWG---SRDRI---SPAN-----
340 350 360 370 380
cry2ab2_820. STFLPPLLTFFVRMSLDGSDREGVATVNNQTESPETILGRSGAF---TARGNSNYFP
370 380 390 400 410 420
54695305 SQPIELISGQHTTATQITILGRN-IFRVDSCACNLNDTVGVNRAVFFVHDAESQSRVY
390 400 410 420 430 440
cry2ab2_820. DYFIRNISGV-PLVV-----RNEOLRRPLHYNEIRNIASPSGTPGGARAYMVSVHN
430 440 450 460 470

48880 EGYIRT-TGIDPRVQNTINYLPGENSIDPTPEDYTHI--LSTTINLTGLPROV---ASN
450 460 470 480 490
cry2ab2_820. RKNNIHAVHSGSMIHLAPNDYTGFTISPIHATQV---NNQTR-----TFISEKFGNQDS
48880 RRSLL--VMYGWTHKSLARNN---TINPDRIQTQIPKVDITRGTGVSVYNDPFGFIGAL
500 510 520 530 540
cry2ab2_820. LRFQNNNTIARYTLAGNSNLYL-LFVSSIGNSTIRVTINGRVYAT-NNVTITNDGV
530 540 550 560 570 580 590
48880 LQRTDHGSLGVLKRVQFPFLHLRQQYRIRVRYASTINIRLSVNGSEFGTISQNLSPSTWRLGED
550 560 570 580 590 600
cry2ab2_820. NDNGARESDINIGNVASSNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
590 600 610 620 630
48880 LRYGSAFIREFNTSIRPTASPDQIRLTIEPSFIRQEVVVDRIEFIPVNPTRAKEDLEAA
610 620 630 640 650 660
cry2ab2_820.pcp
SW:8469164
8469164 description="PESTICIDIAL CRYSTAL PROTEIN CRY9AA PRECURSOR (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIXA(A)) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)" library="NA species="Bacillus thuringiensis serovar galleriae"
source="swissprot_prot" version="NA type="PRI
SCORES Init1: 97 Initn: 127 Opt: 167 z-score: 184.8 E(): 0.053
>>SW:8469164
Initn: 127 Init1: 97 Opt: 167 Z-score: 184.8 expect(): 0.053
Smith-Waterman score: 206; 24.1% identity in 444 aa overlap
(171-578:184-602)
cry2ab2_820. PNRNAVPLSITSSVNTMQQLFLNLPQFGYQVOLLPLPFAQANLHLSFIRDLINAD
8469164 ELRTFRIDSEFDRLITRGSITNGGSLARQNAQIILLPSPASAFHLLLDATRYGT
160 170 180 190 200 210
cry2ab2_820. EWGISAAT-LRTYRDYLNKTYRDSNYCINTYOSAFKGLNTRLHD---MLEFRTY---MF
8469164 NWGLYNATPFINTYOSKLVLELYDYCVHWYNGRNELRQGTSAWLEFHYREMT
220 230 240 250 260 270
cry2ab2_820. LNVFEYVSIWLSFKYQSLVSSGANL---YASGSPQQTQFTSQDWPFYLSFQVNSN
8469164 LNVLDIVASFSSLDITNYPIETDFOLSRVYTFPIGVRHSSLRGESW-FSP-VNEANFS
280 290 300 310 320 330
cry2ab2_820. YVINGFSGARLSNTPFNIVGLPGSTT---THALLAARVNYSGISGSDIGASPNQNFNC
8469164 DLENAIPNRPSPWFLNNMIISTGSLTLEVPSPSTDRARVWG---SRDRI---SPAN-----
340 350 360 370 380
cry2ab2_820. STFLPPLLTFFVRMSLDGSDREGVATVNNQTESPETILGRSGAF---TARGNSNYFP
370 380 390 400 410 420

8469164
SOFITLISGQHTTATQTLGRN--IFRVDQACNLNDITYGVNRAVYHDSGQSQRVY
400 410 420 430 440
cry2ab2_820. DYFIRNISGV--PLVV-----RNEDLRPLHYNEIRNIASPGTPGCGARAYVSVHN
430 440 450 460 470
8469164
EGYIKT--TGIDNPRVQNTYLPGENSDIPTEDYTHI--LSTINLTGQLRV---ASN
450 460 470 480 490
cry2ab2_820. RKNNIHAVHENGSMIHLAANDYFTTISPATQV---NNQTR---TFISEKFGNQDS
480 490 500 510 520
8469164
RRSSL--VMYGWTHKSLARN--TINPDRITQPLTKVDTGTGVSYYNDPFGIGGAL
500 510 520 530 540
cry2ab2_820. LQRTDHGSLGVLRVQFPLHLRQOYRIRVYASTNIRLSVNGSFGTISQNLSTWELGED
530 540 550 560 570 580 590
8469164
LRYGSFAIRFNTSIRPTASPDQIRLTIEPSFIQOYVVDRIEFTVPNPTREAKEDLEAA
610 620 630 640 650 660
cry2ab2_820.pcp
NRAA:46132845
40271

40271 source="GENBANK_P01" delta-endotoxin CryIG protoxin [Bacillus
thuringiensis]gi|8469164|sp|Q99031|CR9AA BACTG Pesticidal crystal protein
cry3Aa precursor (insecticidal delta-endotoxin CryIXA(a)) (Crystalline
entomocidal protoxin) (130 kDa crystal protein)gi|228273|prf||1802272A delta
endotoxin
SCORES Initl: 97 Initn: 127 Opt: 167 z-score: 184.8 E(): 0.053
>>NRAA:40271
Initn: 127 Initl: 97 opt: 167 z-score: 184.8 expect(): 0.053
Smith-Waterman score: 206; 24.1% identity in 444 aa overlap
(171-578:184-602)

cry2ab2_820. PNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVILNAD
150 160 170 180 190 200
40271
ELRTPRIADSEFDRLITRGLTNGSLAQNAQIILLPSFASRAFFHLLLLDTRVGT
160 170 180 190 200 210

cry2ab2_820. ENGISAAT--LRIVDYLNKTYRDSNYCINTYQSAFKGNTLRHD---MLEFTY---MF
210 220 230 240 250
40271
NMGLYNATPFTNYQSKLVELIELYDYCVHWYNRGFNELRQGTSAWLEPHRYREMT
220 230 240 250 260 270

cry2ab2_820. LNVFVYSWLSFKYQSLVSSGANL---YASGSPQQTQSTQSQWFLYSLFQVNSN
260 270 280 290 300
40271
LWVLDIVASFSSLDITNYPIETDFQLSRVYITDFIGVHRSSLRGSM--FSF--VNPANFS
280 290 300 310 320 330

310 320 330 340 350 360

cry2ab2_820. VYLNGFSGAELSNTPFNIVLPGSTT---THALLAARNVYSGGSSGDIGASFFNPNFC
370 380 390 400 410 420
40271
DLENAINPRPSPFLNINISTISLTPSPSTDRARYWG---SRDRI--SPAN-----
340 350 360 370 380

cry2ab2_820. STEFLPPLITPFVPSWLDGSDREGVAVTNWQTESFETTLGASGAF---TARGNSNYFP
370 380 390 400 410 420
40271
SOFTIELISGQHTTATQTLGRN--IFRVDQACNLNDITYGVNRAVYHDSGQSQRVY
390 400 410 420 430 440

cry2ab2_820. DYFIRNISGV--PLVV-----RNEDLRPLHYNEIRNIASPGTPGCGARAYVSVHN
430 440 450 460 470
40271
EGYIKT--TGIDNPRVQNTYLPGENSDIPTEDYTHI--LSTINLTGQLRV---ASN
450 460 470 480 490

cry2ab2_820. RKNNIHAVHENGSMIHLAANDYFTTISPATQV---NNQTR---TFISEKFGNQDS
480 490 500 510 520
40271
RRSSL--VMYGWTHKSLARN--TINPDRITQPLTKVDTGTGVSYYNDPFGIGGAL
500 510 520 530 540

cry2ab2_820. LQRTDHGSLGVLRVQFPLHLRQOYRIRVYASTNIRLSVNGSFGTISQNLSTWELGED
530 540 550 560 570 580 590
40271
LRYGSFAIRFNTSIRPTASPDQIRLTIEPSFIQOYVVDRIEFTVPNPTREAKEDLEAA
610 620 630 640 650 660

cry2ab2_820.pcp
NRAA:46132845
40271
LRYGSFAIRFNTSIRPTASPDQIRLTIEPSFIQOYVVDRIEFTVPNPTREAKEDLEAA
610 620 630 640 650 660
cry2ab2_820.pcp
NRAA:46132845
46132845 source="GENBANK_P01" hypothetical protein Raet03002841 [Ralstonia
eutropha JMP134]
SCORES Initl: 92 Initn: 130 Opt: 161 z-score: 184.5 E(): 0.056
>>NRAA:46132845
Initn: 120 Initl: 92 opt: 161 z-score: 184.5 expect(): 0.056
Smith-Waterman score: 168; 24.6% identity in 179 aa overlap
(55-226:20-184)

cry2ab2_820. HDPFQFHKSLDVTQKENTWKKNNHSLYLDN--GTVASFLLKKVGSLSVGNLSLR
30 40 50 60 70 80
46132845
MGPAFPAHADGALGKLPVTDPMEDLNTILNVLAETPVVGA--MSAV
10 20 30 40 50 60

cry2ab2_820. NLIPESGSLNLMODILRETEKFLNRLTDTLARVNAELTGLQANVESNNOVDNFAEN
90 100 110 120 130 140
46132845
GLLVPEFADVWEIRQKVEALIEQKINDAVISLKSLLDG-----KNNKLY
50 60 70 80 90

cry2ab2_820. RNAVPLSITSS---VNTMQQLFLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVIL
150 160 170 180 190
Initl: 97 Initn: 127 Opt: 167 z-score: 184.8 E(): 0.053

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40352 DWLNCQNNQYGGDPETFDSELSAYTIWGVTLTGFGFTPLGLALIG---FGTLIP 50 60 70 80 90 100

cry2ab2_820. LIFFP-GSTNLMODILRETEKFPNQRLNTDTLARVALETGLQANVEEFNRQVDNLFN-P 90 100 110 120 130 140

40352 VLFPAOOSNTWDSDFITQTKIIKKEASTYISNANKILNRSFNVISTVHNHLKTWENNPP 90 100 110 120 130 140

cry2ab2_820. NRNAVPLSTSTSVNTMQQLFNLRLPQF-----QMCGYQLLLLLLPLFAQAANLHLSFI

	170	180	190	200	210	220
NIQRQIQ DVRIQZQVIRIIM QAVRQZQNCINT SSGSRRSSRSRQZQ						

40352 NQAVKPEVLLKNRRQDFLEPLPTADIDYVPLTKAIEDYTNVCVTYK---KGLNLIKTT
230 230 240 250 260 270
CRY2AB2_820_--TRLHMLEFRITVFLNPFVYSINSLFKYOSLLVSSGANLYAGSGPQOT----QSGFT
240 250 260 270 280 290

40352 PDSNLGNINWNTY---NTRYKMTTAVLDVWALFENYDCKYPIGVQSELREIYQVLN
280 290 300 310 320 330
CY2ab2 820. SQDWPFLYSIFQWNYLNGVFGSARLNTFFNIVGL----PGSTTHALLAARVN-XSG
300 310 320 330 340

40352 FEESPYYDFOQED-----SLTRRPHLFTWLSLNFYEKQTITNNEFFSHYNMWHI
340 350 360 370 380
civ2ab2 820. GISSGDIGASPNNFNGSTLPL-LTPVRSWLDS--GSDREGVATVNMQTSFET
350 360 370 380 390 400

40352	TLDNISQKSVFG-NHNVTDKLSGLATNIIYFLNLSLDKNLYNDYNNISKMDFFII	390	400	410	420	430	440	450	460
rv2ab2	LGLRSAGFTARGNSVFFDYFRINISGVPLVVRNEDLRRLPHVNEIRNIASPGTGGAR	820	410	420	430	440	450	460	

40352	NGTRLLKEKETAGSGQIYDVNKVIFGLPILKLRKRENGNPILFTFYDNY--SHLSLSPFK	450	460	470	480	490	500
rv2ab2	AMVYVNRKNNTTHAVHENGSMTHIALNDYDTGFTTSPHATOVVNO--RTFIFSEKNGOG	470	480	490	500	510	520

40352 SLSIPA-TYKTQVYTFAWTHSSVDPKNTIYTHLT-TQIPAYKANSLGTASKVVQPGHGTG
510 520 530 540 550 560

cry2ab2 820. -DSLRFEQN-NTTARYTLRGNNGSYNLYLRVSSIGNSTIRVTIN---GRVYTATNVNTT

```

cr2ab2_820. -TNNQGVNDGAPSPDINGNVVA-SNSDVPDIN---VTNNSTGFDLMLNMLVFTNIN
570 580 590 600 610 620 630

```

	680
	670
	660
	650
	640
	630

cry2ab2_820. SPLX
40352 REDREKOKLETVOQIINTFYANPIKNTLOSELTDYDIDQANLVCEISEELYPEKEMLL
630 700 710 720 730 740
cry2ab2_820. pep
NR4A:21685485
21685485 source="GENBANK:U00001" pest:crystal protein cry4AA (Bacillus thuringiensis serovar israelensis) [121628] (a) (130 kDa)
crystal protein cry4Aa (insecticidal delta endotoxin cry4Aa) (Crystalline entomocidal protein) (135 kDa crystal protein) [121628] (a) (130 kDa)
insecticidal protein (ISR4) [Bacillus thuringiensis serovar israelensis] [225983] [prf] [1405201B insecticidal protein ISR4]
SCORES Initl: 63 Initn: 199 Opt: 159 Z-score: 175.6 E(): 0.17
>>NR4A:21685485
Initn: 199 Initl: 63 Opt: 159 Z-score: 175.6 E(): 0.17
Smith-Waterman score: 201; 20.8% identity in 630 aa overlap
(57-633:76-681)
cry2ab2_820. PFSQHKSLDVTQKWEKKNHSLYLDPIVGTV-ASF-LLKKVGV-SLVGKRLSELN
21685485 DMLNWCQOQOYGGDFETFDISGELSAYTIIVGVLGTGFTPLGLALIG---FGLLIP
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
cry2ab2_820. LIPPS-GSTNLMQDILRETEKFLNQRNTDILARVNAELTGLQANVEEFNRQVDFLN-P
21685485 VLFPADQOSNTWSDFTQTQKIIKEIASYISNANKILNRSFNSTYHNHLKTWNPP
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
cry2ab2_820. NRNAVPLSITSSVNTMQQLFNLRLPQF-----OMQGYQLLLPLFAQANLHLSFI
21685485 NPQNTQ-DVRTQIQLOVHYHFQNVIPELVNSCPNPSPDCDYNYILVSSYQAQANLHLTVL
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
cry2ab2_820. RDVI-----LNADWEGISAATLRTYRDYLNKYNR---DYSNYCINTYOSAFKGLN-----
21685485 NOAVKFEAYLKNRQFDYLEPLFTAIDYYPVLTKAIEDYNYCVITYK---KGLNLKTT
230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
cry2ab2_820. --TRLDHMLERTYMFNLNFEVVSWSLFKYQSILVSSGANLYASSGPOOT---OSFT
21685485 PDSNLDGNINWNTY---NRYRKMTAVLDLVALFPNDYVGVPGVGOSELTRFIVQLN
280 290 300 310 320 330 340 350 360 370 380 390 400
cry2ab2_820. SODWFLYSLFQVNSVNLNGFSGARLNTFPNIVGL----PGSTTHALLAARVN-YSG
21685485 FEESPXYVDFOYQED-----SLTRRPHLFTWLDLSLNFYKQAQITPNPFTSHYMFHY
340 350 360 370 380 390 400
cry2ab2_820. GISSGDIGASPNONFNCSTFLPL-LTPFVRSLDS--GSREGVAIVTWQTESFEIT
21685485 TLDNISQKSSVFG-NHNVTDKLSGLATNIYIFELNVLKSLONKYLNDYNNYSKMOFFIT
390 400 410 420 430 440

