

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 150 of 361

```

AJ130970_1  VALFNYDSRRYPIRTVSQLTREIYTNFVLENFDGSGFRGSAQGIERSIRSHLMDILNSI
          250      260      270      280      290      300      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  SGARLSNTFFNIIVGLPGSTTHALLAARVNSGGISS---GDIGASPFNFQNCST---
          320      330      340      350      360      370      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  TI--YTDARHGYYYWSG---HQIMASPVGFGSGPEFTFPLGYGTMGNAAPQORIVAQLGQG
          310      320      330      340      350      360      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  FLPPLLTPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSYFPDYFIR
          370      380      390      400      410      420      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  VYRTLSSTFYRRPFENIGINNQQL-SVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPPO
          360      370      380      390      400      410      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  NISGVPLVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS-VHNRK--NNIHAVHE--
          430      440      450      460      470      480      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  N--NWP--PROGFSHRLSHVSMFRSGSSNSV-SIIRAPMFSWIHRSAEFNIIASDSIT
          420      430      440      450      460      470      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGSLRPEQN
          490      500      510      520      530      540      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  QIPAVKGNFLFNGSVIS-GFG-FTGGDLVRLNSSGNIIQNRGYIEVP-----IHFP--
          480      490      500      510      520      530      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  NTIARTILRGNGNSYN-LYLRVSSIGNSTIRVINGRYVYATNVTTNNND-GYNDNGAR
          540      550      560      570      580      590      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  STSTRYRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
          530      540      550      560      570      580      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  FSDINIGNVASSNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
          600      610      620      630      640      650      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
AJ130970_1  FTS-SLGNIVGVNRFSGTAGVIIDRFEPFIVTATLEAEYNLERAQKAVNALFTSTNQLGL
          580      590      600      610      620      630      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.pep
TXNS:M73249_1
Description: M73249 Bacillus thuringiensis Bacillus thuringiensis gene,
complete CDS. 4/1993
Accession/ID: M73249
=====General comments=====
LOCUS M73249_1 [BACKURS]
DEFINITION Bacillus thuringiensis gene, complete CDS. . .
SCORES Init1: 128 Initn: 128 Opt: 230 z-score: 239.8 E(): 1.9e-07
>>TXNS:M73249_1
initn: 128 Init1: 128 opt: 230 z-score: 239.8 expect(): 1.9e-07
Smith-Waterman score: 254; 22.9% identity in 584 aa overlap
(60-604:41-591)
cry2ab2_820. FOHKSLDVTQKEWTEKNNHSLYLDPIVGTVASFLKKGSLVKGKILSELNLIFFSG
          30      40      50      60      70      80
M73249_1 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIWGIF
          20      30      40      50      60      70
```

```

cry2ab2_820.  STNLMDILRETEKFLNORLNTDTLARVNAELTGL-----QANVEEFNRQVDNFLNPRNA
          90      100      110      120      130      140      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  GPSOWDAFLVQLEQLINQRIEFPARNCAISRLGLESLNLYQIYAESFREWADPTNP---A
          70      80      90      100      110      120      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  VPSITTSVNTWQQLFLNRLPQFQMQYQLLLPLFAQAANHLHSFIRVDILNADWEGIS
          150      160      170      180      190      200      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  LREEMRIQFNDWNSALTITAIPLAVQNYQVPLLSVYQAANHLHSVLDRDVSFQGRWGFD
          130      140      150      160      170      180      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  AATLRTYRDLYKNYTRDYSNYCINTYQSAFK---GLNTLHDML---EFTYMFNLNVEY
          210      220      230      240      250      260      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  AATINSRYNDLTRLIGNYTDYAVRWYNTIGLERVWGPDGR--DWRYNQFRRETLIVLDI
          190      200      210      220      230      240      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  VSIWSLF---KYQSLVSS-GANIYASGSGPQQTQSTFSQDMPFLYSLFQVNSNYVLNGF
          260      270      280      290      300      310      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  VALFPNYDSRYPIRTVSQLTREIYTNFVLENFDGSGFRGSAQGIERSIRSHLMDILNSI
          250      260      270      280      290      300      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  SGARLSNTFFNIIVGLPGSTTHALLAARVNSGGISS---GDIGASPFNFQNCST---
          320      330      340      350      360      370      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  TI--YTDARHGYYYWSG---HQIMASPVGFGSGPEFTFPLGYGTMGNAAPQORIVAQLGQG
          310      320      330      340      350      360      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  FLPPLLTPFVRSWLDGSDREGVATVNWQTESFETTLGLRSGAFTARGNSYFPDYFIR
          370      380      390      400      410      420      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  VYRTLSSTFYRRPFENIGINNQQL-SVLDGTEFAYGTSSNLPSSAVYRKSGTVDLSDEIPPO
          360      370      380      390      400      410      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  NISGVPLVRNEDLRRLPHYNEIRNIASPGTGGARAYMVS-VHNRK--NNIHAVHE--
          430      440      450      460      470      480      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  N--NWP--PROGFSHRLSHVSMFRSGSSNSV-SIIRAPMFSWIHRSAEFNIIASDSIT
          420      430      440      450      460      470      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  -----NGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQGSLRPEQN
          490      500      510      520      530      540      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  QIPAVKGNFLFNGSVIS-GFG-FTGGDLVRLNSSGNIIQNRGYIEVP-----IHFP--
          480      490      500      510      520      530      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  NTIARTILRGNGNSYN-LYLRVSSIGNSTIRVINGRYVYATNVTTNNND-GYNDNGAR
          540      550      560      570      580      590      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  STSTRYRVRYASVTPHILNVN-WGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
          530      540      550      560      570      580      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.  FSDINIGNVASSNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
          600      610      620      630      640      650      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
M73249_1  FTS-SLGNIVGVNRFSGTAGVIIDRFEPFIVTATLEAEYNLERAQKAVNALFTSTNQLGL
          580      590      600      610      620      630      :|:::  :|:::  :|:::  :|:::  :|:::  :|:::
cry2ab2_820.pep
TXNS:Q9R826
```


Description: Q9R826 bacillus thuringiensis, crystal toxin protein. 6/2001

Accession ID: Q9R826

ID: Q9R826

AC: Q9R826

DT: 01-MAY-2000

PRELIMINARY;

RT: 1178 AA.