cry2ab2_820. LGLRSGAFTARGSNFYDFYIRNIGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGAR
21685485 NGRTRLEKEITAGSGOITTYVNNKNIIFGLPIKRRNQGNPTLFFTYDNY---SHILSPFK
450 460 470 480 490 500
cry2ab2_820. AYMSVNRKNNIHAVHENGSMIHLANDYTGFTISPIHATQVANO--TRTFISEKFGNOG
21685485 SUSIPA-TYKIQVITFAWTHSSVDPKNTIYIHLT-TQIPAVKANSLGTASKVVOQFGHTG
510 520 530 540 550 560 570 580 590 600 610 620
cry2ab2_820. -DSLRFEON-NTTARYTLRGNGSNYLVRSVNSIGNSTIRVTIN---GRVYATNVNIT
21685485 GLIDFKDHFKITCOHS--NFQOSYFIRIRYASNGSANTRAVINLSIPGVAELGMALNPT
570 580 590 600 610 620
cry2ab2_820. -TNNQGVNDNGARPSDINIGNVVA--SSNSDVPLDIN---VILNSGTQFDLMNIMLVPTNI
21685485 FSGTDITNLKQDFQYLEFSENEVPAPNQISLVFNRSVDVNTVITVLIDKIEFLPITRSI
630 640 650 660 670 680
cry2ab2_820. SPLX
21685485 REDREKOKLETVOQIINTFYANPIKNTLOSELTDYDIDQANLVCEISEELYPEKEMLL
690 700 710 720 730 740
cry2ab2_820. pep
SW:117544
117544 description="PESTICIDIAL CRYSTAL PROTEIN CRY4AA (INSECTICIDIAL DELTA-ENDOTOXIN CRY4Aa)" (Crystalline entomocidal protein) (135 kDa crystal protein) [121628] (a) (130 kDa)
source="swissprot:prot" version="NA type=PRT
SCORES Initl: 63 Initn: 199 Opt: 159 Z-score: 175.6 E(): 0.17
>>SW:117544
Initn: 199 Initl: 63 Opt: 159 Z-score: 175.6 E(): 0.17
Smith-Waterman score: 201; 20.8% identity in 630 aa overlap
(57-633:76-681)
cry2ab2_820. PFSQHKSLDVTQKWEKKNHSLYLDPIVGTV-ASF-LLKKVGV-SLVGKRLSELN
117544 DMLNWCQOQOYGGDFETFDISGELSAYTIIVGVLGTGFTPLGLALIG---FGLLIP
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
cry2ab2_820. LIPPS-GSTNLMQDILRETEKFLNQRNTDILARVNAELTGLQANVEEFNRQVDFLN-P
117544 VLFPADQOSNTWSDFTQTQKIIKEIASYISNANKILNRSFNSTYHNHLKTWNPP
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
cry2ab2_820. NRNAVPLSITSSVNTMQQLFNLRLPQF-----OMQGYQLLLPLFAQANLHLSFI
117544 NPQNTQ-DVRTQIQLOVHYHFQNVIPELVNSCPNPSPDCDYNYILVSSYQAQANLHLTVL
170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400

```
>>NRAA:17977981
initn: 122 init1: 82 opt: 152 z-score: 171.5 expect(): 0.29
Smith-Waterman score: 173; 20.8% identity in 212 aa overlap
(70-263:86-297)

cry2ab2_820. KENTWKKNNHSLVDPVIGTVASFLKKVGLVSK--RLSELNLIFFSGSTINLMQDI
              40 50 60 70 80 90
17977981 PLCTIDTDSKLVAIAKVIAGFAFKSMFGCAAVGLVSKFSFTIIPILWPKDKPIWKEF
              60 70 80 90 100 110
              120 130 140 150
cry2ab2_820. LRETEKFLNQSLNTDLA---RVNAELTGLQANVEEFNRQVDNFPNRNAVPLSITSS
              100 110 120 130 140 150
17977981 TKGQLFRPELGRDAIEIIGNDVQAEVNSLEIMMRDFENKFANWESNRTFANAIAVTTA
              120 130 140 150 160 170
              180 190 200 210 220 230
cry2ab2_820. VNTMQQLFNLRFQFMQGYQL-LLLPLFAQAANLHLSFIRDVILNADEW-----GIS
              160 170 180 190 200
17977981 FSTVNTQIIRLKERFLIAPENRPAFLNLYAQTANIDILLYQSGVYGDKWADINNRSTS
              180 190 200 210 220 230
              240 250 260 270 280 290
cry2ab2_820. AALRTYRDYLNKTRDYSNYCINTYQSAFKGLNTRLH---DMLE-FSTYMLNVEYVS
              210 220 230 240 250 260
17977981 PFSSKDYQSLGKIKDYNTNYCAETIRNSLTILKAKPHIQWIDYRNYRREALGLDLVA
              240 250 260 270 280 290
              300 310 320 330 340 350
cry2ab2_820. IWSLFKYQSLVSSGANLYASGSGPQQTQSQTSDQWPFYLSLFQVNSNYLVNFGSGARLS
              270 280 290 300 310 320
17977981 LFNVDYICYPYPTQRTLTETKRYKVPYFYLQALQORDIETVENQLTHPPSLFTLWLNELNY
              300 310 320 330 340 350
              360 370 380 390 400 410
cry2ab2_820.pcp
NRAA:50285081
50285081 source="GENBANK_PROT" unnamed protein product [Candida glabrata
glabrata]gi|49524271|emb|CAG57862.1| unnamed protein product [Candida glabrata
CBS138]

SCORES Init1: 37 Initn: 37 Opt: 144 z-score: 167.1 E(): 0.51
>NRAA:50285081
initn: 37 init1: 37 opt: 144 z-score: 167.1 expect(): 0.51
Smith-Waterman score: 144; 26.7% identity in 191 aa overlap
(430-607:5-189)

cry2ab2_820. ESFETTLGLRSGAFTARGNSNYFPDYFIRNISGVPLVVRNEDLRRLP-HYNEIRNIASPS
              400 410 420 430 440 450
50285081 MPCKIISIPFLAQNEDMDRYLVKYNEKNTKENS
              10 20 30
              460 470 480 490 500 510
cry2ab2_820. GTPGGARAYVSVHNRKNNIHAVH--ENGSMIHLAPNDYTGFTTISPIHATQNNQTRTFI
              460 470 480 490 500 510
50285081 NASNAANNSR-SRRHGVNFRHFHYAKNGFGNSMV-DLSLYFNNRNFNAP-VSSSTNNEM
              40 50 60 70 80 90
              520 530 540 550 560
cry2ab2_820. SEKFGNGQSLRF-----EQNNTTARYTLRGNGNSYNLYLRVSSIGNSTIRVTING
              520 530 540 550 560
```

50285081
GNKINJNENSKYNGYXNDPGQSNLLMATTQLQAAYS-QLYYNVANKGNEANVA-SG

[illegible]crv2ab2 820. MLVPTNISPLY
630

50285081
FETLSRSGSLNTYSRNEALMFLDOLLSNSNSPYBFGKTDSDMDTKGMKNLNIEH
210 220 230 240 250 260

cry2ab2_820.pep
NRAA:26554299

26554299 source="GENBANK_PROT" hypothetical protein M928450 [Mycoplasma penetrans HF-2]g|2645308[dbj|BAC44637.1| conserved hypothetical protein [Mycoplasma penetrans HF-2]

```

SCORES      Init1: 48      Initn: 48      Opt: 147      Z-score: 162.5 E(): 0.93
>>NRAA:26554299
Init1: 48      Initn: 48      Opt: 147      Z-score: 162.5 expect(): 0.93 (1084 aa)
Smith-Waterman score: 162; 21.4% identity in 429 aa overlap
(249-616;424-831)

```

crv2ab2_820_YTRDYSFYCINTQSAFGLNTRIHDMLPRTYMFANVFVYSIWSLFXQS-----L
220 230 240 250 260 270
TSNGNIYGYDVDSQNALTPSFIROSTTSDKQFYELLPILSVGSGTQFLGLQQNKKSINPL
26554299 : ::::: :

```

cry2ab2_820..LVSSGANLYASGGPQQTQSTSDWFLYSLFQVNSWVLNGSGARLNTFPPIVGLP
280          290          300          310          320          330
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
VNOGSGVQVSSGGAMVLRKNVYRTNNVTKWAF-CKNYLPSSSTFWTSVSVF-DISSIN
26554299

```

```

      340          350          360          370
cry2ab2_820. GSTTHALLAARVNVSGIGSSGDICAS-----PNQNFNCSTFLPPLL---TTPVFPSW
      :|::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
ATTSFSL-ASQVNNNDGTLSPRTFTSYVNSLGNLSGFSTFYINGLYDFESSNPFVSFW
26554299

```

```

390      cry2ab2_820. LDGS-----DREGVATVNQTSFETTLGLSGAFTARGSNFYFDYIRINISGVPLV    430
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : : : : : : : : : : : : : : : : : : : : : : : : :
          ||| |         : : : : ~~~~~~GNOIARTDIENFIYSVTIKKVDGTGIT    470
          ||| |         : : : : ~~~~~~GNOIARTDIENFIYSVTIKKVDGTGIT    510
          ||| |         : : : : ~~~~~~GNOIARTDIENFIYSVTIKKVDGTGIT    550
          ||| |         : : : : ~~~~~~GNOIARTDIENFIYSVTIKKVDGTGIT    590
          ||| |         : : : : ~~~~~~GNOIARTDIENFIYSVTIKKVDGTGIT    630

```

[illegible]

```

cry2ab2_820.  APNDYGTFTSPIHATQVNNQIRTFISEKFGNQDGLRFEQNNTTARYT 500 510 520 530 540
               : | | | : : : | | : : | | : : | | : : | | : : | | :

```

26554299 SSVNST-FTKT-IYPSQL---TKTQVINFLNVGSSISKNNDSWITISEADDIKGTLKL
690 700 710 720 730

```

cy2ab2_820.  YNLYRVSSIGN-STIRVINGRYVATNNTVNDGVNGARFSDINIGNVASSNS
550 560 570 580 600
SVSNKTSQITNFSPLDITQITQITATEVYVSFKISSNSGWS---MPNVITDFNGT
740 750 760 770 780 790
26554299

```

cry2ab2_820. DVPLDI-----NVTLSGTQFDLMNIMLVPTNISPLY
610 620 630

26554299 YLPSEIWGQYKAYINGLVNESDVILLKNINFILTSISNLNIVCLNENSCDSGYLDLQIS

26554299 IKDGSKTVDYDGTQYTTSDGKLVFSSEFLANSGITPYKQVWNITTANKYFYIVDRKTN 860 870 880 890 900 910

cry2ab2_820.pep
NPAA_66821693

66821693 source="GENEBANK_PROT" hypothetical protein DDB0217588 [Dictyostelium discoideum]gi|128828526|gb|AAO51134.1| similar to Dictyostelium discoideum (slime mold). Homeobox-containing protein (Fragment)gi|160472437|gb|EAL70390.1| hypothetical protein DDB0217588 [Dictyostelium discoideum]

```

SCORES      Inl1: 80      Inltn: 105      Opt: 145      z-score: 160.1      E(): 1.3
>>NPAA:66821693
Inl1: 105      Inltn: 80      Opt: 145      z-score: 160.1      expect(): 1.3
Smith-Waterman score: 145;      25.8% identity in 159 aa overlap
NPAA:66821693-A111

```

500
 490
 480
 470
 460
 450
 440
 430
 420
 410
 400
 390
 380
 370
 360
 350
 340
 330
 320
 310
 300
 290
 280
 270
 260
 250
 240
 230
 220
 210
 200
 190
 180
 170
 160
 150
 140
 130
 120
 110
 100
 90
 80
 70
 60
 50
 40
 30
 20
 10
 0

[illegible]

~~cry2ab2_820..TIRVTNGRYVYATNVTTTNDGARGFSSIMGVAS--SNSQVPIDINVNTIN~~

620 630

[illegible]

cry2ab2_820.pep
NRAA:37527939

37527939	source="GENBANK_PROT"	hypothetical protein plu4092	[Photorhabdus
luminescens	subsp. laumondii	TT01 gi 36787375 emb CA216464.1	unnamed protein

Figure 1 is a line graph showing the number of cases of COVID-19 in the United States from March 2020 to March 2021. The y-axis is labeled "Number of cases" and ranges from 0 to 1,400,000 in increments of 200,000. The x-axis is labeled "Date" and shows dates from March 2020 to March 2021. The graph shows a sharp increase in cases starting in March 2020, peaking in May 2020 at approximately 1,350,000 cases, followed by a decline and then a second, smaller peak in November 2020 at approximately 1,100,000 cases. Cases then decline again, with a small uptick in March 2021.

cry2ab2_b20.pep
 NR04:50309745
 50309745|source="GENBANK|PROT|unnamed protein product|kluyveromyces
 lacticis|accession=U05644|emb|CAG99972.1|unnamed protein product|kluyveromyces lacticis

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NR04_1-11401

SCORES Initl: 45 Initn: 45 Opt: 132 z-score: 153.2 E(): 3.1
>>NR04:50309745 (374 aa)
initn: 45 initl: 45 opt: 132 z-score: 153.2 expect(): 3.1
Smith-Waterman score: 132; 23.0% identity in 164 aa overlap
(470-625:31-187)

cry2ab2_820. EDRLRLHYNEIRINSPSGTGGARVWVYHNRKKNTHKENGSMIHLAPNDYTGFT 440 450 460 470 480 490
50309745 MPQGLVNVFFSVEQEDMDYLRKPLTKQKQSGQNHYPQAAHRYNSQVKNNGHYSSYT 450 460 470 480 490
cry2ab2_820. ISPIHATVNNQTRFISEKFGNGDGLRFRQNTATRYKRGNGSNLYLR--VNSIG 500 510 520 530 540 550
50309745 NSQ-HQNQ--HQOHNRKKNYNN-GITFT-QNNYNYKATVQOENALYKQOQOQSVTSWY 510 520 530 540 550

cry2ab2_820. NSTIRVTINGRYVATVNTITNNDGVNDN-----GARFSDINTINGVVA--SSNDVFPQD 560 570 580 590 600 610
50309745 NKSVHQOITYSSGYA-GYNSTNSYSSNSIGNANFNVAHLNDTNGNDNGYNNI-TPTDGG 560 570 580 590 600 610

cry2ab2_820. NVTLNSGTQFDLMIMLVPTNISPLY 620
50309745 NSAHNSLSLQNLGNNVNNMSQLPASHIPFSPSTSVTPPTPSRLSLSLSSVSGSSVS 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
NR04:6435735

6435735 source="GENBANK_PROT" Chain A, Crystal Structure Of Invasin: A Bacterial Integrin-Binding Protein

SCORES Initl: 67 Initn: 67 Opt: 133 z-score: 152.4 E(): 3.4
>>NR04:6435735 (492 aa)
initn: 67 initl: 67 opt: 133 z-score: 152.4 expect(): 3.4
Smith-Waterman score: 139; 21.0% identity in 262 aa overlap
(393-636:1-259)

cry2ab2_820. NFNCSTFLPLLTPTFVRSWLDGSDREGVATVNNQTESPETTLGRSGARTAGNSNYF 370 380 390 400 410 420
6435735 SVTVQQQLTLTAIVIGDGA-PANGKTAIT 370 380 390 400 410 420

cry2ab2_820. PDYFIENISGVPL-----VVRNEDLRPLHYNEIRN---IA--SPSGTPGGARVWVSVH 430 440 450 460 470
6435735 VFTVADFEKGLAQEQEWITNNGALPNKITEKTANGVARIALTNTTGDVTVVTAEE 430 440 450 460 470

cry2ab2_820. NRKNHIAVHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTF-ISEKFGNQ--GDSLRF 480 490 500 510 520
6435735 GQKQSVDTHFVKGTTIA--ADKSTLAAVPTSIIADGLMASTITLLEKDYTGDPQAGANVAF 480 490 500 510 520

cry2ab2_820. EQNNTATRYTLRGNGSNLYLRVSSIGNSTIRVTINGRYVATVNTITNNDGVNDN- 530 540 550 560 570 580
6435735 DTILGNMGVITDHDNGTYSAPLTSTTLGVAITVVKVGAAPSVPSVTVNTADPIPDAGR 530 540 550 560 570 580

cry2ab2_820. ARPS-----DINIGNVAVASSNDVPLDINVTLSNGTQFDLMIMLVPTNISPLY 590 600 610 620 630
6435735 SFTVSTPDIADGIMSSTLSFVPVDKNGHFISGMQGLSFTONGVPSVISPITEQPDYSY 590 600 610 620 630

6435735 ATVVGNSVDVITTPQVDTLILSTLQKKISLFFVPTLTGLVNGQNFATDKGPKTIFKN 270 280 290 300 310 320 330

cry2ab2_820.pep
NR04:41055126

41055126 source="GENBANK_PROT" similar to dual specificity phosphatase 4 [Danio rerio]gi|3085156|gb|AAH52477.1| similar to dual specificity phosphatase 4 [Danio rerio]gi|6839699|ref|XP_707628.1| PREDICTED: similar to Dual specificity protein phosphatase 4 (Mitogen-activated protein kinase phosphatase-2) (MAP kinase phosphatase-2) (MKP-2) (Dual specificity protein phosphatase RVH2) isoform 2 [Danio rerio]gi|6839699|ref|XP_684742.1| PREDICTED: similar to Dual

SCORES Initl: 59 Initn: 59 Opt: 130 z-score: 151.1 E(): 4
>>NR04:41055126 (367 aa)
initn: 59 initl: 59 opt: 130 z-score: 151.1 expect(): 4
Smith-Waterman score: 137; 23.0% identity in 270 aa overlap
(48-337:93-348)

cry2ab2_820. VGTVAFLKLVKGVSGVGRILSELRLNLIFFPSGNTLMQDILRETEKFLNQLNTIARV 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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cry2ab2_820. ALLAAVNYSGISGDIAGSPNQNFNCSTFLPPLITPPVRSWLDSSGSDREGVATVNW
41055126 NQPSLTVLQSPITTSPC
350 360 370 380 390

cry2ab2_820.pep
NRAA:66805041

66805041 source="GENBANK_PROT" hypothetical protein DB0219415 [Dictyostellium
discoideum]gi|60464691|gb|EAL62818.1| hypothetical protein DB0219415
[Dictyostellium discoideum]

SCORES Init1: 101 Initn: 128 Opt: 133 z-score: 151.0 E(): 4.1
>>NRAA:66805041 (593 aa)
initn: 128 init1: 101 opt: 133 z-score: 151.0 expect(): 4.1
Smith-Waterman score: 139; 20.8% identity in 212 aa overlap
(140-327:91-297)

cry2ab2_820. NTDTLARNVNAELTGLQANVEFNQVDNPLNPNNAVPLSLTSSVNTMOQLFLNRLPQ--
66805041 LEKIEIVQGNVFSNFTITSYDSRTLWKNPNDSITKKNLSDSDNLEDILRXYLNSS
70 80 90 100 110 120

cry2ab2_820. -FOMQGYQLLLPLFAQAANLHLSFIRDVILNADENWGISAAITLYR-----DYLKN
66805041 VFTKGLYSTLMFLFAMATLIILLRDGITNGLSWGMSGENREYKFFSTCITDVKH
130 140 150 160 170 180

cry2ab2_820. YTRDYSNICYQSAFKGINTLHDMLEFRTYMFNVFYSVMSLFKYOSLLVSSGAN
66805041 LXAHDVCTEIRSKSEFG-KSKFDSIVCINSHSFIKT-KVSTLCS--NYRNVAESVFD
190 200 210 220 230

cry2ab2_820. L-----YASGSGPQQTQSFDQ-----WFFLYSLFQVNSN---YVLNGFSGARLNTFP
66805041 LADSWYSLDNG-KFSKQFSGKNRYLWSSYGLPVDNSKETSIYKVGNIKNYTYTPSYA
240 250 260 270 280 290 300 310 320

cry2ab2_820. NIVGLPGSTTHALLAARVNYSGISGDIAGSPNQNFNCSTFLPPLITPPVRSWLDG
66805041 SUGENFINENDQYKPYAGVKINHDSNWIYSIQIPFKDPLNGRVDGVKGVQVETESLT
300 310 320 330 340 350

cry2ab2_820.pep
NRAA:8928013

8928013 source="GENBANK_PROT" Pesticidal crystal protein cry25Ba (Insecticidal
delta-endotoxin CryxxVa(a)) (Crystalline entomocidal protoxin) (76 kDa crystal
protein) (Insecticidal protein Jegg74)gi|366835|gb|AAC61892.1| insecticidal
protein Jegg74 [Bacillus thuringiensis serovar Jeggathesan]

SCORES Init1: 72 Initn: 129 Opt: 133 z-score: 150.1 E(): 4.6
>>NRAA:8928013 (675 aa)
initn: 129 init1: 72 opt: 133 z-score: 150.1 expect(): 4.6

Smith-Waterman score: 166; 19.9% identity in 589 aa overlap
(100-636:105-661)

cry2ab2_820. GSLVGRILSELRLNLPFGSGNINLMQDILRETEKFLNQRLNTDTLARNVNAELTGLQAN--
8928013 SPSIGDAFALVSSIGEYVETKTSFPLSVADVARNLRIREALDQNAIRATGKFGNGLMDTYN
80 90 100 110 120 130

cry2ab2_820. ---VEEPNRQVDNPL--NPNRNA-VPLSLTSSVNTMOQLFLNRLP-QFOMQGYQLLLPL
8928013 TVYLNQDWDYTRIPANPQGSQSLREARSLSEIEIERDFKALAGEFAEAGSQIVLLPI
140 150 160 170 180 190

cry2ab2_820. FQAANLHLSFIRDVILNADENW-----ISAAITLYRDLKNYTRDYSNYCINTYQ
8928013 YQAQANIHLILKIDAMQFRTDLGLIRPVGVPVITTSADPFSEFLLRIKKYTDHCISYVD
200 210 220 230 240 250

cry2ab2_820. SAFKGLINTLAD-----MLEERTYMFNVFYSVMSLFKYOSLLVSSGANL-YASGSG
8928013 DGLAKIRSGSDGETWWEFNKFRREMTLTVLDLVLPYTHNKLXPIPTQTELSRVVYTD
260 270 280 290 300 310

cry2ab2_820. PQQTQSFTSQMPEFLYSLFQVNSVNLNGFSGARLNTFPNIVGLPGSTTHALLAARVN
8928013 PVGCTGNRKSD---IFS--RLNFDYLENRLTRPREPNVYLNQVLFASVTSNS-----
320 330 340 350 360

cry2ab2_820. YSGGSSGDIAGSPNQNFNCSTFLPPLIT--PF-VRSW-LDSGSDREGVATVNWQ---
8928013 NNGEVLIRNLAKNIMFEGGWTSRSGDGVTTGTTPFTMDWSYCGWYPRKHYAEITSRQAL
370 380 390 400 410 420

cry2ab2_820. ---TESFETTLGL---RSGAFTARGNSNY-FPDYFIRNISGV---PLV-VRNED---LRRP
8928013 PGLNNSIHVIGIDSFRAIGPGSQGDHTFSLPGDMYDCGKVQINPLEDYRNSDHWISDM
430 440 450 460 470 480

cry2ab2_820. LHYNEIRNIAGSPGPGARAYMVSVNHRKNTHAVHENGSMIHLAPNDYTGFTISPIHA
8928013 MTINQSVQLASNPQTQTFAFSALSLGMW-----HSSAGNR-----NVVYDKITQIPA
490 500 510 520

cry2ab2_820. TVNNQTRTISEKFGNQGDSLRFQNNNTIARYTLRNGNS-----YNYLVRVSSIGN
8928013 TKTVREHPIKPGFTG-GDLADLSSNSDILQYDLKSLDDRLTEDVFPFIRIRCASIGV
530 540 550 560 570 580

cry2ab2_820. STIRVTINGRYVYATNNVITTN--DGVNDNGARFSDINIGNVVASSNSDVPFLDINVTLS
8928013 STISVDNNGSSSPQVTVAATAASLDTLKYESFQVVSIP-GNYVYFDSAPTRL-----LRQ
590 600 610 620 630 640

[illegible]

CRY2AB2_820.pep
SW:8928013

	530	550	570	580
8928013 description="PESTICIDAL CRYSTALLIN PROTEIN CRY5AA (INSECTICIDAL DELTA-ENDOTOXIN CRYXA(A)) (CRYSTALLIN BENTHOCIDAL PROTOTOXIN) (76 KDA CRYSTAL PROTEIN) (INSECTICIDAL PROTEIN SEG-4)." library=NA species="Bacillus thuringiensis serovar jegathesan" source="SwissProt protob" version=NA type=PRT				

```

SCORES      Init: 72      In1tn: 129      Opt: 133      Z-score: 150.1      E: 4.6
>SW:8928013      In1tn: 129      In1tl: 72      opt: 133      Z-score: 150.1      expect(): 4.6
Smith-Waterman score: 166;      19.9% identity in 509 aa overlap
(100-636:105-661)
CRY2AB2_820..GTQFDLNMIMLVPTNISPLY
:::      :::::
519..LNMGGSGQFVIVSGHAAALGAGLGGQIVGII 630
6266615      610      620      630      640

```

[illegible]

```

130      140      150      160      170      180
---VEEENRQVDNFI--NPNRNA-VPLSTSSVNTMQQLFLNRLP-QFMQGYQLLLPL
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
8928013 TVYLNKIQYDITRIIPANPQGSQLEAREARRSLEETIERDFKALGEAFAGSQVLLPL
      140      150      160      170      180      190      200      210      220      230

4589753 source="GENBANK_PROT" pectate lyase [Bacillus sp.]
      SCORE= 117.49      Initn= 49      Opt= 128      z-score= 149.3 E(): 5.1
      >>NR4_058753
      Initn= 49      Init1= 49      Opt= 128      Z-score= 149.3 expect(): 5.1
      Smith-Waterman score= 128.21      21.3% identity in 230 aa overlap

```

~~8928013 YAOAMNHILLKDMQFRTDLGRIPGVPTTSAEDPFESEFLRIKKYTHDCLISYYD
200 210 220 230 240 250
CRY2ab2.820 LDGSDRGVATVTWQTESFFMLGURGAFTARGNSNYPDPYFRNRISGVPLVRNRD
360 370 380 390 400 410 420 430 440
4589753 NERKIDDTGTSCYSANKIDVTNTNVSVIGVGKTGFNGEFGIKVKVRANNIRN--
90 90 100 110 120 130 140~~

[illegible][illegible][illegible]

TYNPPYNYISLLNNVKNVSEVINSAGVGKNP | 4589753 500 490 480 470 460 450

320 330 340

cry2ab2_820.pep
NRAA:66825667

66825667 source="GENBANK PROT" hypothetical protein DDB0190469 [Dictyostelium discoideum]gi|60474256|gb|EAL72193.1| hypothetical protein DDB0190469 [Dictyostelium discoideum]

```

SCORES      Init1: 48      Initn: 75      Opt: 133      z-score: 148.0 E(): 6
>>NRAA:66825667
Initn: 75      Init1: 48      Opt: 133      z-score: 148.0 expect(): 695 aa)
Smith-Waterman score: 139;      21.5% identity in 340 aa overlap
(109-625:246-572)

```

```

cry2ab2_820.  LVASGCGPQQTQSTQDWPFLYSIFQNSVNYLVNGFSCALNSLTFFNINVLGFGSTTTTAA
                280    290    300    310    320
66825667      SPSSSITTTTNTTNTTNTLKNPKYGNLSLLINFDPLPGRSFRYSISPKTITFSV
                220    230    240    250    260    270

```

[illegible]

cry2ab₂_820. GVATVNNQTESFETTLGSGAFTAGNSNYFDIFIRNTSLGVPLVVNRDURRLH-Y
+ : : : : : + : : : : : + : : : : : + : : : : : + : : : : : + : : : : :
66825667 GNEIVTVLNDNYY-LYDLKK-N-YSKEYSDLYDFKDSNQKN-----KKKKKRSNHSR
 340 350 360 380

```

450      460      470      480      490
cry2ab2_820.  NEIRNIASPGTFCGAPARWVSVHNRKNH-----AVHENG-----MHLAPNDYTG
66825667      GHSRINSGSGGGRSHRSGSSSSGCGVGSINDSGRPSRSSIVSRITSNSSG-
430      440      450      460      470      480      490

```

```
cry2ab2_820..TSPHATQVNNQTRTFEISEKFGNODSLAEQNNTARYTLRGNGSNLYLRSSGN
      :|::||::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~SSCN
66825667SNDGSGNE-SNKDTF-DSENKNPIFKTGKLNKKRKKRKKAKTDSOISL--SSCSN
```

```
cry?ab2_0z0..SIRVINGRYTATWNTITDGVNDGARGSDINIGVNASDV.PLOI--NVTL
|.|.: :.: :.:|||.:.: |.: :.: :.: ||.: :.: :.: 
66825667.SSIGSSNSSSSNNN>NNNNNNNNNNNNNNNNNNNNNPITPITSPISLNFDTF
```

```

cry2ab2_820.  NSGTQFDLNMILVPTNISFLY      620      630
      || : : : |
66825667  NSDSPFMKKEEQQEDDKKEIEIKDYKTKDDKEENGINSDENIKEKEEQEEQEG
      570      580      590      600      610      620

```

cry2ab2.820.pep
NPAA:155443
155443 source="GENPANK PROT" invasin C (alt.)

155443 source="GENBANK PROT" invasin C (alt.)

```

SCORES      Intl: 67      Inltn: 98      Opt: 133      z-score: 147.4 E(): 6.4
>>NPPA:15543
inltn: 98      Intl: 67      Opt: 133      z-score: 147.4 expect(): 6.4
Smith-Waterman score: 139; 21.0% identity in 262 aa overlap
(193-636:476-734)

```

```
cir2ab2_820. NFNCSTFLPPLTPFVRSLDGGSRGVAIVTNWQTESFTTIGLRSGAFTARGNSNF  
                :|: |: |: |: |: |: |:  
RVTDLTANFYSLASALVHDQNRSNFTLSVTVOQPQLITAAVIGDGA-PANGKTAIT  
155443          450   460   470   480   490   500
```

```
cry2ab2_B20. PDYFIRNISGVL-----VVRNEDRLRPLHNEIRN---IA--SPSGTGGARAYMVSH
      : : : | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
155443 VEFTVADEPGKPLAGOEVIITNNAGA.PNKITEKTDPANGVARIALNTINTDGVTVTAETVE
```

```

cry2ab2_020. NRKNNIHAVHNGSMTHLAPNDYTGFTSIPIHATQVNNQTRTF.ISKFGNQ--GDSLRFP
::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: ::: :::
GQRQSVDFHFVKGTIA--ADKSTLAAVFTSIADGLMASTITLFLKQTITGDPQAGANAVAF
155443
570 580 590 600 610 620

```

```
cry2ab2_820. EQNNTATYTLRGNGNSLYLURVSSIGNSTIRVTWTKGVYATNNVTNTTNDGVNDG-  
      :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :  
155443 DTTLCNGVIITHDNDGTSGAPLTSTLLGVAIVKVDGAAPSVPSTVFNTAIPIDAGR  
      630    640    650    660    670    680
```

```

590      600      610      620      630
cry2ab2_820. ARFS---DINIGNVASSNDVDINVTNGSTQFDLMNMLVFNINISPLY
155443      SSFTVSTPILADGTSSTLSPVDKNGHFISSMOGLSFTQNGVPVISGIPTEQDPSY
590      600      610      620      630

```

155443 ATVGNNSVDVTTTPQVDLLILSTLQKLSLFPVPLTILGILVNGONFATDKGPKFTIFKN
750 760 770 780 790 800
crv2ab2 820 .pep

155442 source="GENBANK PROT" invasin B (alt.)

```

SCORES      Inil: 67      Initr: 98      Opt: 133      z-score: 147.4      E(): 6.4
>>NRAA.15542
initr: 98      Inil: 67      Opt: 133      z-score: 147.4      expect(): 6.4
Smith-Waterman score: 139; 21.0% identity in 262 aa overlap
(391-636,478-736)

```

```

cry2ab2_820.  NFNCSFTLPPLLTFRSMDSGDREGVATVNWQTESFETTLGSGAFTARGNSFTF
                370      380      390      400      410      420
                |||  |||  |||  |||  |||  |||
RVTDITLNFYSLSALAVDHQGRNSFTSLVQVQPLQLTAAVIGDGA-PANGKTAIT
155442
                450      460      470      480      490      500

```

```

cry2ab_820. PDYFNITSGVPL-----VVRNEDLRPLHNEIRN--IA--SPSGTGGGARAYMVSVH
155442 VFTVADEGKPLAGOWWITNGALPNKITEKDANGVARTALNTDGVVTAAEVE

```


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[illegible]

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[illegible]

CRY2AB2_820.pep
NRAA:58042545
58042545 source="GENBANK" phage ABC transporter-like [Citrobacter sp. MY-5]
SCORES Initl: 54 Initn: 80 Opt: 126 Z-score: 144.1 E(): 9.9
>NRAA:58042545
Initn: 54 Initl: 54 Opt: 126 Z-score: 144.1 E(): 9.9
Smith-Waterman score: 136; 26.0% identity in 173 aa overlap
(379-617:1-250)
CRY2AB2_820. GISSGDIGASPFQNFNCSTFLPPLTPFVSMNSGSDGAGVATVNNWTFESFNLGL
58042545 KSLVDSNN-AGDQKSLHNDGVNDRH
CRY2AB2_820. MVSVHNK-NIHAVHENGSMIHLAPNDYGTFTSPIHATQVNNQRTFISEKFN-----IN
58042545 MIGLDLADATADAVIENNNGTIFANDSFATVLTGVGHVNVGTVIADGVTSGLIK
CRY2AB2_820. QGSLRFEQNTTARTYLRNGNS---YNYLRVSSIGNSTIRVT-----IN
58042545 QGDSINVEGMNGN-----NGNSSEVHYGYTLDPVFKNTVSVTSGSDEAGGSMNEN
CRY2AB2_820. GRVYATNTNTNDGND---NGARFSDINIGNVASSNSDVPLDINVLNSGTQFDL
58042545 GYV-VGINVNGSAGKLVNNSMNGVESVEINGTAGTADTTVSFD-NVVEGSNLTAD
CRY2AB2_820. MNIMLVPTNISPLY
58042545 AITSTSVVATKAGSTDASGNVDVTMSKNAYTDVATDASVNDIAKALDAGYTNNELFTSLN
CRY2AB2_820.pep
NRAA:68350387
68350387 source="GENBANK PROT" hypothetical protein TP03_0414 [Theileria parva]gi|71027581|ref|XP_763434.1| hypothetical protein TP03_0414 [Theileria parva]
SCORES Initl: 80 Initn: 108 Opt: 126 Z-score: 144.1 E(): 9.9
>NRAA:68350387
Initn: 108 Initl: 80 Opt: 126 Z-score: 144.1 E(): 9.9
Smith-Waterman score: 126; 26.0% identity in 173 aa overlap

(452-612:113-278)
CRY2AB2_820. PPDYFTRISGVPVLVVRNEDLRRLPHYNEIRNIASPSGTGGGARAYMVSVHNRKNNIHAV
68350387 TGDNTSNTENTQNTQNAQANTENTGYTQNTONNGSVTGMGYGIPMGVYMSPIYAT
CRY2AB2_820. HE--NGSMIHLAPNDYGTFTSPIHATQVNNQRTFISEKFNQGSLSRFE---QNNTTA
68350387 FTVPDITDTCNDPNTN---TAGVDDITPLVNNLGTFFSVRFITAVNSFISNLGTPTNTY
CRY2AB2_820. RYTLRNGNSYNYLYRVSSISGNSITIRVTI-----NGRVYATNTNTNDGVNDNGAR
68350387 TYTNTFPNT-NYANTGTNTNTSYTFFSTPGSNRYRVYNTSNTQNTNTNTNDSNVN
CRY2AB2_820. FSDINIGNVASSNSDVPL-DINVLNSGTQFDLMNIMLVPTNISPLY
68350387 TNNITDTTNVAS---DVPTADINTDLSLPHTVSDPNARMEELINEFEKIERLIGDVINSI
CPU time used: 0:08:58.5
Database scan: 0:00:19.5
Post scan processing: 0:09:38.1
Total CPU time: 0:09:56.1
Output File: cry2ab2_820_allpeptides

Distributed over 1 thread.
Start time: Mon May 1 16:43:57 2006
Completion time: Mon May 1 16:51:34 2006

Information of Monsanto Company

Title

Assessment of the *in vitro* Digestibility of the Cry1A.105 Protein in Simulated Gastric Fluid

Authors

Shefalee A. Kapadia, Elena A. Rice, Ph.D.