Created:

SCORES Initl: 128

>TXN5:Q9R826

Initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

initl: 128

Monsanto Company

Final Report

Product Characterization Center

Study No. 06-01-62-01

MSL No. 20307

Page 152 of 361

```
cry2ab2_820. 300 310 320 330 340 350
PFLYSFQVNSVNLNGFSGARLSNTFFNIVGLPSTTHALLAARVNSGG--ISSGDI
M73252_1 300 310 320 330 340 350
VINITDYRGVGFENIENSAIRS---PHLMDFLNLTIDTLRGVHVWAGHRVTSHT
cry2ab2_820. 360 370 380 390 400 410
GASPFNQFNCSTFLPPLLTFFVRSWLDGSDREGVATVNWQTESFETTLGRSGAFTA
M73252_1 330 340 350 360 370
GSSQV-----ITTP-QYGTANAEPRRTIAPSTPFGNLFRYL---SNPFR
cry2ab2_820. 420 430 440 450 460 470
RGSNSYFPDYPFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVSVNRK
M73252_1 380 390 400 410 420
RSE-NITPTLGINVVGVGFIQPNNA--EVLVRSRGTVDSLNLPLIDGENSLVGVSHL
cry2ab2_820. 480 490 500 510
NNIHAVHE--NGSMHLPNDYTGf-----TISPIHATQV-----NNQTRTIFSEK
M73252_1 430 440 450 460 470
SHVLTLSRLYNITSLTPTFVWTHHSATNTNTINPDIIITQIPLVKGRFGGTSVIKPG
cry2ab2_820. 520 530 540 550 560 570
FGNGDLSLRFQONNTTARYTLRGNGS----YNLYRVSSIGNSTIRVTINGRVYATN
M73252_1 490 500 510 520 530 540
FTG-GDILR--RNTIGEFVLOVNIENSPITQRYRLEFRYASRDARITVAIGQIRVDMT
cry2ab2_820. 580 590 600 610 620 630
VNTITNDGVNDGARFSDINIGVVA--SSNSDVPLDINVLNSGTQFDLMNMLVPTNI
M73252_1 550 560 570 580 590 600
LEKTMET--GESLTSRTFTSYNFPFSFRANPDIIIRIAELPIRGGLYIDKIELILADA
cry2ab2_820. SPLV
TFBEEYDLERAQKAVNALFTSTNGLKTDVTDYHIDQVSNLVECLSDFECLDEKRELSE
cry2ab2_820.pcp
TXN5:006894
Description: 006894 bacillus thuringiensis. crylea4. 6/2001
Accession/ID: 006894
ID 006894 PRELIMINARY;
AC 006894; PRT; 1171 AA.
DT 01-JUL-1997 (TremBLrel. 04, Created)

SCORES Init1: 117 Initn: 117 Opt: 227 z-score: 236.6 E(): 2.8e-07
>TXN5:006894
Initn: 117 Init1: 117 opt: 227 z-score: 236.6 expect(): 2.8e-07
Smith-Waterman score: 234; 22.0% identity in 605 aa overlap
(32-607:13-576)

cry2ab2_820. QAMDNSVLNSGRITICDAYVAADHPFSGHKSLLDTGVOKWETKKNKXSLYLDPIVGTV
006894 MEIVNNQOCVPCVCLNNPENELDIERSNSTVAIN--IALE
```

```
cry2ab2_820. 70 80 90 100 110 120
ASFLKKYGVSLVGRKRIILSELNLIPIPSGTSNLMODILRETEKFLNQRINTDITLARVNAEL
006894 50 60 70 80 90
ISRLLASATPIGG--ILLGLFPAIWSIGPSQWDLFLEQIEILLIDOKI--BEFAR-NOAI
cry2ab2_820. 130 140 150 160 170
TGLQANVEEFNRQVDFN---LNPNNVPLSITSSVNTMQQLNRLPQFQMGYQLLL
006894 100 110 120 130 140 150
SRLEGISLYGIYTEAFREWEADPTNPALKEEMRTQFNDMNSILVTAIPLESVQVQVPF
cry2ab2_820. 180 190 200 210 220 230
LPLFAQANHLHSFIRDVILNADENGISAATLRTYRDYLNKYTRDYSNYCINTYQSAFKG
006894 160 170 180 190 200 210
LSVYQAAANLHSLVRDVSFVQAGFDIATINSRYNDLTRLPIPIYIDYAVRWY---G
cry2ab2_820. 240 250 260 270 280 290
LATRLHDLMEFTYMFNLVNFVYVSWLSFKYQSLVSSGANLYASGSPQQTQSFTSQDW
006894 220 230 240 250 260 270
LD-RLPRTGGLRNARENQFRRELTSVLDIISFFRNYSRLYPIFTSSOLTRVYT-DP
cry2ab2_820. 300 310 320 330 340 350
PFLYSLFQVNSVNLNGFSGARLSNTFFNIVGLPSTTHALLAARVNSGG--ISSGDI
006894 280 290 300 310 320 330
VINITDYRGVGFENIENSAIRS---PHLMDFLNLTIDTLRGVHVWAGHRVTSHT
cry2ab2_820. 360 370 380 390 400 410
GASPFNQFNCSTFLPPLLTFFVRSWLDGSDREGVATVNWQTESFETTLGRSGAFT
006894 330 340 350 360 370 380
GSSQV-----ITTPQYGN--QNAEPRRTIAPSTPFGNLFRYL---SNPFF
cry2ab2_820. 420 430 440 450 460 470
ARGNSYFPDYPFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPGTGGARAYMVSVNRH
006894 370 380 390 400 410 420
RESE-NITPTLGINVVGVGFIQPNNA--EVLVRSRGTVDSLNLPLIDGENSLVGVSHR
cry2ab2_820. 480 490 500 510
NNIHAVHE--NGSMHLPNDYTGf-----TISPIHATQV-----NNQTRTIFSE
006894 430 440 450 460 470 480
LSHVLTLSRLYNITSLTPTFVWTHHSATNTNTINPDIIITQIPLVKGRFGGTSVIKGP
cry2ab2_820. 520 530 540 550 560 570
KFGNGDLSLRFQONNTTARYTLRGNGS----YNLYRVSSIGNSTIRVTINGRVYAT
006894 490 500 510 520 530 540
GTG-GDILR--RNTIGEFVLOVNIENSPITQRYRLEFRYASRDARITVAIGQIRVDM
cry2ab2_820. 580 590 600 610 620 630
VNTITNDGVNDGARFSDINIGVVA--SSNSDVPLDINVLNSGTQFDLMNMLVPTN
006894 550 560 570 580 590 600
TLEKTMET--GESLTSRTFTSYNFPFSFRANPDIIIRIAELPIRGGLYIDKIELILAD
cry2ab2_820. ISFLY
```


006899 ATFEEDYLERAQKAVNALFTSTNLQGLKTDVTDYHIDQVSNLVECLSDFECLDEKRELSE 610 620 630 640 650 660

cry2ab2_820.pep
TXN5:C1EA_BACTX

Description: Q57458 bacillus thuringiensis (subsp. kenyae), pesticidal
crystal protein cryIe
Accession/ID: Q57458
-----General comments-----
ID C1EA_BACTX STANDARD; PR1 117
AC Q57458; Q03741; . . .

SCORES Initl: 117 Inltn: 117 Opt: 227 Z-score: 236.6 E(): 2.8e-07
>TXN5:C1EA_BACTX (117 aa)
Initl: 117 Inltn: 117 Opt: 227 Z-score: 236.6 expected: 2.8e-07
Smith-Waterman score: 234; 21.9% identity in 604 aa overlap
(32-607:13-576)

cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADHPFSQHKSLDTVQKRWETWKKNNHSLYDPIVGVG 10 20 30 40 50 60
C1EA_BACTX MEIVNNQNCVPYNCNLPENPEILDIERSNSTVATN-IAAE 10 20 30 40

cry2ab2_820. ASFLKKVGLSVGKRLISELRLNLIFFSGSTNLMDILRETKFLNORLNTDILARVNAEL 70 80 90 100 110 120
C1EA_BACTX ISRLIASATPIGG--ILLGLFDAIWSIGPSQWDLFLEQIELLDQKI--REPAR-NOAI 100 110 120 130 140 150

cry2ab2_820. TGLQANVEEFNRQVDMF----LNPNNRNVPLSITSSVNTMQQLFLNRLPQFMQGVQLLL 130 140 150 160 170
C1EA_BACTX SRLEGISLXGIVTEAFREWEADPTNPALKEEMRTQFNDMNSILVTAIPLESVQNYQVFP 100 110 120 130 140 150

cry2ab2_820. LPLFAQANLHLSFIEDVILNADENGISAATLRTYRDYLNKTRDYSNYCINTYQSAFKG 180 190 200 210 220 230
C1EA_BACTX LSVYQAAANLHLSVLRDVSFVCGAAGFDIATINSRYNDLRLPIPIYDYVRWYNT---G 160 170 180 190 200 210

cry2ab2_820. LNTRLHMDLEFRTYMFNFVEYVSIWSLKYQSLLVSSGANLYAGSGPQOQTFTSQDW 240 250 260 270 280 290
C1EA_BACTX LD-RLPRTGGLRWARNQFRRELITISVLDIISFFRNYDSRLYPIPTSQLTREVIT-DP 220 230 240 250 260 270

cry2ab2_820. PFLYSLFOVNSYVNLNGFSGARLSNFTFNIVGLPGSTTHALLARVNYSGG--ISSGDI 300 310 320 330 340 350
C1EA_BACTX VINITDVRVGPSPENIENSAIRS----PHLMDFLNLLITDILIRGVHYWAGHRVTSHT 280 290 300 310 320 330

cry2ab2_820. GASPFQNFNCSTPLPPLLTTPFVRSLWDSGSDREGVATVNWQTSFETTLGLSAGFTA 360 370 380 390 400 410
C1EA_BACTX GSSQV-----ITTP-QYGITANPEPRITAPSTFPGLNLFYRTL---SNPFFR 330 340 350 360 370

cry2ab2_820. RGSNSYFPDYFIRNIGSVPLVWNEDLRRPLHYNEIRNIASPSGTFGGARAYMVSVNMRK 420 430 440 450 460 470
C1EA_BACTX RSE-NITPTLGINVQGVGIQPNNA---EVLRSRGTVDSLNELPIDGENSLVGYSHRL 380 390 400 410 420 430

cry2ab2_820. NNHVAHVE--NGSMIHLAPNDYTGf-----TISPIHATQV-----NNOTRTFISEK 480 490 500 510
C1EA_BACTX SHYTLRSLYNTNITSFTFWTHHSATNTNINFDIITQIPLVKGRGLGGTSVIKPGG 430 440 450 460 470 480

cry2ab2_820. FGNQGSILRFEQNNITARYTLRGNS-----YNYLVRVSSIGNSTIRVTINGRVYTATN 520 530 540 550 560 570
C1EA_BACTX FTG-GDILR--RNTIGFEVSLQVNIINSPIQRYRFRFYASSRDKARITVAIGGQIRVDMT 490 500 510 520 530 540

cry2ab2_820. VNTTNNQGVNDNGARFSDINIGNVVA--SSNSDVPDLNIVTLNSGTQFDLMIMLVPTNI 580 590 600 610 620 630
C1EA_BACTX LEXTMEI--GESLTSRTSTSYTNFSNPFSPRANPDIIIRIAEELPIRGGELYIDKIELILADA 550 560 570 580 590 600

cry2ab2_820. SPLY TFEEYDLERAQKAVNALFTSTNLQGLKTDVTDYHIDQVSNLVECLSDFECLDEKRELSE 610 620 630 640 650 660
cry2ab2_820.pep
TXN5:U94323_1

Description: U94323_1 Bacillus thuringiensis Bacillus thuringiensis protoxin
CryIeA4 (cryIeA4)
Accession/ID: U94323_1
-----General comments-----
LOCUS U94323_1 [BTU94323.1] 331 bp
DEFINITION Bacillus thuringiensis protoxin CryIeA4 (cryIeA4) gene, complete . . .