Study Completed On

November 2, 2005

Performing Laboratory

**Monsanto Company
Product Characterization Center
800 North Lindbergh Boulevard
St. Louis, Missouri 63167**

Laboratory Project ID

**MSL-19929
Study 05-01-62-02**

The text below applies only to use of the data by the United States Environmental Protection Agency (US EPA) in connection with the provisions of the Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA).

Statement of No Data Confidentiality Claim

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA § 10(d)(1)(A), (B), or (C).

We submit this material to the United States Environmental Protection Agency specifically under the requirements set forth in FIFRA as amended, and consent to the use and disclosure of this material by EPA strictly in accordance with FIFRA. By submitting this material to EPA in accordance with the method and format requirements contained in PR Notice 86-5, we reserve and do not waive any rights involving this material that are or can be claimed by the company notwithstanding this submission to EPA.

Company: Monsanto Company

Company Agent: _____

Title: _____

Signature: _____ Date: _____

Statement of Compliance

This study meets the US EPA Good Laboratory Practice requirements as specified in 40 CFR Part 160.

Submitter: _____

Date: _____

Sponsor
Representative: _____

Date: 11/2/05

Study Director: _____

Date: 11/02/2005

001 Proprietary Information of Monsanto Company

Quality Assurance Statement

Study Title: Assessment of the *in vitro* Digestibility of the Cry1A.105 Protein
in Simulated Gastric Fluid

Study Number: 05-01-62-02

Reviews conducted by the Quality Assurance Unit confirm that the final report accurately describes the methods and standard operating procedures followed and accurately reflects the raw data of the study.

Following is a list of reviews conducted by the Monsanto Regulatory Quality Assurance Unit on the study reported herein.

Dates of Inspection / Audit	Phase	Date Reported To:	
		Study Director	Management
08/04/2005	Digestive Fate	08/04/2005	08/04/2005
07/27/2005	Western Blot	08/04/2005	08/04/2005
10/19/2005	Raw Data Audit	10/25/2005	10/25/2005
10/19/2005	Draft Report Audit	10/27/2005	10/27/2005

Jean M. Rejda-Heath
Quality Assurance Unit
Monsanto Regulatory, Monsanto Company

November 2, 2005
Date

Study Information Page

Study Number: 05-01-62-02

Title: Assessment of the *in vitro* Digestibility of the CryIA.105 Protein in Simulated Gastric Fluid

Primary Testing Facility: Monsanto Company
Product Characterization Center
800 North Lindbergh Boulevard
St. Louis, MO 63167

Study Director: Elena A. Rice, Ph.D.
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800 North Lindbergh Boulevard
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Principal Investigator: Shefalee A. Kapadia
Monsanto Company
Product Characterization Center
800 North Lindbergh Boulevard
St. Louis, Missouri 63167

Study Initiation Date: July 15, 2005

Study Completion Date: November 2, 2005

Records Retention: All study specific raw data, protocol, amendments, deviations, final report, and facility records will be retained at Monsanto, St. Louis.

Specimen Retention: Specimens will be retained at Monsanto, St. Louis, as specified in section 5.2.

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Study Certification Page

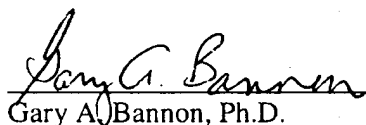
The results reported in this Final Report accurately reflect the data generated under study number 05-01-62-02.

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Abbreviations¹

CEW	Corn earworm
CFR	Code of Federal Regulations
DF	Dilution factor
EC ₅₀	Effective protein concentration to inhibit the growth of the target insect by 50%
ECL	Enhanced chemiluminescence
<i>E. coli</i>	<i>Escherichia coli</i>
EPA	Environmental Protection Agency
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act
HRP	Horseradish peroxidase
IgG	Immunoglobulin G
LOD	Limit of Detection
ILSI	International Life Science Institute
LB	Laemmli buffer
MALDI-TOF MS	Matrix assisted laser desorption/ionization – time of flight mass spectrometry
NFDM	Non-fat dry milk
PBST	Phosphate buffered saline containing Tween-20
SDS-PAGE	Sodium dodecyl sulfate-polyacrylamide gel electrophoresis
SGF	Simulated gastric fluid
SOP	Standard operating procedure
T	Time
TCA	Trichloroacetic acid
US	United States
1 × LB	Laemmli buffer [62.5mM Tris-HCl, 5% (v/v) 2-mercaptoethanol, 2% (w/v) sodium dodecyl sulfate, 0.005% (w/v) bromophenol blue, 10% (v/v) glycerol, pH 6.8].
5 × LB	Five times concentrated 1 × LB

¹ Standard abbreviations, e.g. units of measure, concentration, mass, time, etc., are used without definition according to the format described in "Instructions to Authors" in The Journal of Biological Chemistry.

1.0 Summary

Monsanto has developed plants that produce the Cry1A.105 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* Cry1A protein with 93.6 % overall amino acid sequence identity to the Cry1Ac protein.

The purpose of this study was to assess the *in vitro* digestibility of the Cry1A.105 protein in simulated gastric fluid (SGF) containing the proteolytic enzyme pepsin. The Cry1A.105 protein used in this study was produced in and purified from *E. coli*. The *E. coli*-produced Cry1A.105 protein was characterized prior to the digestibility study. Digestibility of the Cry1A.105 protein in SGF was assessed using stained SDS-polyacrylamide gel and western blot analysis.

The results of this study demonstrated that the full-length Cry1A.105 protein was rapidly digested during incubation in SGF. At least 99.3% of the full-length Cry1A.105 protein was digested within 30 seconds when analyzed using Colloidal Brilliant Blue G stained polyacrylamide gels. Greater than 95% of the Cry1A.105 protein was digested in SGF within 30 seconds when specimens were analyzed using western blot. A faint ~4.5 kDa band was observed between the 30-second and 20-minute digestion time points when analyzed using a Colloidal Brilliant Blue G stained polyacrylamide gel. Neither this band, nor any other immunoreactive band was detected using western blot analysis.

2.0 Introduction

Monsanto has developed plants that produce the Cry1A.105 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* Cry1A protein with 93.6 % overall amino acid sequence identity to the Cry1Ac protein.

Currently, proteins introduced into commercial food crops through the techniques of biotechnology are evaluated for safety, including an assessment of the potential to be allergenic. One aspect of this assessment includes analysis of the digestibility of the target protein in an SGF assay containing pepsin. The correlation between protein allergenicity and protein stability in an *in vitro* pepsin digestion assay has been previously established (Astwood et al., 1996). Proteins that are highly digestible are expected to be less likely to cause sensitization or allergenic reaction when consumed. Recently, the International Life Science Institute (ILSI) standardized the pepsin digestibility assay protocol in a multi-laboratory evaluation (Thomas et al., 2004). The SGF formulation, time course, and experimental parameters used in this study followed the conditions used in the ILSI multi-laboratory evaluation.

3.0 Purpose

The purpose of this study was to assess the stability of the Cry1A.105 protein in simulated gastric fluid containing the proteolytic enzyme pepsin.

4.0 Materials

4.1 Test Substance

The test substance was the Cry1A.105 protein. The Cry1A.105 protein (Analytical Protein Standard lot 20-100073) was isolated from a fermentation batch of *E. coli* containing pMON96851 expression plasmid. This protein has been characterized and has a total protein concentration of 1.2 mg/ml and a purity of 92 %. Functional activity was confirmed using an insect bioassay with the larvae of a susceptible pest, corn earworm (CEW). The EC_{50} value was 5.8 ng/ml of diet. Prior to its application to the test system, the test substance was stored in a -80°C freezer in a test substance storage buffer containing 25 mM CAPS, 1 mM benzamidinium-HCl, 0.1 mM EDTA, and 0.2 mM DTT, pH ~10.3.

4.2 Control Substance

There was no control substance for this study.

4.3 Reference Substance

There was no reference substance for this study. Analytical reference standards (e.g., molecular weight markers) used in this study were documented in the data and are described in this report.

4.4 Characterization of the Test Substance

The characterization of the physicochemical and functional properties of the test substance was performed under characterization plan 20-100073 and is described on the Certificate of Analysis. The following properties were established for the Cry1A.105 protein: identity (N-terminal sequencing, MALDI-TOF mass spectrometry (MS), immunodetection), concentration (amino acid analysis), purity (SDS-PAGE/densitometry), molecular weight (SDS-PAGE/densitometry, MALDI-TOF MS), stability (SDS-PAGE/densitometry) and activity (CEW bioassay).

5.0 Test System

The test system for this study was simulated gastric fluid (SGF) that contains the proteolytic enzyme pepsin. The SGF was prepared using a highly purified form of pepsin (Catalog number P-6887, Sigma Company, St. Louis, MO). The SGF was formulated so that ten units of pepsin activity per microgram of total protein from the test substance would be present in the digestion reactions. The amount of pepsin powder used to

prepare SGF was calculated from the specific activity reported on the product label. One unit of activity is defined as a change in $A_{280\text{ nm}}$ of 0.001 per minute at 37 °C, measured as trichloroacetic acid (TCA) soluble products using hemoglobin as the substrate. The stock SGF solution was prepared by adding pepsin powder (26.6 mg) to 33.2 ml of an acidic sodium chloride solution (2 mg/ml NaCl, 10 mM HCl, pH 1.3). After the activity of pepsin in SGF was confirmed, the stock SGF solution was diluted to provide approximately 1500 units pepsin activity/ml of solution.

5.1 Justification for Selection of the Test System

In vitro digestion models are used widely to assess the nutritional value of ingested proteins based on their amino acid bioavailability. Also, the correlation between protein allergenicity and protein stability in an *in vitro* pepsin digestion assay has been previously established (Astwood et al., 1996). Recently the pepsin digestibility assay protocol was standardized by ILSI in a multi-laboratory evaluation test (Thomas et al., 2004). This multi-laboratory test showed that results of the *in vitro* pepsin digestion assay are reproducible when a common protocol is followed. The SGF formulation, time course, and experimental parameters used in this study followed the conditions used in the ILSI multi-laboratory evaluation test.

5.2 Specimens

Specimens were generated by incubating the test substance with the test system for the times specified in section 5.3. See Sections 6.0 through 7.0 for details on the preparation and analysis of specimens. Specimens will be retained in a -80 °C freezer one year, after which they will no longer afford analytical evaluation and may be discarded.

5.3 Procedure for Identification of Specimens

Alphanumeric codes were used to distinguish incubation time points: (where T = time, P = protein only, and N = no protein):

<u>Targeted Incubation Time Point</u>	<u>Designation(s)</u>
0 min	T0, P0, N0
30 sec	T1
2 min	T2
5 min	T3
10 min	T4
20 min	T5
30 min	T6
1 h	T7, P7, N7

6.0 Experimental Design

6.1 Digestibility of the Test Substance in SGF

Digestion of the test substance in SGF was evaluated over time by analyzing specimens from all incubation time points. The target digestion temperature was $37 \pm 2^\circ\text{C}$.

The test substance protein was diluted to 0.6 mg total protein /ml by mixing 200 μl of the protein at 1.2 mg/ml and 200 μl of storage buffer (25 mM CAPS, 1 mM benzamidine-HCl, 0.1 mM EDTA, and 0.2 mM DTT, pH 10.3) and then heated at 44.5°C for 10 minutes. Digestion samples were prepared by adding 200 μl of the diluted test substance to a tube containing 800 μl of SGF. The tube contents were vortex mixed and immediately placed in a 37.2°C water bath and subsequently vortex mixed every 30 - 60 sec throughout the digestion experiment. Samples (100 μl) were removed at targeted times of 0.5, 2, 5, 10, 20, 30, and 60 min (specimens T1 to T7, respectively) and placed in a tube containing quenching mixture. Quenching mixture contained 35 μl of carbonate buffer [700 mM Na_2CO_3 , pH 11.0], and 35 μl of 5 \times Laemmli buffer (LB) [312.5 mM Tris-HCl, 25% (v/v) 2-mercaptoethanol, 10% (w/v) sodium dodecyl sulfate, 0.025% (w/v) Bromophenol Blue, and 50% (v/v) glycerol, pH 6.8].

The zero incubation time point (T0) was prepared in a separate tube. SGF (80 μl) was quenched by adding 35 μl of carbonate buffer and 35 μl of 5 \times LB prior to the addition of 20 μl of the diluted test substance.

All quenched samples were heated to $75\text{-}100^\circ\text{C}$ for 5-10 min, frozen on dry ice, and stored in a -80°C freezer until analyzed.

6.2 Experimental Controls

Experimental controls were prepared to determine the stability of the test substance in the test system buffer lacking pepsin [10 mM HCl, 2 mg/ml NaCl, pH 1.3]. These experimental controls were identified with the letter "P". The zero incubation time point (P0) was prepared in a separate tube. Test system buffer (80 µl) was quenched by addition of 35 µl of carbonate buffer and 35 µl of 5× LB prior to the addition of 20 µl of the diluted test substance. The 60 min incubation time point (P7) was prepared by adding 20 µl of the diluted test substance to test system buffer lacking pepsin (80 µl). The tube was vortex mixed and immediately placed in a 37.1 °C water bath. After 60 min of incubation, the sample was quenched by addition of 35 µl of carbonate buffer and 35 µl of 5× LB.

Additional experimental controls were prepared to evaluate the stability of the pepsin in the test system (SGF) lacking the test substance and to determine if non-specific interaction occurs between the test system components and the antibodies during western blot analysis of the specimens. These experimental controls contained an aliquot of the test system incubated with test substance storage buffer instead of the test substance and were identified with the letter "N". The zero incubation time point (N0) was in a separate tube. Test system (80 µl) was quenched by addition of 35 µl of carbonate buffer and 35 µl of 5× LB prior to addition of 20 µl of the storage buffer (25 mM CAPS, pH 10.3, 1 mM benzamidine-HCl, 0.1 mM EDTA, and 0.2 mM DTT). The 60 min incubation time point (N7) was prepared by adding 20 µl storage buffer to 80 µl of test system. The tube was vortex mixed and placed in a 37.1 °C water bath. After 60 min of incubation, the sample was quenched by addition of 35 µl of carbonate buffer and 35 µl of 5× SB.

All experimental controls were heated at 75-100 °C for 5-10 min, frozen on dry ice, and stored in a -80 °C freezer until analyzed.

7.0 Analytical Methods

Activity of the SGF was assessed using a pepsin activity assay. The digestibility of the Cry1A.105 protein in SGF was assessed using stained polyacrylamide gels and western blot analysis. The limit of detection (LOD) of the Cry1A.105 protein for these methods was determined concurrently.

7.1 SGF Activity Assay

The SGF activity assay was used to confirm the suitability of the test system before its use with the test substance. Acceptable activity was defined as a pepsin activity per mg of pepsin powder (0.03 mg of powder per ml of diluted SGF) equal to the activity of pepsin per mg of pepsin powder as determined by the manufacturer (± 1000 units/mg). One unit of pepsin activity in this assay is defined as the amount of pepsin that will produce a change in the absorbance at

280 nm of 0.001 per min at pH 1.2-2.0 at 37 ± 2 °C. The assay is used to estimate the amount of soluble peptides present in a TCA solution after pepsin digestion of denatured hemoglobin. Undigested hemoglobin was precipitated with TCA, and the amount of soluble peptides was estimated by measuring the absorbance at 280 nm. The amount of soluble peptide is directly proportional to the amount of protease activity.