SCORES Initl: 117 Inltn: 117 Opt: 227 Z-score: 236.6 E(): 2.8e-07
>TXN5:U94323_1 (117 aa)
Initl: 117 Inltn: 117 Opt: 227 Z-score: 236.6 expected: 2.8e-07
Smith-Waterman score: 234; 22.0% identity in 605 aa overlap
(32-607:13-576)

cry2ab2_820. QAMDNSVLNSGRITTCDAYNVAADHPFSQHKSLDTVQKRWETWKKNNHSLYDPIVGVG 10 20 30 40 50 60
U94323_1 MEIVNNQNCVPYNCNLPENPEILDIERSNSTVATN-IAAE 10 20 30 40 50 60

cry2ab2_820. ASFLKKVGLSVGKRLISELRLNLIFFSGSTNLMDILRETKFLNORLNTDILARVNAEL 70 80 90 100 110 120
U94323_1 ISRLIASATPIGG--ILLGLFDAIWSIGPSQWDLFLEQIELLDQKI--REPAR-NOAI 50 60 70 80 90 100

cry2ab2_820. TGLQANVEEFNRQVDMF----LNPNNRNVPLSITSSVNTMQQLFLNRLPQFMQGVQLLL 130 140 150 160 170
U94323_1 SRLEGISLXGIVTEAFREWEADPTNPALKEEMRTQFNDMNSILVTAIPLESVQNYQVFP 100 110 120 130 140 150

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 154 of 361

```
180      190      200      210      220      230
cry2ab2_820. LPFAQANLHLSFTIRVILNADEWGISAAALTRDYKYNTRYDYNICYNTYQSAFGK
U94323_1  LSVYQANLHLSVLRDVSFVGQAFDIATINSRYNDLTRLIPIYTDYAVRWYNT--G
160      170      180      190      200      210
240      250      260      270      280      290
cry2ab2_820. LNTLRHDLMEFRYFMFNVFEVSIWLSLFKYQSLVSSGANLYASGSGPOQTQSFSDQM
U94323_1  LD-RLPTGGLRWAFNQFRELTSVLDIISFFRNVDLSLYPIPTSSQLTREVT-DP
220      230      240      250      260      270
300      310      320      330      340      350
cry2ab2_820. PFLYSLFQNSNYVLNMGFSGARLSNTFPNIVGLFGSTTHALLAARVNYSGG-ISSGDI
U94323_1  VINITDVRVGFSPENIENSAIRS---PFLMDFLNLLTDTDLIRGVHYWAGHRVTSHT
280      290      300      310      320      330
360      370      380      390      400      410
cry2ab2_820. GASPNQFNCSFTPLPLTP-FVRWLDGSDREGVAVTNWQTESFETTLGLRGAF
U94323_1  GSSGV-----ITTFQYGN--QNAEPRTIAPSTFPGLNLFYRTL---SNPFF
330
420      430      440      450      460      470
cry2ab2_820. ARGNSYFPDPIFRNISGVPLVVRNEDRLRPLHYNEIRNIASPSGTPGARAYMVSVHNR
U94323_1  RSE-NITPTLGINVQGVGFIQPNNA---EVLRSRGTVDSLNELPIDGENSLVGYSHR
370      380      390      400      410      420
480      490      500      510
cry2ab2_820. KNIHAVHE--NGSMHLPANDYTGF-----TISPIHATQV-----NNQTRIFSE
U94323_1  LSHVTLTRSLYNTNITSLTPFWTHHSATNTINPDIITQIPVKGFLRGGTSVKGKP
430      440      450      460      470      480
520      530      540      550      560      570
cry2ab2_820. KFGNQGDSLRFQNNHTARTYLRGNNS-----YMLYLRVSSIGNSTIRVTINGRVYAT
U94323_1  GFTG-GDILR--RNTIGFVSLQVNIINSPIRTORYLRFRYASSRDAITVAIGGQIRVDM
490      500      510      520      530      540
580      590      600      610      620      630
cry2ab2_820. NVNITNDGVNDNGAREFDINIGNVA--SSNSDVPFLDINTVNLNSQTFDLMNIMLVPTN
U94323_1  TLEKTEI--GESLTSRTFSYTNFSNPFSPRANPDIIIRIAEELPIRGGELYDKIELLAD
550      560      570      580      590      600
610      620      630      640      650      660
cry2ab2_820. ISPLY
U94323_1  ATFEEDYDLERAQKAVNALFTSTNQLGLKTDVTDYHIDQVSNLVECLDEFLDKRELIS
610      620      630      640      650      660
820      830      840      850      860      870
cry2ab2_820.pcp
TXNS:M35524_1
```

Description: M35524 Bacillus thuringiensis B. thuringiensis delta-endotoxin
gene, complete cds
Accession/ID: M35524
=====General comments=====

```
LOCUS      M35524_1 [BACRYIA]
DEFINITION B.thuringiensis delta-endotoxin gene, complete cds; . . .

SCORES      Init1: 128      Initn: 128      Opt: 225      z-score: 234.5 E(): 3.7e-07
>TXNS:M35524_1
Initn: 128      Init1: 128      Opt: 225      z-score: 234.5 expect(): 3.7e-07
Smith-Waterman score: 257;      22.9% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FQHKSLDTVQKEWEMKKNHLSYLDPIVGVASFLLKVKVSLGKRLSELRLIPPSG
M35524_1  IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLISEF--VPGAGFVLGLVDIIGCIF
30      40      50      60      70      80
90      100      110      120      130      140
cry2ab2_820. STNLMDILRETEKFLNRLNTDTLARNVAELTG----QANVEEFNRQVDNFLNPRNA
M35524_1  GFSQWDAFVQLQELINQRIEERFARNQALSRLEGLSNLYOYIAESFREWEADFPNP---A
70      80      90      100      110      120
150      160      170      180      190      200
cry2ab2_820. VFLSITSSVNTMQOLFNRLPQPMQVQGLLLPLFAQANLHLSPIRDVINADWGIS
M35524_1  LREEMRIQFNDMSALTTAIPLLAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF
130      140      150      160      170      180
210      220      230      240      250
cry2ab2_820. AATLRTYDYLNKTYRDSNYCINTYQSAFK---GLNTRLHMDL---EFRYMFNLVFEY
M35524_1  AATINSRYNDLTRLIQNTYDTHAVRWYNTGLERWVGDSR--DWVRYNQFRRELTLVLDI
190      200      210      220      230      240
260      270      280      290      300      310
cry2ab2_820. VSIWSLF---KYQSLVSS--GANLYASGSGPQQTQSFSDQWFFLYSLFQNSNYVLNGF
M35524_1  VALFENYDSRRYPIRTVTSQITREIYTNVLENFDGSPRGSAGIERSIRSPHLMIDLNSI
250      260      270      280      290      300
320      330      340      350      360
cry2ab2_820. SGARLSNTFPNIVGLFGSTTHALLAARVNYSGGIS---GDIGASPPNQNFNCST---
M35524_1  TI--YTDHARGYYWSG---HOIMASPVGSGPEFTFPPLYCTMGNAAPQQRIVVAQLGQG
310      320      330      340      350
370      380      390      400      410      420
cry2ab2_820. FPPLLTFFVRSMWLDGSDREGVAVTNWQTESFETTLGLRGAFRTAGNSNYFPDYFIR
M35524_1  VYRTLSSTFYRRPFIQNNQQL-SVLDTGEFAYGTSSNLPASVYRKSGTVDLSDEIPPO
360      370      380      390      400      410
430      440      450      460      470      480
cry2ab2_820. NTSGVPLVVRNEDRLRPLHYNEIRNIASPSGTPGARAYMVS-VHNRK--NNIHAVHE--
M35524_1  N-NNVP--PROGSHRLSHSVWFRSGSSSVSI--IRAPMFSWIHRSAEFNNIIASDSIT
420      430      440      450      460      470
490      500      510      520      530
cry2ab2_820. -----NGSMHLPANDYTGTISPIHATQVNNQTRIFISEKFGNQGDSLREQN
M35524_1  QIPAVKGNFLFNGSVIS-GPG-FTGGLVLRNLSGNNIGNRGYIEVP-----IHFP--
480      490      500      510      520
```