Briefly, the SGF was diluted to 0.03 mg of solid material (pepsin) per ml of SGF [the dilution factor (DF) was 26.7]. Acidified hemoglobin [2% (w/v), 5 ml] was added to each of three replicates of the test sample and blank samples and pre-warmed at 37 ± 2 °C for 5-10 minutes prior to starting the reactions. Diluted SGF (1 ml) was added to each replicate of test samples and both test and blank samples were incubated at 37.0 °C for an additional 10 min. The reaction was stopped by addition of 10 ml of chilled 5% (v/v) TCA to the test and blank samples. Diluted SGF (1 ml) was then added to the blank samples. Samples were mixed and then incubated another 5-10 min at 37.4 °C. Precipitated protein was removed by filtering the test and the blank samples using 0.8 µm syringe filters. Samples of the clarified test and blank samples were read at 280 nm in a Beckman DU-650 Spectrophotometer. The activity of pepsin was calculated using the following equation:

$$\frac{\text{Mean Test}_{A_{280\text{nm}}} - \text{Mean Blank}_{A_{280\text{nm}}}}{0.001 \times 10 \text{ min} \times 1 \text{ ml}} \times \text{DF},$$

where 0.001 is the change in the absorbance at 280 nm per min at pH 1.2-2.0 and 37 ± 2 °C produced by one unit of pepsin activity; 10 min is the reaction time, 1 ml is the amount of SGF added to the reaction; and, DF is the dilution factor for the SGF.

7.2 SDS-PAGE

Samples containing 1× LB from the SGF *in vitro* digestion of the Cry1A.105 protein were separated by SDS-PAGE using pre-cast tricine 10-20% polyacrylamide gradient mini-gels and tricine running buffer (Invitrogen, Carlsbad, CA). The protein loaded per lane was based on the pre-digestion total protein concentration of the Cry1A.105 protein. All experimental controls were loaded at the same volume as those containing Cry1A.105 protein so that all other components would be comparable. All samples were heated at 100.3 °C for 5 min prior to loading on the gels. Protein markers were used to estimate the relative molecular weight. Electrophoresis was performed at a constant voltage of 125 V for 85 minutes. After electrophoresis, proteins were either visualized by staining the gel with colloidal Brilliant Blue G (section 7.3), or the gel was subjected to electrotransfer of proteins to nitrocellulose membrane for western blot analysis (section 7.4).

7.3 Colloidal Brilliant Blue G Staining

The colloidal Brilliant Blue G staining method was selected because it is an effective method for detecting nanogram quantities of protein on a gel (Neuhoff et al., 1988). Mark12 molecular weight markers (Invitrogen, Carlsbad, CA) were used to estimate the relative molecular weight of visualized proteins and peptides. Based on pre-digestion concentrations, approximately 0.7 µg of total protein was loaded per lane. After separation of proteins, the gels were fixed in a solution containing 7% (v/v) acetic acid and 40% (v/v) methanol for 30 min and stained for approximately 20 h in 1× Brilliant Blue G-colloidal stain solution containing 20% (v/v) methanol. The gels were briefly destained for 30 s in a 10% (v/v) acetic acid, 25% (v/v) methanol solution and completely destained for ~5 h in a 25% (v/v) methanol solution. Images were captured using a Bio-Rad GS-800 densitometer. The results of the *in vitro* digestibility of Cry1A.105 protein were determined by visual examination of the stained gels.

The approximate molecular weights of the full-size protein and proteolytic fragment observed on the colloidal Brilliant Blue G stained gels were visually determined relative to the positions of the molecular weight markers.

The LOD of the Cry1A.105 protein using the colloidal Brilliant Blue G staining procedure was determined. Various dilutions of the zero time point (T0) digestion specimen were loaded onto a separate gel that was run concurrently with the gel used to assess digestibility. Aliquots of the T0 digestion sample representing approximately 700, 350, 100, 50, 20, 10, 5, and 2.5 ng total protein were used for the stained LOD gel.

7.4 Western Blot Analysis

Specimens from the SGF *in vitro* digestions were also analyzed using western blotting. Based on pre-digestion concentrations, approximately 20 ng of total protein were loaded per lane. Following electrophoresis, pre-stained molecular weight markers (Precision Plus Protein Standards, Bio-Rad, Hercules CA) were used to verify electrotransfer of proteins to the membrane. Proteins were electrotransferred to nitrocellulose membranes (0.45 µm pore size, Invitrogen) for 90 min at a constant voltage of 25 V.

Membranes were blocked overnight in a 4 °C refrigerator with 5% (w/v) non-fat dry milk (NFDM) in phosphate buffered saline containing Tween-20 (PBST) buffer. All subsequent incubations (described below) were performed at room temperature. Membranes were incubated with rabbit anti-Cry1A.105 antibody (lot 070705JL) diluted 1:2,000 in PBST containing 1% (w/v) NFDM for 1 h. Excess serum was removed by three 10 min washes with PBST. The membrane was incubated with HRP-conjugated goat anti-rabbit IgG (Sigma) at a dilution of 1:10,000 in PBST containing 1% (w/v) NFDM for 1 h and again washed

(three 10 min washes) with PBST. Immunoreactive bands were visualized using the enhanced chemiluminescence (ECL) detection system (Amersham Biosciences) and exposed (2, 5, and 10 minutes) to Hyperfilm ECL high performance chemiluminescence film (Amersham Biosciences). Films were developed using a Konica SRX101A automated film processor (Tokyo, Japan).

The approximate molecular weights of the full-size protein observed on the western blots were visually determined relative to the positions of the molecular weight markers.

The LOD for the Cry1A.105 protein using the western blot analysis procedure was determined. Various dilutions of the zero time point (T0) digestion specimen were loaded onto a separate gel that was run concurrently with the digestion western blot gel and subjected to the same western blot procedure as described above. Aliquots of the T0 digestion sample representing approximately 7, 3.5, 2, 1, 0.5, 0.2, 0.1, and 0.05 ng total protein were used for the western blot LOD analysis.

7.5 Statistical Methods

No statistical analysis was performed.

8.0 Control of Bias

Measures taken to control bias in this study were the inclusion of both stability and test system experimental controls to account for any effects due to the model in the absence of the pepsin enzyme and the absence of the test substance. Digestion specimens and lower limit of detection samples were analyzed concurrently to eliminate run-to-run variation.

9.0 Rejected Data

One set of data, which included determination of pepsin activity, *in vitro* digestibility of Cry1A.105 in SGF, and western blot analysis of Cry1A.105 SGF digestions was rejected because this set of data was generated before the protocol was amended to include dilution of the test substance and vortexing of the digestion tube throughout the duration of the digestion to improve exposure of the test protein to the test system. One set of SDS-PAGE gels was rejected because the band representing pepsin in the T7 specimen was not observed on the gel, which most probably was a result of a loading error. One set of western blots was rejected because a significant reduction in the amount of the full-length Cry1A.105 protein in the T0 specimen was observed. This was likely caused by a loading error.

10.0 Protocol Amendments

The protocol contained a few typographical errors, which were corrected by amendments. Section 6.1, describing digestibility of the test substance in SGF, was amended to address the possibility of test substance precipitation and/or aggregation at low pH. There was no negative impact on the study as a result of these changes.

11.0 Protocol Deviations

Throughout the experimental phase of the study, one protocol deviation occurred. The preparation of the T0 specimen and experimental controls P0, P7, N0, and N7 followed the amended procedure for the digestibility of the test substance, even though they were not specifically referenced in the amendment. This deviation improved the quality of the study data, because the T0 specimen and experimental controls were prepared in a similar manner to the study specimens.

12.0 Results and Discussion

12.1 Pepsin Activity in SGF

The pepsin activity in SGF was evaluated before conducting the digestion trials to assess the suitability of the test system used in this study. The experimentally observed activity was 2429 units per mg pepsin powder, which was within the acceptable interval of pepsin activity (2280 to 4280 units per mg pepsin powder). Therefore, the test system was shown to be suitable for use in this study.

12.2 Assessment of the Extent of Digestion of the Cry1A.105 Protein by Pepsin using Colloidal Brilliant Blue G Gel Staining of SDS-PAGE

The extent of digestion of the Cry1A.105 protein was evaluated by visual analysis of colloidal Brilliant Blue G stained polyacrylamide gels (Figure 1). The SDS-PAGE for the digestibility assessment (Figure 1A) was run concurrently with a separate SDS-PAGE to determine the LOD of Cry1A.105 protein (Figure 1B). The limit of detection of the full-length (~130 kDa) Cry1A.105 protein was visually estimated to be 0.005 µg or approximately 1% of the total protein loaded:

$$\frac{0.005 \mu\text{g} \times 100\%}{0.7 \mu\text{g}} \cong 0.7\%$$

The gel used to assess the stability of the Cry1A.105 protein to pepsin (Figure 1A) was loaded with ~0.7 µg (based on pre-digestion concentrations) for each of the digestion time points. Visual examination of the stained gel showed that the full-length (~130 kDa) Cry1A.105 protein was digested below LOD within 30 seconds of digestion in SGF (Figure 1A, lane 5). Therefore, at least 99.3% (100% – 0.7% = 99.3%) of the full-length Cry1A.105 protein was digested within 30 seconds of incubation of Cry1A.105 protein in SGF based on the Colloidal Brilliant Blue G Gel stained SDS-PAGE analysis. A faint band with a molecular weight of approximately 4.5 kDa was observed at a very low level

between the 30-second and 20-minute digestion time points (Figure 1A, lanes 9). No protein band was visible at the 30-minute digestion time point (Figure 1A, lane 10).

No change in the full-length Cry1A.105 protein band intensity was observed in the absence of pepsin in the experimental controls P0 and P7 (Figure 1A, lanes 3 and 12). This indicates that digestion of the Cry1A.105 protein was due to the proteolytic activity of pepsin present in SGF and not due to the instability of the test substance at pH 1.3 and 37°C.

The experimental controls evaluating the stability of the pepsin in the test system (SGF) lacking the test substance demonstrated that pepsin was observed as the stained protein band at ~38 kDa throughout the experimental phase (Figure 1A, lanes 2 and 13). The amount of pepsin slightly decreased between 30 and 60 min of the digestion, most probably due to enzyme auto-digestion.

12.3 Assessment of the Extent of Digestion of the Cry1A.105 Protein by Pepsin using Western Blot Analysis

The extent of digestion of the Cry1A.105 protein was also evaluated by a western blot method (Figure 2). The western blot used to assess the stability of the Cry1A.105 protein to pepsin digestion (Figure 2A) was run concurrently with a western blot to determine the LOD of Cry1A.105 protein (Figure 2B). The LOD of full-length (~130 kDa) Cry1A.105 protein was visually estimated to be 1 ng or 5 % of the total protein loaded:

$$\frac{1 \text{ ng} \times 100\%}{20 \text{ ng}} = 5\%$$

The gel used to assess the Cry1A.105 protein *in vitro* digestibility by western blot was loaded with 20 ng total protein of the test substance (based on pre-digestion concentrations) for each of the digestion time points. Western blot analysis demonstrated that the Cry1A.105 protein was digested below the LOD within 30 seconds of incubation in SGF (Figure 2A, lane 5). Based on the western blot LOD for the Cry1A.105 protein in SGF and the observation that no full-length protein or immunoreactive bands were observed on the western blot at the 30-second digestion time point, it was concluded that at least 95% (100% - 5% = 95%) of the full-length Cry1A.105 protein was digested within 30 seconds.

No change in the full-length Cry1A.105 protein band intensity was observed in the absence of pepsin in the experimental controls P0 and P7 (Figure 2A, lanes 3 and 12). This indicates that the test substance was stable in the test system without pepsin at pH 1.3 and ~37 °C over the course of the experiment.

No immunoreactive bands were observed in specimens N0 and N7 that represent test system experimental controls (Figure 2A, lanes 2 and 13). This indicates that

non-specific interactions between the test system components and the antibodies were not observed under these experimental conditions.

13.0 Conclusions

The results of this study demonstrated that the full-length Cry1A.105 protein was rapidly digested after incubation in SGF. At least 99.3% of the full-length Cry1A.105 protein was digested within 30 seconds when analyzed using Colloidal Brilliant Blue G stained polyacrylamide gels. Greater than 95% of the Cry1A.105 protein was digested in SGF within 30 seconds when specimens were analyzed using western blot analysis. A faint ~4.5 kDa band was observed between the 30-second and 20-minute digestion time points when analyzed using Colloidal Brilliant Blue G stained polyacrylamide gels. Neither this band, nor any other immunoreactive band was detected when using western blot analysis.

14.0 References

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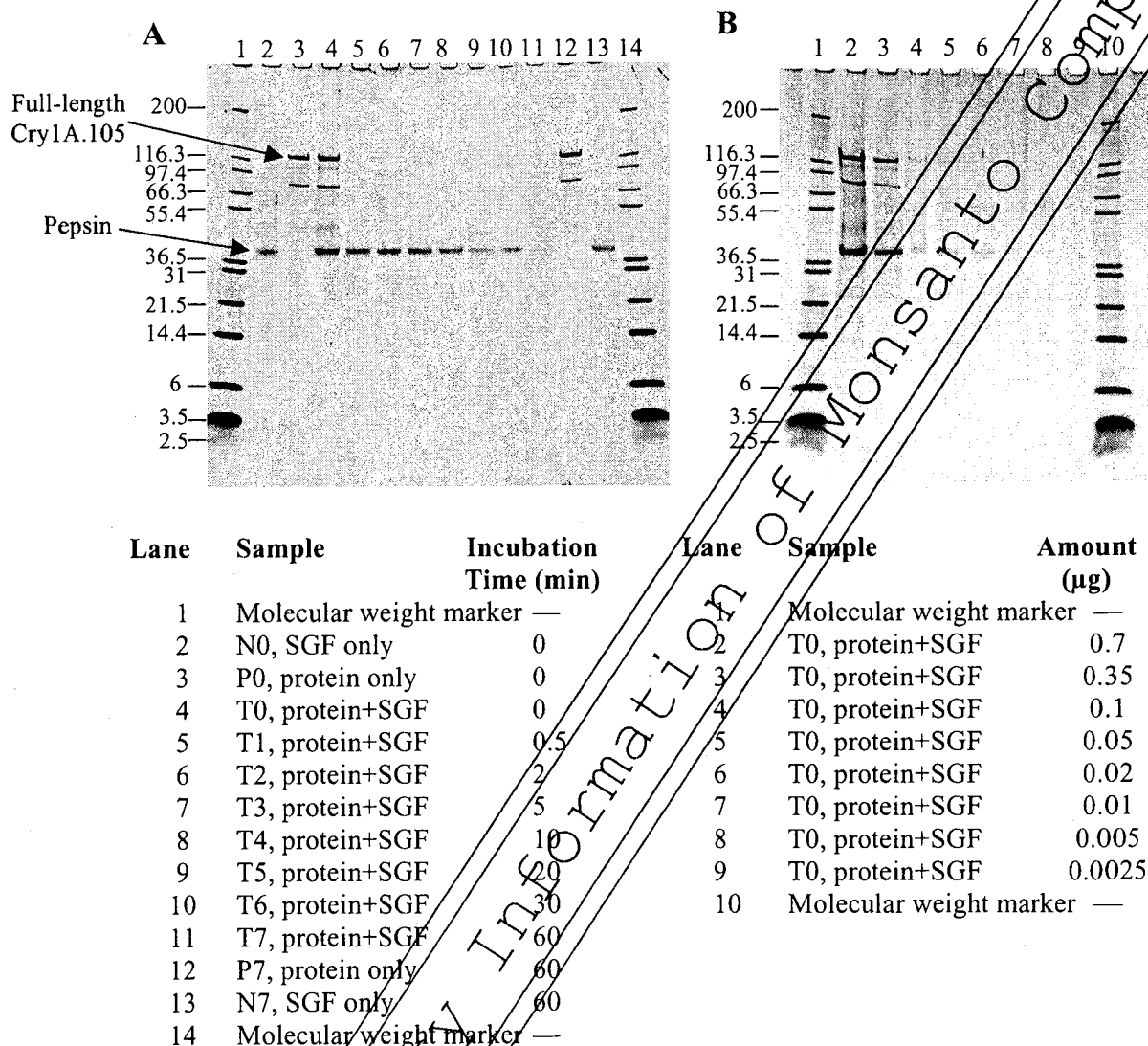
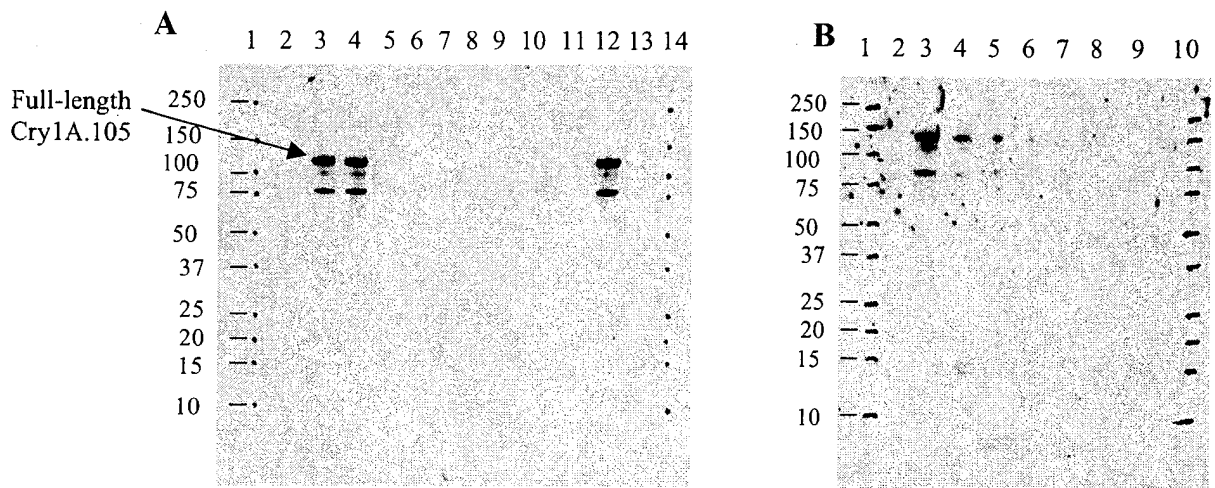


Figure 1. Colloidal Brilliant Blue G stained SDS-polyacrylamide gels

Panel A corresponds to Cry1A.105 protein digestion in SGF. Based on pre-digestion protein concentrations, ~0.7 µg (total protein) was loaded in lanes containing Cry1A.105 protein. The incubation times are indicated. Panel B corresponds to the limit of detection of Cry1A.105 protein. Approximate molecular weights (kDa) are shown on the left and correspond to the markers loaded in each gel. In both gels, Cry1A.105 protein migrated to approximately 130 kDa and pepsin to approximately 38 kDa (indicated by the arrows on the left). Blank or empty lanes were cropped and lanes renumbered.



Lane	Sample	Incubation Time (min)	Lane	Sample	Amount (ng)
1	Molecular weight marker	—	1	Molecular weight marker	—
2	N0, SGF only	0	2	T0, protein+SGF	7
3	P0, protein only	0	3	T0, protein+SGF	3.5
4	T0, protein+SGF	0	4	T0, protein+SGF	2
5	T1, protein+SGF	0.5	5	T0, protein+SGF	1
6	T2, protein+SGF	2	6	T0, protein+SGF	0.5
7	T3, protein+SGF	5	7	T0, protein+SGF	0.2
8	T4, protein+SGF	10	8	T0, protein+SGF	0.1
9	T5, protein+SGF	20	9	T0, protein+SGF	0.05
10	T6, protein+SGF	30	10	Molecular weight marker	—
11	T7, protein+SGF	60			
12	P7, protein only	60			
13	N7, SGF only	60			
14	Molecular weight marker	—			

Figure 2. Western blot analysis

Panel A corresponds to Cry1A.105 protein digestion in SGF. Based on pre-digestion protein concentrations, 20 ng (total protein) was loaded in lanes containing Cry1A.105 protein. The incubation times are indicated. Panel B corresponds to the limit of detection of the Cry1A.105 protein. Approximate molecular weights (kDa) are shown on the left and correspond to the markers loaded in each gel. In both gels, Cry1A.105 migrated to approximately 130 kDa. A 10 min exposure is shown. Blank or empty lanes were cropped and lanes renumbered.

Appendix. List of Applicable SOPs

BR-ME-0388-02	Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis
BR-ME-0392-01	Western Blot Analysis (Immunoblotting)
BR-ME-0460-02	Assay for Pepsin Activity in Simulated Gastric Fluid
BR-ME-0527-01	Brilliant Blue G-Colloidal Staining of Polyacrylamide Gels
BR-ME-0924-01	Electrotransfer of Proteins to Membranes
BR-ME-0973-01	Drying of Polyacrylamide Mini Gels Using Invitrogen Gel Drying System (Adaptation of Invitrogen Gel Drying Procedure)
BR-EQ-0599-02	Bio-Rad GS-710 and GS-800 Densitometers
BR-EQ-0857-01	Beckman Coulter DU-650 Spectrophotometer

Title

Assessment of the *in vitro* Digestibility of the Cry1A.105 Protein
in Simulated Intestinal Fluid

Authors

Shafalee Kapadia
Elena A. Rice, Ph.D.

Study Completed On

November 2, 2005

Performing Laboratory

Monsanto Company
Product Characterization Center
800 North Lindbergh Boulevard
St. Louis, Missouri 63167

Laboratory Project ID

MSL-19930

Study 05-01-62-03

The text below applies only to use of the data by the United States Environmental Protection Agency (US EPA) in connection with the provisions of the Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA).

Statement of No Data Confidentiality Claim

No claim of confidentiality is made for any information contained in this study on the basis of its falling within the scope of FIFRA 10(d)(1)(A), (B), or (C).

We submit this material to the United States Environmental Protection Agency specifically under the requirements set forth in FIFRA as amended, and consent to the use and disclosure of this material by EPA strictly in accordance with FIFRA. By submitting this material to EPA in accordance with the method and format requirements contained in PR Notice 86-5, we reserve and do not waive any rights involving this material that are or can be claimed by the company notwithstanding this submission to EPA.

Company: Monsanto Company

Company Agent: _____

Title: _____

Signature: _____ Date: _____

Statement of Compliance

This study meets the US EPA Good Laboratory Practice standards requirements as specified in 40 CFR Part 160.

Submitter: _____

Date: _____

Sponsor
Representative: _____

Date: 11/2/05

Study Director: _____

Date: 11/02/2005

001 Proprietary Information of Monsanto Company

Quality Assurance Statement

Study Title: Assessment of the *in vitro* Digestibility of the Cry1A.105 Protein
in Simulated Intestinal Fluid

Study Number: 05-01-62-03

Reviews conducted by the Quality Assurance Unit confirm that the final report accurately describes the methods and standard operating procedures followed and accurately reflects the raw data of the study.

Following is a list of reviews conducted by the Monsanto Regulatory Quality Assurance Unit on the study reported herein.

Dates of Inspection / Audit	Phase	Date Reported To:	
		Study Director	Management
07/20/2005	Digestive Fate	07/21/2005	07/21/2005
07/21/2005	Western Blot	07/22/2005	07/22/2005
09/14/2005	Raw Data Audit	09/27/2005	09/27/2005
09/14/2005	Draft Report Review	09/28/2005	09/28/2005

Joan M. Rejda-Heath
Quality Assurance Unit
Monsanto Regulatory, Monsanto Company

November 2, 2005
Date

Study Information

Study Number: 05-01-62-03

Title: Assessment of the *in vitro* Digestibility of the CryIA.105 Protein in Simulated Intestinal Fluid

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Record Retention: All study specific raw data, protocol, amendment, final report, and facility records will be retained at Monsanto, St. Louis.

Specimens Retention: Specimens will be retained at Monsanto, St. Louis, as specified in section 5.2.

Study Initiation Date: July 15, 2005
Study Completion Date: November 2, 2005

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Study Certification

The results reported in this Final Report accurately reflect the data generated under study number 05-01-62-03.

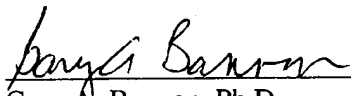
Approved By:



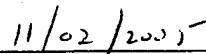
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Abbreviations and Definitions¹

APS	Analytical Protein Standard
CEW	Corn earworm
CFR	Code of Federal Regulations
COA	Certificate of Analysis
EC ₅₀	Effective protein concentration to inhibit the growth of the target insect by 50%
ECL	Enhanced chemiluminescence
<i>E. coli</i>	<i>Escherichia coli</i>
EPA	Environmental Protection Agency
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act
HRP	Horseradish peroxidase
IgG	Immunoglobulin G
LOD	Limit of detection
MALDI-TOF MS	Matrix assisted laser desorption and ionization - time of flight mass spectrometry
NFDM	Non-fat dry milk
PBST	Phosphate buffered saline containing Tween-20
PVDF	Polyvinylidene difluoride
SIF	Simulated intestinal fluid containing pancreatin
SDS-PAGE	Sodium dodecylsulfate polyacrylamide gel electrophoresis
SOP	Standard operating procedure
T	Time point
TCA	Trichloroacetic acid
U	Unit (of enzyme activity)
US	United States
1 × LB	Laemmli buffer [62.5mM Tris-HCl, 5% (v/v) 2-mercaptoethanol, 2% (w/v) sodium dodecyl sulfate, 0.005% (w/v) bromophenol blue, 10% (v/v) glycerol, pH 6.8].
5 × LB	Five times concentrated 1 × LB

¹ Standard abbreviations, e.g., units of measure, concentration, mass, time etc., are used without definition according to the format described in "Instructions to Authors" in The Journal of Biological Chemistry.

1.0 Summary

Monsanto has developed plants that produce the Cry1A.105 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* Cry1A protein with 93.6% overall amino acid sequence identity to the Cry1Ac protein.

The purpose of this study was to assess the *in vitro* digestibility of the Cry1A.105 protein in simulated intestinal fluid (SIF) containing a mixture of proteolytic enzymes known as pancreatin. The Cry1A.105 protein used in this study was produced in and purified from *E. coli*. The *E. coli*-produced Cry1A.105 protein was characterized prior to the digestibility study. Digestibility in SIF was assessed using western blot analysis.

The results of this study demonstrate that the full-length Cry1A.105 protein was digested within 5 min of incubation in SIF, yielding fragments with molecular weights of approximately 60, 32, and 30 kDa. At least 99.5% of the full-length Cry1A.105 protein was digested in SIF within 5 minutes. The ~60 kDa fragment, migrating as a doublet, which represents the trypsin resistant core of the Cry1A.105 protein, was observed for up to 24 hours of digestion. The ~32 kDa fragment was undetectable at the 2-hour digestion time point. The amount of the ~30 kDa fragment, migrating as a doublet, while greatly diminished over the course of the digestion, was still faintly visible at the 24-hour time point.

2.0 Introduction

Monsanto has developed plants that produce the Cry1A.105 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry1A.105 is a modified *Bacillus thuringiensis* Cry1A protein with 93.6% overall amino acid sequence identity to the Cry1Ac protein.

Potential allergenicity and toxicity of the introduced protein are evaluated using various methods, including digestibility of the protein by various proteases in simulated gastric and intestinal fluid assays (Astwood et al., 1996). Simulated intestinal fluid (SIF) is an *in vitro* digestion model where proteins undergo digestion at neutral pH by a mixture of proteases known as pancreatin. The relationship between protein allergenicity and protein stability in the *in vitro* SIF study is limited, because the protein has not been first exposed to the acidic denaturing conditions of the stomach, as would be the case *in vivo* (FAO/WHO, 2001).

3.0 Purpose

The purpose of this study was to assess the stability of the Cry1A.105 protein in simulated intestinal fluid containing a mixture of proteolytic enzymes called pancreatin.

4.0 Materials

4.1 Test Substance

The test substance was the Cry1A.105 protein. The Cry1A.105 protein (Analytical Protein Standard lot 20-100073) was isolated from a fermentation batch of *E. coli* containing pMON96851 expression plasmid. This protein has been characterized and has a total protein concentration of 1.2 mg/ml and a purity of 92 %. The activity was confirmed using an insect bioassay with the larvae of a susceptible pest, corn earworm (CEW). The EC_{50} value was 5.8 ng/ml of diet. Prior to its application to the test system, the test substance was stored in a -80°C freezer in a test substance storage buffer containing 25 mM CAPS, 1 mM benzamidine-HCl, 0.1 mM EDTA, and 0.2 mM DTT, pH ~10.3.

4.2 Control Substance

There was no control substance for this study.

4.3 Reference Substance

Analytical reference standards (e.g., molecular weight markers for SDS-PAGE) used in this study were documented in the data and are described in this report.

4.4 Characterization of Test Substance

The characterization of the physicochemical and functional properties of the test substance was performed under characterization plan 20-100073 and is described on the Certificate of Analysis. The following properties were established for the Cry1A.105 protein: identity (N-terminal sequencing, MALDI-TOF mass spectrometry (MS), immunodetection), concentration (amino acid analysis), purity (SDS-PAGE/densitometry), molecular weight (SDS-PAGE/densitometry, MALDI-TOF MS), stability (SDS-PAGE/densitometry) and activity (CEW bioassay).

5.0 Test System

The test system for this study was simulated intestinal fluid (hereafter referred to as SIF), which contains a mixture of proteolytic enzymes known as pancreatin. Normal proteolytic digestion of consumed food proteins starts with pepsin-mediated hydrolysis in the acidic environment of the stomach, and continues with neutral pH enzymatic digestion in the small intestine. The denaturing environment of the stomach (low pH) alters protein characteristics and facilitates proteolytic digestion in the small intestine by pancreatic enzymes. The physiological relevance of protein digestion in the *in vitro* SIF study is limited, because these experimental conditions do not first expose the protein to the acidic denaturing conditions of the stomach, as would be the case *in vivo*.

SIF was prepared according to the method described in The United States Pharmacopoeia (1995). The pancreatin enzyme used for the preparation of SIF was obtained from Sigma Company (Catalog number P1500, St. Louis, MO). The SIF was formulated so that 55.3 µg of pancreatin powder would be present per 1 µg of test substance (total protein) in the digestion reactions. The SIF was prepared by adding pancreatin powder (0.304 g) to 30.4 ml (final volume) of 50 mM monobasic potassium phosphate solution) adjusted to pH 7.5 with sodium hydroxide. Activity of the SIF was assessed using an SIF activity assay. The assay was used to confirm activity before initiation of the digestion of the test substance.

5.1 Justification for Selection of the Test System

In vitro digestion models are widely used to assess the digestibility of ingested substances and SIF has been used for *in vitro* studies to assess the digestion of food components (Yagami et al., 2000; Okunuki et al., 2002).

5.2 Specimens

Specimens were generated by incubating the test substance with the test system for the times specified in section 5.3. See sections 6.0 and 7.2 for details on the preparation and analysis of specimens. Specimens will be retained in a -80 °C freezer for one year from the end of study after which they will no longer afford analytical evaluation and may be discarded.

5.3 Procedure for Identification of Specimens

Alphanumerical codes were used to distinguish incubation time points (where T = time, P = protein only, and N = no protein):

<u>Targeted Incubation Time Point</u>	<u>Code(s)</u>
0 min	T0, P0, N0
5 min	T1
15 min	T2
30 min	T3
1 h	T4
2 h	T5
4 h	T6
8 h	T7
12 h	T8
24 h	T9, P9, N9

6.0 Experimental Design

6.1 Digestibility of the Test Substance in SIF

Digestion of the test substance in SIF was evaluated over time by analyzing specimens from all incubation time points. The target digestion temperature was $37 \pm 2^\circ\text{C}$.

The digestion was prepared by adding 200 μl of the test substance to a tube containing 1.33 ml of SIF. The tube contents were vortex mixed and immediately placed in a $37 \pm 2^\circ\text{C}$ water bath. Digestion specimens (100 μl) were removed at 5, 15, and 30 min (specimens T1, T2, and T3, respectively), and 1, 2, 4, 8, 12, and 24 hours (specimens T4 to T9, respectively). Each 100 μl sample was immediately quenched by adding to 25 μl of 5 \times LB [312.5 mM Tris-HCl, 25% (v/v) 2-mercaptoethanol, 10% (w/v) sodium dodecyl sulfate, 0.025% (w/v) bromophenol blue, and 50% (v/v) glycerol, pH 6.8] and heating to $92.4\text{--}94.0^\circ\text{C}$ for 5 min.

The zero incubation time point (T0) was prepared in a separate tube by first quenching 66 μl of SIF with 19 μl of 5 \times LB followed by heating to 93.9°C for 5 min prior to the addition of 10 μl of the test substance.

All specimens were frozen on dry ice and stored in a -80°C freezer until analysis.

6.2 Experimental Controls

Experimental stability controls were prepared during the incubation period to characterize the stability of the test substance in the test system (SIF) that lacks the pancreatin enzymes. Specimens from this experimental control were identified with the letter "P" and were prepared in separate tubes. To prepare the zero incubation control time point (P0), test system buffer (66 μl) was quenched by addition of 5 \times LB (19 μl) followed by heating to 93.8°C for 5 min prior to the addition of 10 μl of the test substance. The 24-hour incubation time point (P9) was prepared by adding 10 μl of the test substance to the test system buffer (66 μl). The tube was immediately placed in a $37 \pm 2^\circ\text{C}$ water bath. After 24 hours of incubation the sample was quenched by addition of 19 μl of 5 \times LB and heat denaturation at 92.6°C for 5 min in a water bath.