Monsanto Company

Final Report

Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 155 of 361

©01

cry2ab2_820. NTATATLRGNGNSYN-LYLAVSSIGNSTIRVTINGRVYATNVTNTTND-GVNDNGAR
M35524_1. STSTRYVVRVYASVPIHNLVWGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA
Q45735. VRTLSSTFYRRPNFNNQQL-SVLDTGFAYGTSSNLPFSAYVRKSGTVDSLDEIPPO

cry2ab2_820. FSDINIGNVWASSNSDVPLDINVTLSNGTQFDLMNMLVPTNISPLY
M35524_1. FTS-SLGNIVGVNFGSTAGVYVORRPSIVTATLEAEYNLERAKQAVNALFTSTNQLGL
Q45735. N-NVYP--PROGFSHRLSHVSMFRSGSSSVSI--IPAPMFSWIHRSAEFNIIASDSIT

cry2ab2_820.pap
TXN5:Q45735
Description: Q45735 bacillus thuringiensis delta-endotoxin. 6/2001
Accession/ID: Q45735
ID Q45735 PRELIMINARY;
AC Q45735 PRELIMINARY;
DT 01-NOV-1996 (TREMELrel. 01, Created)

SCORES Initl: 128 Initn: 128 Opt: 225 z-score: 234.5 E(1): 3.7e-07
>>TXN5:Q45735
Initn: 128 Initl: 128 Opt: 225 z-score: 234.5 expect(1): 3.7e-07
Smith-Waterman score: 257; 22.9% identity in 584 aa overlap
(60-604:41-590)

cry2ab2_820. FOHKSLEDTVQKEWTEWKKNNHSLYLOPIVGTVASFLKKKGLVSKRLSELRLNLIFFSG
Q45735. IPYNCLSNPEVEVLGGERIETGTPIDISLTLQFLSEF--VPGAGFVLGLVDIIWGIF

cry2ab2_820. STNLMQDIURETEKFLNORLNTDTLARVNAELTGL---QANVEEFNRQVDNPLNRNA
Q45735. GPSCWDALFVQLEQLINQRIEFARNOAISRLGLSNLYQIYAESFREWEADPTNP--A

cry2ab2_820. VPLSITSSVNTWQQLFLNRLPQFMQOGYQLLLPLFAQAANHLHSFIRDVILNADEWGIS
Q45735. LRREMIQFNDNNALTAIPLAVQNYQVPLLSVYVQAANHLHSVLRDVSVFGQWGF

cry2ab2_820. AATLRTRDYLNKNTDYNSYCINTQSAFK---GLNTRLHDM---EFTYVFLNVEPY
Q45735. AATINSRYNDLTRIGNYTDHVRWYNTGLERVWGPDSR--DWVRVYQFRRLTLTLVLDI

cry2ab2_820. VSWLSLF---KYQSLVSS--GANLYASGGPQQTQSFTSQDWPFLLYLFQVNSNYLVNGF
Q45735. VALFPNYSRRYPRTYSOLTRIEYTNPVLENFQSGFRGSAQGIERSIRSPHLMILNSI

cry2ab2_820. SGARLSNTPFNIVGLPGSTTHALLAARVNYSGISS-----GDIGASPNQFNCSIT---
Q45735. TI--YTDARHGYIYWSG-----HOIMASPVGSGPEFTFPLYGTMGNAAPQQRIVLAQGGQ

cry2ab2_820. FLUPPLLTFFRSMWLDSSDREGVATVWVQTESFETTLGLRSGAFTARGNSYFPDYPIR
Q45735. VRTLSSTFYRRPNFNNQQL-SVLDTGFAYGTSSNLPFSAYVRKSGTVDSLDEIPPO

cry2ab2_820. NISGVPLVVRNEDLRLHYLRNIRNIASPGTGGAGAYVVS-VNHRK--NNIHAVE--
Q45735. N-NVYP--PROGFSHRLSHVSMFRSGSSSVSI--IPAPMFSWIHRSAEFNIIASDSIT

cry2ab2_820. NGSMIHLAPNDYTGFTTSPHATQVNNQTRTFISEKFGNOGDSLRFEON
Q45735. QIPAVKGNFLNGSVIS-GFG-FTGGDLVRLNLSGNNIQNRGYIEVP-----IHFP--

cry2ab2_820. NTATATLRGNGNSYN-LYLAVSSIGNSTIRVTINGRVYATNVTNTTND-GVNDNGAR
Q45735. STSTRYVVRVYASVPIHNLVWGNSSIFS--NTVPATATSLDNLQSSDFGYFESANA

cry2ab2_820. FSDINIGNVWASSNSDVPLDINVTLSNGTQFDLMNMLVPTNISPLY
Q45735. FTS-SLGNIVGVNFGSTAGVYVORRPSIVTATLEAEYNLERAKQAVNALFTSTNQLGL

cry2ab2_820.pap
TXN5:Q45735
Description: X94146_1
Accession/ID: X94146_1
LOCUS X94146_1 (CBMT7)
DEFINITION C.bifermentans cbm71 gene.
DATE 17-JUN-1996

SCORES Initl: 114 Initn: 114 Opt: 207 z-score: 220.6 E(1): 2.2e-06
>>TXN5:X94146_1
Initn: 114 Initl: 114 Opt: 207 z-score: 220.6 expect(1): 2.2e-06
Smith-Waterman score: 215; 19.4% identity in 575 aa overlap
(77-630:44-606)

cry2ab2_820. KNNHSLVLDIPVGTVASFLKKKGLVSKRLSELRLNLIFFSGSTNIPMDILKSTSEL
X94146_1. KGVASVFKVIDTTHNISKNNNFNILTDQFIIDTILSLWELNENETFSMEDGETT

cry2ab2_820. NORLNTDLAR--VNAELTGLQANV--EENROVQNFNLNPNNAVPLSSTNVTNCGP
X94146_1. NKNLSAQTEKGLLNSNFGFLKFKFYNNAFRSWIDNY-NPTSIDDVYRFKDVNGSICE--

cry2ab2_820. LNRLPQFMQOGYQLLLPLFAQAANHLHSFIRDVILNADEWGISAAATLRTRDYLNKNTYR

Information of Monsanto Company

Study No. 06-01-62-01
MSL No. 20307
Page 156 of 361

SCORES	Initl: 114	Initn: 114	Opt: 207	z-score: 220.6 E(): 2.2e-06		
>>TXNS:CGAA_CLOBI				(613 aa)		
Initn: 114	initl: 114	opt: 207	Z-score: 220.6	expect(): 2.2e-06		
Smith-Waterman score: 215;			19.4% identity in 589 aa	overlap		
(77-630:44-606)						
cry2ab2_820.	110	120	130	140	150	160
CGAA_CLOBI	20	30	40	50	60	70
cry2ab2_820.	110	120	130	140	150	160
CGAA_CLOBI	80	90	100	110	120	130
cry2ab2_820.	170	180	190	200	210	220
CGAA_CLOBI	140	150	160	170	180	190
cry2ab2_820.	280	290	300	310	320	330
CGAA_CLOBI	250	260	270	280	290	300
cry2ab2_820.	340	350	360	370	380	390
CGAA_CLOBI	310	320	330	340	350	360
cry2ab2_820.	400	410	420	430	440	
CGAA_CLOBI	370	380	390	400	410	
cry2ab2_820.	450	460	470	480	490	
CGAA_CLOBI	420	430	440	450	460	
cry2ab2_820.	500	510	520	530	540	550
CGAA_CLOBI	480	490	500	510	520	
cry2ab2_820.	560	570	580	590	600	610
CGAA_CLOBI	530	540	550	560	570	

```

Description: Q45882 clostridium bifermentans. pesticidal crystal-like protein
             cry16aa (insec
Accession/ID: Q45882
=====General comments=====
ID   CGAA_CIOBI        STANDARD;          PRI;   613 AA.
AC   Q45882;          .

```


Study No. 06-01-62-01

MSL No. 20307

Page 157 of 361

CKAA_BACUF
YYWGNQFLSNGTSLNLYGRSDGR---TTFNVS--NIDIFRVNTHTHIGGAPTDYDGLGH
350 360 370 380 390 400

cry2ab2_820.
R-EGV-ATVTNNQTESFETTLGLRSAGFTARGSNYPDPVFIRNISGVPLVRVEDLRPP
390 400 410 420 430 440

CKAA_BACUF
RAEFICANTQNORTSLYSVEIPSSHFFENHTVFLPE-----SGLEPRERYTHRLF
410 420 430 440 450

cry2ab2_820.
LHYNEIRTIASPGTGGAARAYMVSVYHKNNIHAVHGSMIHLHPNDYTGFTISPIHA
450 460 470 480 490 500

CKAA_BACUF
QMNVES--VNPNAR---GRVFLHWATHRSRLR---RTNG-----LRSQQILQI---PAVK
460 470 480 490 500

cry2ab2_820.
TVNNQTRTFISERFGNGDS-LRPQNNMTARTYL-----RNGNSYNLYLRVSSNGS
510 520 530 540 550

CKAA_BACUF
TISNGGDRAWLV---NYGENIMKLONLTIGLSYKLTAVDSEASNTRFIVRVRYASVMNN
510 520 530 540 550

cry2ab2_820.
TIRVTINGRVYTATNVNTITNDGVNDNGARESDINIGNY-VASSNSDVPDLINVNLN-
560 570 580 590 600 610

CKAA_BACUF
KMLNLVNGAQIASLNVEHTVQR-----GGSLTDLOVGNFKYATFAGFMKGSSILGIF
560 570 580 590 600 610

cry2ab2_820.pep
KEPNIIDSLVDLKIELIPSFMSSLSEQTONYNTYNOQTIIYTHNGQDYTDYDNSSGMVHQSY
620 630 640 650 660 670
TXN5.U82518_1

Description: U82518 Bacillus thuringiensis Bacillus thuringiensis
mosquitocidal toxin gene, complete cds.
Accession/ID: U82518
=====General comment=====

LOCUS U82518.1 (BtU82518)
DEFINITION Bacillus thuringiensis mosquitocidal toxin gene, complete cds.