Additional test system experimental controls were prepared with the test system lacking the test substance. An aliquot of the test system incubated with storage buffer instead of the test substance was quenched at the beginning and at the end of the incubation period. These test system experimental controls were identified with the letter "N" and were used to determine if non-specific interaction occurs

between the test system components and the antibodies during western blot analysis of the specimens. For the zero incubation time point (N0), the test system (66 μ l) was quenched by addition of 5 \times LB (19 μ l) followed by heat denaturation prior to addition of the storage buffer (10 μ l). The 24-hour incubation time point (N9) was prepared by adding 10 μ l storage buffer to 66 μ l of the test system and placing in a 37 ± 2 °C water bath. After 24 hours of incubation, the sample was quenched by addition of 19 μ l of 5 \times LB and heated to 92.6 °C for 5 min.

All controls were frozen on dry ice and stored in a -80 °C freezer until analysis.

7.0 Analytical Methods

Activity of the SIF was assessed using an SIF activity assay. The digestion of the Cry1A.105 protein in SIF was assessed using western blot analysis. The limit of detection (LOD) of the Cry1A.105 protein was determined for the western blot.

7.1 SIF Activity Assays

The SIF activity assay was used to confirm the suitability of the test system before its use with the test substance. According to SOP "Assay for Proteolytic Activity in Simulated Intestinal Fluid", acceptable activity was defined as $11,000 \pm 3,000$ U/ml. One unit of pancreatin activity in this assay is defined as an increase in the absorbance at 574 nm of 0.001 per min at 37 ± 2 °C.

The assay is based on the estimation of the amount of soluble peptide present in a trichloroacetic acid (TCA) solution after pancreatin digestion of resorufin-labeled casein (Roche Molecular Biochemicals, Mannheim, Germany). Undigested resorufin-labeled casein is precipitated with TCA and the amount of soluble peptide is estimated in the supernatant by measuring the absorbance at 574 nm. The amount of soluble peptide is directly proportional to the amount of proteolytic activity.

Both blank and activity replicates contain resorufin-labeled casein. Three activity replicates were incubated with 0.05 \times SIF for 15 min at 37.5 °C. Three blank replicates were incubated with 50 mM KH_2PO_4 , pH 7.5 in place of SIF. The reaction was quenched by addition of chilled 5% (w/v) TCA to activity and blank replicates. Supernatant recovered after centrifugation was neutralized by the addition to assay buffer [500 mM Tris-HCl, pH 8.8] and the absorbance of the clarified activity and blank replicates was read at 574 nm using a Beckman DU-650 spectrophotometer. The activity of SIF was calculated using the following equation:

$$\frac{\text{Mean Activity}_{A574nm} - \text{Mean Blank}_{A574nm}}{0.001 \times 15 \text{ min} \times 0.1 \text{ ml} \times 0.05}$$

where 0.001 is the change in the absorbance at 574 nm per min at $37 \pm 2^\circ\text{C}$ produced by one unit of pancreatin activity, 15 min is the reaction time, 0.1 ml is the amount of $0.05 \times$ SIF added to the reaction, and 0.05 is the SIF dilution factor.

7.2 Western Blot Analysis

Specimens from the SIF *in vitro* digestion of the Cry1A.105 protein were separated by SDS-PAGE using pre-cast 4-20% tris-glycine gradient mini-gels (Invitrogen, Carlsbad, CA) with tris-glycine SDS running buffer. The protein loaded in each lane was based on pre-digestion concentrations of the Cry1A.105 protein (total protein). The digestion samples were diluted with $1 \times$ LB to a concentration of $\sim 2 \text{ ng}/\mu\text{l}$ and $\sim 20 \text{ ng}$ of total protein was loaded in each lane. The experimental controls were loaded in the same volumes as the digestion samples. All samples were heated to 99.2°C for 5 min prior to loading on the gels. Electrophoresis was performed at 125 V for 60 min and 150 V for 40 min. After electrophoresis, proteins were electrotransferred to a polyvinylidene difluoride (PVDF) membrane (Novex) for 90 min at a constant voltage of 25 V. Prestained molecular weight markers (Precision Plus All Blue Protein Standards, Bio-Rad, Hercules, CA) were used to verify electrotransfer of proteins to the membrane.

Proteins transferred to a PVDF membrane were analyzed by western blot. The membrane was blocked overnight at 4°C with 5% (w/v) non-fat dry milk (NFDM) in PBST buffer. All subsequent incubations (described below) were performed at room temperature. Rabbit anti-Cry1A.105 antibody (lot 070705JL) was incubated with the membrane for 60 min at a dilution of 1:2,000 in 1% (w/v) NFDM in PBST. Excess serum was removed by three 5 min washes with PBST. The membrane was incubated with HRP-conjugated goat anti-rabbit IgG (Sigma, St. Louis, MO) at a dilution of 1:7,500 in 1% (w/v) NFDM in PBST for 60 min, and again washed (three 5 min washes) with PBST. Immunoreactive bands were visualized using the enhanced chemiluminescence (ECL) detection system (Amersham Bioscience, Piscataway, NJ) and exposed to Hyperfilm ECL high performance chemiluminescence film (Amersham Biosciences). Films were developed using a Konica SRX101A automated film processor (Tokyo, Japan). The films were scanned using a Bio-Rad GS-800 densitometer to produce electronic images to be used as figures for reporting purposes.

The approximate molecular weights of the full-size protein and proteolytic fragments observed on the western blot were visually determined relative to the positions of the molecular weight markers.

The limit of detection (LOD) for the western blot analysis procedure was determined for the Cry1A.105 protein by loading various dilutions of the zero time point (T0) digestion specimen onto a separate gel. This gel was run concurrently with the digestion western blot gel and subjected to the same western blot procedure as described above. The following approximate total protein loadings of the T0 digestion sample were used for the western blot LOD analysis: 10, 5, 2, 1, 0.5, 0.2, 0.1, and 0.05 ng.

7.3 Statistical Methods

No statistical analysis was performed.

8.0 Control of Bias

Measures taken to control bias in this study included the inclusion of both stability and test system experimental controls to account for any effects due to the model in the absence of the pancreatin enzyme and the absence of the test substance. Digestion specimens and lower limit of detection samples were analyzed concurrently to eliminate run-to-run variation.

9.0 Amendments and Deviations

The description of the test substance storage buffer contained a typographical error, which was corrected by the amendment to the protocol. There was no impact on the study.

10.0 Results and Discussion

10.1 SIF Activity

In order to assess the suitability of the test system used in this study, the pancreatin activity in SIF was evaluated before use. The experimentally observed activity was 10,618 U/ml and was within the acceptable interval of SIF activity (8,000 to 14,000 units per ml of SIF). Therefore, the test system was shown to be active and suitable for use in this study.

10.2 Assessment of Digestibility by Western Blot Analysis

The digestion of the Cry1A.105 protein was evaluated by a western blot method, as described in Section 7.2 (Figure 1). A western blot to determine the LOD (Figure 1A) of the Cry1A.105 protein was run concurrently with the western blot used to assess the Cry1A.105 protein *in vitro* digestibility in SIF (Figure 1B). The LOD was visually estimated to be 0.1 ng. This value represents 0.5% of the total protein loaded:

$$\frac{0.1 \text{ ng} \times 100\%}{20 \text{ ng}} = 0.5\%$$

The gel to assess the Cry1A.105 protein *in vitro* digestibility by western blot was loaded with 20 ng total protein of the test substance (based on pre-digestion concentrations) for each of the digestion time points. Western blot analysis demonstrated that a band corresponding to the full-length Cry1A.105 protein was digested below the LOD within 5 minutes of incubation in SIF (Figure 1B, lane 5). Therefore, at least 99.5% ($100\% - 0.5\% = 99.5\%$) of the full-length Cry1A.105 protein was digested within 5 minutes. Proteolytic fragments with approximate molecular weight of ~60, 32 and 30 kDa were observed at the 5 minute digestion time point. The ~60 kDa fragment, migrating as a doublet, which represents the trypsin resistant core of the Cry1A.105 protein, was observed for up to 24 hours of digestion. The ~32 kDa fragment was digested and undetectable at the 2-hour time point (Figure 1B, lane 9). The ~30 kDa fragment, migrating as a doublet, was observed for up to 24 hours of digestion, however, the intensity of the signal corresponding to this fragment diminished as digestion progressed.

No change in the full-length Cry1A.105 protein band intensity was observed in the absence of pancreatin in the experimental controls P0 and P9 (Figure 1B, lanes 3 and 14). This indicates that the test substance was stable in the test system without pancreatin at ~37 °C over the course of the experiment.

No immunoreactive bands were observed in specimens N0 and N9 that represent test system experimental controls (Figure 1B, lanes 2 and 15). This indicates that no non-specific interaction occurs between the test system components and the antibodies.

11.0 Conclusions

The results of this study demonstrate that the full-length Cry1A.105 protein was digested within 5 min of incubation in SIF, yielding fragments with molecular weights of approximately 60, 32, and 30 kDa. At least 99.5% of the full-length Cry1A.105 protein was digested in SIF within 5 minutes. The ~60 kDa fragment, migrating as a doublet, which represents the trypsin resistant core of the Cry1A.105 protein, was observed for up to 24 hours of digestion. The ~32 kDa fragment was undetectable at the 2-hour digestion time point. The amount of the ~30 kDa fragment, migrating as a doublet, diminished over the course of the digestion, however, it was still present at the 24-hour time point at a very low level.

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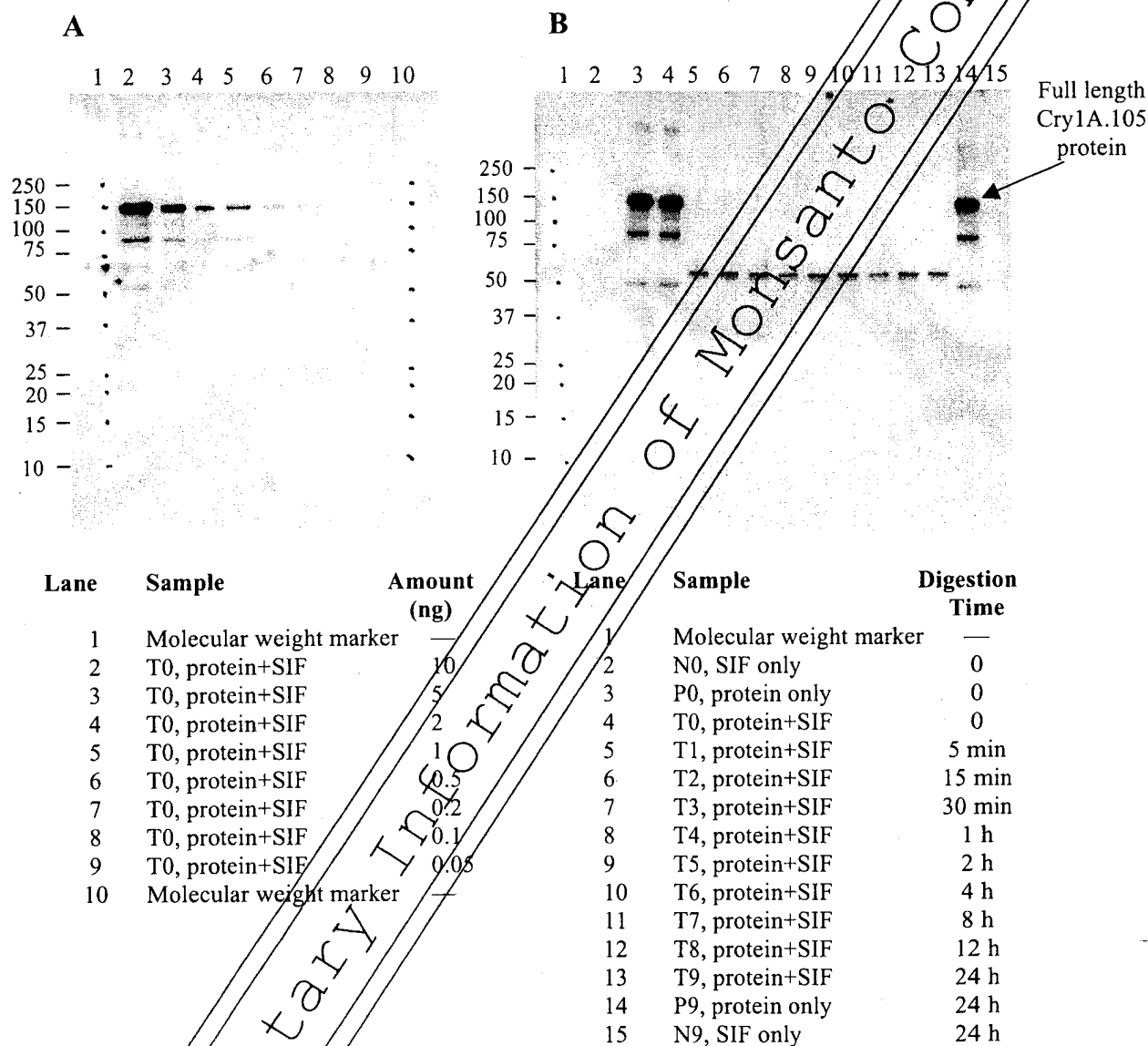


Figure 1. Western Blot Analysis

Panel A corresponds to the limit of detection of Cry1A.105 protein. Panel B corresponds to Cry1Ab protein digestion in SIF. Based on the pre-digestion protein concentration, 20 ng (total protein) was loaded in lanes containing Cry1A.105 protein. The digestion times are indicated. Approximate molecular weights (kDa) are shown on the left and correspond to the markers loaded on each gel. In both gels, Cry1A.105 protein migrated to approximately 130 kDa. A 10 min exposure is shown. Blank and empty lanes were cropped and lanes were renumbered in figure 1A.

Appendix

List of Applicable SOPs

BR-ME-0388-02	Sodium Dodecyl Sulfate Polyacrylamide Gel Electrophoresis
BR-ME-0392-01	Western Blot Analysis (Immunoblotting)
BR-ME-0461-03	Assay for Proteolytic Activity in Simulated Intestinal Fluid
BR-EQ-0599-02	Bio-Rad GS-710 and GS-800 Densitometers
BR-EQ-0857-01	Beckman Coulter DU-650 Spectrophotometer
BR-ME-0924-01	Electrotransfer of Proteins to Membranes

Title

Assessment of the *in vitro* Digestibility of the Cry2Ab2 Protein in Simulated Gastric Fluid

Authors

Shafalee A. Kapadia, and Elena A. Rice, Ph.D.

Study Completed On

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Performing Laboratory

Monsanto Company
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Laboratory Project ID

MSL- 19931
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Representative: _____

Date: 2/17/06

Study Director: _____

Date: 2/20/2006

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Quality Assurance Statement

Study Title: Assessment of the *in vitro* Digestibility of the Cry2Ab2 Protein
in Simulated Gastric Fluid

Study Number: 05-01-62-04

Reviews conducted by the Quality Assurance Unit confirm that the final report accurately describes the methods and standard operating procedures followed and accurately reflects the raw data of the study.

Following is a list of reviews conducted by the Monsanto Regulatory Quality Assurance Unit on the study reported herein.

Dates of Inspection / Audit	Phase	Date Reported To:	
		Study Director	Management
08/04/2005	Digestive Fate	08/04/2005	08/04/2005
08/01/2005	SDS-PAGE	08/04/2005	08/04/2005
12/14/2005	Raw Data Audit	01/05/2006	01/05/2006
12/14/2005	Draft Report Audit	01/05/2006	01/05/2006

Joan M. Rejda-Heath
Quality Assurance Unit
Monsanto Regulatory, Monsanto Company

Feb. 17, 2006
Date

Monsanto Company
Final Report
Product Characterization Center

Study: 05-01-62-04
MSP: 19931
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Study Certification Page

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

Approved By:

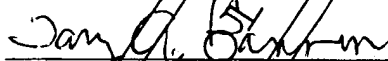


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2/20/2006

Date

Reviewed By:



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Feb 17, 2006

Date

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Study Information Page

Study Number: 05-01-62-04

Title: Assessment of the *in vitro* Digestibility of the Cry2Ab2 Protein in Simulated Gastric Fluid

Primary Testing Facility: Monsanto Company
Product Characterization Center
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Study Initiation Date: July 15, 2005

Study Completion Date: February 20, 2006

Records Retention: All study specific raw data, protocol, amendment, final report, and facility records will be retained at Monsanto, St. Louis.

Specimen Retention: Specimens will be retained at Monsanto, St. Louis, as specified in section 5.2.