SCORES Initl: 101 Inithn: 126 Opt: 207 Z-score: 218.9 E(): 2.7e-06
>>TXN5.U82518_1
Initln: 126 Inith: 101 opt: 207 Z-score: 218.9 eexpect(): 2.7e-06
Smith-Waterman score: 210; 21.1% identity in 653 aa overlap
(24-632:27-631)

cry2ab2_820.
MQAMDNSVLSNGRTTCIDAYNVAADHP-PFOHKSLLDTTSKEWTWPKNNISLYLDA
10 20 30 40 50

U82518_1
MNPQNNDIEDVDPENYDNNLNRYPYANDPVNQ-----NTNYSKNWNGYEELNPSAATA
10 20 30 40 50

cry2ab2_820.
IVGTVASFLKKVSLVG-----KRILESLRN-LIPFSGSNTLMQDIURETEKFNQNN
60 70 80 90 100 110

U82518_1
ILASIG-LINRAVLTVGLNTQEVISIODALGFIRNGTG-NELLITHVEQLIQOTLA
60 70 80 90 100 110

Study No. 06-01-62-01
MSL No. 20307
Page 158 of 361

```

Description: Q45753 bacillus thuringiensis (subsp. darmstadtensis).
pesticidal crystal prote
Accession/ID: Q45753
=====General comments=====
ID      CSAB_BACUD      STANDARD;      PRT; 1289 AA.
AC      Q45753; . . .

SCORES      Init1: 95      Initn: 157      Opt: 196      Z-score: 202.9 E(): 2.1e-05
>>TXNS:CSAB_BACUD
Init1: 157 Init1: 95 Opt: 196 Z-score: 202.9 expect(): 2.1e-05
Smith-Waterman score: 196; 20.6% identity in 228 aa overlap
(87-300:114-335)

cry2ab2_820. 60 70 80 90 100 110
IVGTVASFLKKVGSIVGKRILSELRLNLIFFSGSNLMQDILRETEKFLNQRLNTDLAR
CSAB_BACUD LITLAVPEIGLFTPFIGLFFAALMKHDAPPFNADIDFEAKPKPAIQEMIDRLITADQGIT
90 100 110 120 130 140

cry2ab2_820. 120 130 140 150 160
VNAELTGLQANVEEFNRQVDNF-----LNPNRNVAFLGITSVNTMQQLFLNRLPQF---
cry2ab2_820. 170 180 190 200 210 220
OMQGYQLLLPLFLFAQANLHLHSFIRDVLNADEW-----GISAATLRTYDLYKNLTRYDYS
CSAB_BACUD NTADRTLGLPLFYVAIIASMHMLLRDIIITGPTMDSKINFPTDAISFKTDIKNNIKLYS
210 220 230 240 250 260

cry2ab2_820. 290 300 310 320 330 340
GSGPQOTQSFTSQDWPFYSLYFQVNSYVINGFGSARLSNFTFNIIVGLPGSTTTHALLAA
CSAB_BACUD GSGDISLQKTERILISFPPIRTADGLTLNNTSIDTSNPNFYENGNGAFNPXERILKQFK
320 330 340 350 360 370

cry2ab2_820.pep
TXN5:L07026_1

Description: L07026 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (CryA(b)) g
Accession/ID: L07026
=====General comments=====
LOCUS      L07026_1 [BACCRYVAB]
DEFINITION Bacillus thuringiensis delta-endotoxin (CryA(b)) gene, 5' end

SCORES      Init1: 95      Initn: 157      Opt: 196      Z-score: 202.9 E(): 2.1e-05
>>TXNS:L07026_1
Init1: 157 Init1: 95 Opt: 196 Z-score: 202.9 expect(): 2.1e-05
Smith-Waterman score: 196; 20.6% identity in 228 aa overlap
(87-300:114-335)

cry2ab2_820. 60 70 80 90 100 110
IVGTVASFLKKVGSIVGKRILSELRLNLIFFSGSNLMQDILRETEKFLNQRLNTDLAR

```


©01

L07026_1 LITLAVPEIGIFTPFGIFFAALNKHDAAPPNADKIDFEAMKPAICEMIDRILTADQTF

cry2ab2_820. VNDELGLQANVEDPQVDNF-----LAPNNAVPLSITSSVNTMOQLFLNLPQF---

L07026_1 LGEISGLQANVEDPQVDNF-----LAPNNAVPLSITSSVNTMOQLFLNLPQF---

cry2ab2_820. QMOGQQLLLPLFAQAANLHLSFIRDVILNADEW-----GISAAFLRYRDYLNKNTDYS

L07026_1 NTADRTLLGLFYAILASMHLMRLDRIITKGTMTDSKINFTPDARQSFVTDIKNKIKLYS

cry2ab2_820. NYCINTYQSAFGLNRLHDMLEFRYTMFLNVEYSWGL-----FKYQSLVSSGANLYAS

L07026_1 KTIYDFQKGLASYGTP--SDLESFAKKQ-----KYIEINTHCLDFAFLPFTDPDLYPT

cry2ab2_820. GSGPQQTQSTQSDMPFLYSLFQVNSYVNLGFGSARLSNTFPNIVDGSITTHALLAAR

L07026_1 GSGDISLOKTRILSPFIPTADGLTLNNTSIDTSNPNYENGNGAFNPKERILKQFK

cry2ab2_820.pap

TXN5:L07025_1

Description: L07025 Bacillus thuringiensis

Accession/ID: L07025

LOCUS L07025_1 (BACDRYVA)

DEFINITION Bacillus thuringiensis delta-endotoxin (CryA(a)) gene, 5' end.