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Abbreviations¹

CEW	Corn earworm
CFR	Code of Federal Regulations
COA	Certificate of Analysis
DF	Dilution factor
EC ₅₀	Effective protein concentration to inhibit the growth of the target insect by 50%
ECL	Enhanced chemiluminescence
<i>E. coli</i>	<i>Escherichia coli</i>
EPA	Environmental Protection Agency
FIFRA	Federal Insecticide, Fungicide, and Rodenticide Act (U.S.)
HRP	Horseradish peroxidase
IgG	Immunoglobulin G
ILSI	International Life Science Institute
LOD	Limit of Detection
MALDI-TOF MS	Matrix assisted laser desorption ionization – time of flight mass spectrometry
n/a	Not applicable
NFDM	Non-fat dry milk
PBST	Phosphate buffered saline containing Tween-20
PVDF	Polyvinylidene difluoride
SDS-PAGE	Sodium dodecyl sulfate polyacrylamide gel electrophoresis
SGF	Simulated gastric fluid
SOP	Standard operating procedure
T	Time
TCA	Trichloroacetic acid
US	United States
1× LB	Laemmli buffer [62.5mM Tris-HCl, 5% (v/v) 2-mercaptoethanol, 2% (w/v) sodium dodecyl sulfate, 0.005% (w/v) bromophenol blue, 10% (v/v) glycerol, pH 6.8].
5× LB	Five times concentrated 1× LB

¹ Standard abbreviations, e.g. units of measure, concentration, mass, time, etc., are used without definition according to the format described in "Instructions to Authors" in The Journal of Biological Chemistry.

1.0 Summary

Monsanto has developed plants that produce the Cry2Ab2 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. Cry2Ab2 is a *Bacillus thuringiensis* (subsp. *kurstaki*) protein.

The purpose of this study was to assess the *in vitro* digestibility of the Cry2Ab2 protein in simulated gastric fluid (SGF) containing the proteolytic enzyme pepsin. The Cry2Ab2 protein used in this study was produced in and purified from *E. coli*. The *E. coli*-produced Cry2Ab2 protein was characterized prior to the digestibility study. Digestibility of the Cry2Ab2 protein in SGF was assessed using stained SDS-polyacrylamide gels and western blot analysis.

The results of this study demonstrated that the full-length Cry2Ab2 protein was rapidly digested after incubation in SGF. At least 99.4% of the full-length Cry2Ab2 protein was digested within 30 seconds when analyzed using Colloidal Brilliant Blue G stained polyacrylamide gels. At least 99% of the Cry2Ab2 protein was digested in SGF within 30 seconds when analyzed using western blot analysis. A faint proteolytic band of ~5 kDa was observed only at the 30-second digestion time point when analyzed using a stained polyacrylamide gel. No stable proteolytic bands were observed at any time points by western blot analysis.

2.0 Introduction

Monsanto has developed plants that produce the Cry2Ab2 insecticidal protein and are protected from feeding damage caused by European corn borer (*Ostrinia nubilalis*) and other lepidopteran insect pests. The Cry2Ab2 is a *Bacillus thuringiensis* (subsp. *kurstaki*) protein.

Currently, proteins introduced into commercial food crops through the techniques of biotechnology are evaluated regarding their potential allergenicity. One aspect of this assessment includes analysis of the digestibility of the target protein in an SGF assay containing pepsin. The correlation between protein allergenicity and protein stability in an *in vitro* pepsin digestion assay has been previously established (Astwood *et al.*, 1996). Proteins that are highly digestible are expected to be less likely to cause sensitization or allergenic reaction when consumed. Recently, the International Life Science Institute (ILSI) standardized the pepsin digestibility assay protocol in a multi-laboratory evaluation (Thomas *et al.*, 2004). The SGF formulation, time course of digestion, and experimental parameters used in this study followed the conditions used in the ILSI multi-laboratory evaluation.

3.0 Purpose

The purpose of this study was to assess the stability of the Cry2Ab2 protein in simulated gastric fluid containing the proteolytic enzyme pepsin.

4.0 Materials

4.1 Test Substance

The test substance is the *E. coli*-produced Cry2Ab2 protein. The *E. coli*-produced Cry2Ab2 protein is referred to as Cry2Ab2.820 in the Certificate of Analysis (Analytical Protein Standard lot 20-100071). The protein was isolated from a fermentation batch of *E. coli* containing the pMON70520 expression plasmid. This protein has been characterized and has a total protein concentration of 0.5 mg/ml, and a purity of 87%. Activity was confirmed using an insect bioassay with the larvae of a susceptible pest, corn earworm (*Helicoverpa zea*, CEW). The EC₅₀ value was 0.25 µg/ml of diet. The test substance was stored in a -80 °C freezer in buffer containing 50 mM CAPS, 2 mM DTT, pH 11 prior to use.

4.2 Control Substance

There was no control substance for this study.

4.3 Reference Substance

There was no reference substance for this study. Analytical reference standards (e.g., molecular weight markers) used in this study were documented in the data and are described in this report.

4.4 Characterization of the Test Substance

The characterization of the physicochemical and functional properties of the test substance was performed under characterization plan 20-100071 and is described on the COA. The following properties were established for the Cry2Ab2 protein: identity (N-terminal sequencing, MALDI-TOF mass spectrometry (MS), immunodetection), concentration (amino acid analysis), purity (SDS-PAGE/densitometry), molecular weight (SDS-PAGE/densitometry, and MALDI-TOF MS), stability (SDS-PAGE/densitometry), and activity (CEW bioassay).

5.0 Test System

The test system for this study was simulated gastric fluid (SGF) that contains the proteolytic enzyme pepsin. The SGF was prepared using a highly purified form of pepsin (Catalog number P-6887, Sigma Company, St. Louis, MO). The SGF was formulated so that ten units of pepsin activity per microgram of total protein from the test substance

would be present in the digestion reactions. The amount of pepsin powder used to prepare SGF was calculated from the specific activity reported on the product label. One unit of activity is defined as a change in $A_{280\text{ nm}}$ of 0.001 per minute at 37 °C, measured as trichloroacetic acid (TCA) soluble products using hemoglobin as the substrate. The stock SGF solution was prepared by adding pepsin powder (26.6 mg) to 33.2 ml of an acidic sodium chloride solution (2 mg/ml NaCl, 10 mM HCl, pH ~1.3). After the activity of pepsin in SGF was confirmed, the stock SGF solution was diluted to provide approximately 1944 units pepsin activity/ml of solution.

5.1 Justification for Selection of the Test System

In vitro digestion models are used widely to assess the nutritional value of ingested proteins based on their amino acid bioavailability. Also, the correlation between protein allergenicity and protein stability in an *in vitro* pepsin digestion assay has been previously established (Astwood *et al.*, 1996). Recently the pepsin digestibility assay protocol was standardized by the ILSI in a multi-laboratory evaluation test (Thomas *et al.*, 2004). This multi-laboratory test showed that results of the *in vitro* pepsin digestion assay are reproducible when a common protocol is followed. The SGF formulation, time course, and experimental parameters used in this study followed the conditions used in the ILSI multi-laboratory evaluation test.

5.2 Specimens

Specimens were generated by incubating the test substance with the test system for the times specified in section 5.3. See Sections 6.0 through 7.0 for details on the preparation and analysis of specimens. Specimens will be retained in a -80°C freezer for one year, after which they will no longer afford analytical value and may be discarded.

5.3 Procedure for Identification of Specimens

Alphanumerical codes were used to distinguish incubation time points: (where T = time, P = protein only, and N = no protein):

<u>Targeted Incubation Time Point</u>	<u>Designation(s)</u>
0 min	T0, P0, N0
30 sec	T1
2 min	T2
5 min	T3
10 min	T4
20 min	T5
30 min	T6
60 min	T7, P7, N7

6.0 Experimental Design

6.1 Digestibility of the Test Substance in SGF

Digestion of the test substance in SGF was evaluated over time by analyzing specimens from all incubation time points. The target digestion temperature was 37 ± 2 °C.

Digestion samples were prepared by adding 252 μ l of the test substance to a tube containing 648 μ l of SGF. The tube contents were vortex mixed and immediately placed in a 37.2 °C water bath. The tube with the digestion mixture was regularly vortexed (every 30-60 sec) throughout the digestion experiment to prevent test substance precipitation. Samples (100 μ l) were removed at targeted times of 0.5, 2, 5, 10, 20, 30, and 60 min (specimens T1 to T7, respectively) and placed in a tube containing quenching mixture. Quenching mixture contained 35 μ l of carbonate buffer [700 mM Na_2CO_3 , pH 11], and 35 μ l of 5 \times Laemmli buffer (LB) [312.5 mM Tris-HCl, 25% (v/v) 2-mercaptoethanol, 10% (w/v) sodium dodecyl sulfate, 0.025% (w/v) Bromophenol Blue, and 50% (v/v) glycerol, pH 6.8].

The zero incubation time point (P0) was prepared in a separate tube. SGF (72 μ l) was quenched by adding 35 μ l of carbonate buffer and 35 μ l of 5 \times LB prior to adding 28 μ l of test substance.

All quenched samples were heated at 75-100 °C for 5-10 min, frozen on dry ice, and stored in a -80 °C freezer until analyzed.

6.2 Experimental Controls

Experimental controls were prepared to determine the stability of the test substance in the test system buffer lacking pepsin [10 mM HCl, 2 mg/ml NaCl, pH 1.3]. These experimental controls were identified with the letter "P". The zero incubation time point (P0) was prepared in a separate tube. Test system buffer (72 μ l) was quenched by addition of 35 μ l of carbonate buffer and 35 μ l of 5 \times LB prior to addition of 28 μ l of the test substance. The 60 min incubation time point (P7) was prepared by adding 28 μ l test substance to test system buffer lacking pepsin (72 μ l). The tube was vortex mixed and immediately placed in a 37.2 °C water bath. After 60 min of incubation, the sample was quenched by addition of 35 μ l of carbonate buffer and 35 μ l of 5 \times LB.

Additional experimental controls were prepared to evaluate the stability of the pepsin in the test system (SGF) lacking the test substance and to determine if non-specific interaction occurs between the test system components and the antibodies

during western blot analysis of the specimens. These experimental controls contained an aliquot of the test system incubated with test substance storage buffer instead of the test substance and were identified with the letter "N". The zero incubation time point (N0) was in a separate tube. Test system (72 μ l) was quenched by addition of 35 μ l of carbonate buffer and 35 μ l of 5 \times LB prior to addition of 28 μ l of storage buffer (50 mM CAPS, 2 mM DTT, pH 11). The 60 min incubation time point (N7) was prepared by adding 28 μ l storage buffer to 72 μ l of test system. The tube was vortex mixed and placed in a 37.4 $^{\circ}$ C water bath. After 60 min of incubation, the sample was quenched by addition of 35 μ l of carbonate buffer and 35 μ l of 5 \times LB.

All experimental controls were heated at 75-100 $^{\circ}$ C for 5-10 min, frozen on dry ice, and stored in a -80 $^{\circ}$ C freezer until analyzed.

7.0 Analytical Methods

Activity of the SGF was assessed using a pepsin activity assay. The digestibility of the Cry2Ab2 protein in SGF was assessed using stained polyacrylamide gels and western blot analysis. The limit of detection (LOD) of the Cry2Ab2 protein for these methods was determined concurrently.

7.1 SGF Activity Assay

The SGF activity assay was used to confirm the suitability of the test system before its use with the test substance. Acceptable activity was defined as a pepsin activity per mg of pepsin powder (0.03 mg of powder per ml of SGF) equal to the activity of pepsin per mg of pepsin powder as determined by the manufacturer (\pm 1000 units/mg). One unit of pepsin activity in this assay is defined as the amount of pepsin that will produce a change in the absorbance at 280 nm of 0.001 per min at pH 1.2-2.0 at 37 ± 2 $^{\circ}$ C.

The assay is used to estimate the amount of soluble peptides present in a TCA solution after pepsin digestion of denatured hemoglobin. Undigested hemoglobin was precipitated with TCA, and the amount of soluble peptides was estimated by measuring the absorbance at 280 nm. The amount of soluble peptide is directly proportional to the amount of protease activity.

The SGF was diluted to 0.03 mg of solid material (pepsin) per ml of SGF [the dilution factor (DF) was 26.7]. Acidified hemoglobin [2% (w/v), 5 ml] was added to each of three replicates of the test sample and blank samples and pre-warmed at 37 ± 2 $^{\circ}$ C for 5-10 minutes prior to starting the reactions. Diluted SGF (1 ml) was added to each replicate of test samples and both test and blank samples were incubated at 37.0 $^{\circ}$ C for an additional 10 min. The reaction was stopped by

addition of 10 ml of 5% (v/v) chilled TCA to the test and blank samples. Diluted SGF (1 ml) was then added to the blank samples. Samples were mixed and then incubated another 5-10 min at 37.4 °C. Precipitated protein was removed by filtering the test and the blank samples using 0.8 µm syringe filters. Samples of the clarified test and blank samples were read at 280 nm in a Beckman DU-650 Spectrophotometer. The activity of pepsin was calculated using the following equation:

$$\frac{\text{Mean Test}_{A280\text{nm}} - \text{Mean Blank}_{A280\text{nm}}}{0.001 \times 10 \text{ min} \times 1 \text{ ml}} \times \text{DF},$$

where 0.001 is the change in the absorbance at 280 nm per min at pH 1.2-2.0 and 37 ± 2 °C produced by one unit of pepsin activity; 10 min is the reaction time, 1 ml is the amount of SGF added to the reaction; and, DF is the dilution factor for the SGF.

7.2 SDS-PAGE

Samples containing 1× LB from the SGF *in vitro* digestion of the Cry2Ab2 protein were separated by SDS-PAGE using pre-cast tricine 10-20% polyacryamide gradient mini-gels and tricine running buffer (Invitrogen, Carlsbad, CA). The protein loading per lane was based on pre-digestion total protein concentration of the Cry2Ab2 protein. All experimental controls were loaded at the same volume as those containing Cry2Ab2 protein so that all other components would be comparable. All samples were heated at 95.3 °C for 5 min prior to loading on the gels. Mark12 molecular weight markers (Invitrogen, Carlsbad, CA) were loaded to be used to estimate the relative molecular weight of proteins and peptides visualized by staining. Electrophoresis was performed at a constant voltage of 125 V for 90 min. After electrophoresis, proteins were either visualized by staining the gel with colloidal Brilliant Blue G (section 7.3), or the gel was subjected to electrotransfer of proteins to polyvinylidene difluoride (PVDF) membrane for western blot analysis (section 7.4).

7.3 Colloidal Brilliant Blue G Staining

The colloidal Brilliant Blue G staining method was selected because it is an effective method for detecting nanogram quantities of protein on a gel (Neuhoff et al., 1988). Based on pre-digestion concentrations, approximately 0.8 µg of total protein was loaded per lane. After separation of proteins, the gels were fixed in a solution containing 7% (v/v) acetic acid and 40% (v/v) methanol for 30 min and stained for 15 h in 1× Brilliant Blue G-colloidal stain solution containing 20% (v/v) methanol. The gels were briefly destained for 30 s in 10% (v/v) acetic acid, 25% (v/v) methanol and completely destained for 23 h in a 25% (v/v) methanol solution. Images were captured using a Bio-Rad GS-800 densitometer. The

results of the *in vitro* digestibility of Cry2Ab2 protein were determined by visual examination of the stained gels.

The LOD of the Cry2Ab2 protein using the colloidal Brilliant Blue G staining procedure was determined. Various dilutions of the zero time point (T0) digestion specimen were loaded onto a separate gel that was run concurrently with the gel used to assess digestibility. Aliquots of the T0 digestion sample representing approximately 1, 0.5, 0.2, 0.1, 0.05, 0.02, 0.01, 0.005, and 0.0025 µg total protein were used for the stained LOD gel.

7.4 Western Blot Analysis

Specimens from the SGF *in vitro* digestions were also analyzed using western blotting. Based on pre-digestion concentrations, approximately 20 ng of total protein were loaded per lane. Following electrophoresis, pre-stained molecular weight markers (Precision Plus Protein Standards, Bio-Rad, Hercules CA) were used to verify electrotransfer of proteins to the membrane and estimate size of proteins and peptides. Proteins were electrotransferred to PVDF membranes (0.45 µm pore size, Invitrogen) for 90 min at a constant current of 25 V.

Membranes were blocked overnight in a 4 °C refrigerator with 5% (w/v) non-fat dry milk (NFDM) in phosphate buffered saline containing Tween-20 (PBST) buffer. All subsequent incubations (described below) were performed at room temperature. Membranes were incubated with goat anti-Cry2Ab2 antibody (lot 7227632) diluted 1:3,000 in PBST containing 1% (w/v) NFDM for 70 min. Excess serum was removed by three 5 min washes with PBST. The membrane was incubated with HRP-conjugated anti-goat IgG (Sigma) at a dilution of 1:10,000 in PBST containing 1% (w/v) NFDM for 1 h and again washed (three 5 min washes) with PBST. Immunoreactive bands were visualized using the enhanced chemiluminescence (ECL) detection system (Amersham Biosciences, Piscataway, NJ) and exposed (1, 2, 5, and 10 min) to Hyperfilm ECL high performance chemiluminescence film (Amersham Biosciences). Films were developed using a Konica SRX101A automated film processor (Tokyo, Japan).

The LOD for the Cry2Ab2 protein using the western blot analysis procedure was determined. Various dilutions of the zero time point (T0) digestion specimen were loaded onto a separate gel that was run concurrently with the digestion western blot gel and subjected to the same western blot procedure as described above. Aliquots of the T0 digestion sample representing approximately 10, 5, 2, 1, 0.5, 0.2, 0.1, and 0.05 ng total protein were used for the western blot LOD analysis.