SCORES Initl: 95 Initn: 128 Opt: 196 z-score: 202.3 E(): 2.3e-05

>>TXN5:L07025_1

Initn: 128 Initl: 95 Opt: 196 z-score: 202.3 expect(): 2.3e-05

Smith-Waterman score: 201; 19.0% identity in 585 aa overlap

cry2ab2_820. IVGTASFLKKVGLVGLKILSELNRLIFPSGSTNLMDILRETEKFNQRLNLTDLAR

L07025_1 LITLAVPEIGIFTPFGIFFAALNKHDAAPPNADKIDFEAMKPAICEMIDRILTADQTF

cry2ab2_820. VNDELGLQANVEDPQVDNF-----LAPNNAVPLSITSSVNTMOQLFLNLPQF---

L07025_1 LGEISGLQANVEDPQVDNF-----LAPNNAVPLSITSSVNTMOQLFLNLPQF---

cry2ab2_820. QMOGQQLLLPLFAQAANLHLSFIRDVILNADEW-----GISAAFLRYRDYLNKNTDYS

L07025_1 NTADRTLLGLFYAILASMHLMRLDRIITKGTMTDSKINFTPDARQSFVTDIKNKIKLYS

cry2ab2_820. NYCINTYQSAFGLNRLHDMLEFRYTMFLNVEYSWGL-----FKYQSLVSSGANLYAS

L07025_1 KTIYDFQKGLASYGTP--SDLESFAKKQ-----KYIEINTHCLDFAFLPFTDPDLYPT

cry2ab2_820. GSGP---OQTSQFTSQDWFLYSLFQVNSYVNLGFGSARLSN--TFPNI-----

L07025_1 GSGDISLOKTRILSPFIPTADGLTLNNTSIDTSNPNYENGNGAFNPKERILKQFK

cry2ab2_820. -----VGLPGSITTHALLAARVNS-----GGISSGDIASPNQNFNCSTFLPPLT

L07025_1 LYPWRACQVGLLQFLYALIEVQDSVETRLYGQLPAVDFQAPNYSIDSN---PIIQ

cry2ab2_820. PFVRSWLDSSGREGVATVNTQTESFETTL--GL-----RSGAFTARGNSNYFPD----

L07025_1 INMDTW---XTPQGA---SGWNTLMRGSVSLFLQDGTSLSGMGGGFGADTIYSLP

cry2ab2_820. ---YFIRNLSGVPLVVRNEDLRPLHNEIRNIASP--SGTPG--GARAYMVSVHNRKNNI

L07025_1 ATHLSLYLGTPTQSDN---YSGHVGLAVGVSTPQEATLPNIIGQDPDEQGNVSTMGFPF

cry2ab2_820. HAVNENSGMHLAPNDVTGFTSPHATOVNNTTRIFISEKEFGNOGDSLREONNTTARY

L07025_1 EKASVGTGKELNANAKLSQCSIGIPINVT-----GEYQICRYASNDINVP

cry2ab2_820. TARGNGLYLYLRV---SGLGSTRIVGRVYATVNTTNNNDGNDNGARFSDIN

L07025_1 FNVATGAPNIFQVITLSTVNNNGVNGANG-VYVVKSIATDINS--FTEIPAKTINVH

cry2ab2_820. IGNVVASSNDVPLDINWTLNSGQVNMIMLVNTNIPPLY

L07025_1 LTN---QGSSDVFDRIFETIPSLPIYGLYVYSSGADVWLSNNNNYDIIVNGOAN

cry2ab2_820.pap

TXN5:CSAA_BACUD

Description: Q45760 bacillus thuringiensis (subsp. darmstadtensis).

Accession/ID: Q45760

ID CSAA_BACUD

AC Q45760; . . .

SCORES Initl: 95 Initn: 128 Opt: 196 z-score: 202.3 E(): 2.3e-05

>>TXN5:CSAA_BACUD

Initn: 128 Initl: 95 Opt: 196 z-score: 202.3 expect(): 2.3e-05

Smith-Waterman score: 201; 19.0% identity in 585 aa overlap

Study No. 06-01-62-01
MSL No. 20307
Page 160 of 361

```

cry2ab2_820.   IVGTVASFLKKVGSVLVGKRLISLRNLIFPSSGNLMQDLIRTEFKLNQRNLTDLAR
                  60      70      80      90     100
C5AA_BACUD    LITLAVFEIGITFTFGLFFAALNKHDAPPFPNAKDIIPEAKPAIQEMIDRTILTADEQFT
                  90     100     110     120     130     140
cry2ab2_820.   VNAELTGLQANVEENRQVDNF---LNFNRNAVPLSTTSYNTMQOLFNRLPQF---
                  120     130     140     150     160
C5AA_BACUD    LINGEISGQLNLAARYQSTMDIOIQSHGFKNQVDSGLIKFTFDIVLSNSFYDRLPFVIFTD
                  150     160     170     180     190     200
cry2ab2_820.   QMOQGYQLLLPLFAQAANLIHSFIIRDILNADEW---GISAAATLRYRDLYLNTRYDS
                  170     180     190     200     210     220
C5AA_BACUD    NTAORTLGLPYVAIILASMHMLMRDIITKGPTWDSKINFTPDALDSFKTDIKNNIKLYS
                  210     220     230     240     250     260
cry2ab2_820.   NYCANTVQSFAFKGLNTRLHDMLETRTYFMFNWEIYSWSL--FKYOSLLVSSGANLYAS
                  230     240     250     260     270     280
C5AA_BACUD    KTIIDVFQKGLASYGP-SDLESFAKXQ-----KYIEIMTHCLDFARLPFFTFDPDLXYT
                  270     280     290     300     310
cry2ab2_820.   GSGP---QOTQSFTSQDMPPFLYS--LFQVNSNVLVNGFGSARLNS-TFPNI-----
                  290     300     310     320
C5AA_BACUD    GSGDISLQKTRRLSPPIRATAOGLTLNNTSIDTSNPVNYENGAGAFNPERILKQFK
                  320     330     340     350     360     370
cry2ab2_820.   -----VGLPGSTTHALLAARVNS-----GGISSGDIGASFNQFNCSFTPLPLLIT
                  330     340     350     360     370
C5AA_BACUD    LYPWSRAGQYGSLQLPYLMAIEVQDSVETRLYQGLFAPDVPOAGNVYVSIDSNN---PIIQ
                  380     390     400     410     420     430
cry2ab2_820.   PFVRSWLDSGSDREGVATVTWKOTESFETTL-GL-----RSCAFTARGSNYFPD-----
                  380     390     400     410     420
C5AA_BACUD    INMDTW---XTPPQGA---SGWNILMRGVSGLSFLODRGTRLSAGMGWGGFADITYSLP
                  440     450     460     470     480
cry2ab2_820.   --YFIRNISGVPLVRNEDLRRPLHYNERINIASP--SGTPG--GARAYVNSVHNRRKNI
                  430     440     450     460     470
C5AA_BACUD    ATHYLSLYTGTPQYISDN---YSHCVGALVGVYSTQEATLNIIGQPDEQGNVSTMGTGFF
                  490     500     510     520     530     540
cry2ab2_820.   HAVHENGSMIHILAPNDYTGFILSIPIAHQTUNQOTFTISEKFNOGDSURFPONNTIARY
                  480     490     500     510     520     530
C5AA_BACUD    EKASYGTGVVKWKLNGAMKLSPGSIGIPITNYS-----GEYQIRCRYASNDNTNVF
                  550     560     570     580     590     600
cry2ab2_820.   TLRGNGSNYNILRV---SSITGNSITRVINGSVVATNVMTTNDVNDNGCARFSIN
                  540     550     560     570     580     590
C5AA_BACUD    FNVDTGANDPIFOQINFASTVDNNIGVOQGANG-VVIVKSIAITDNS--FTEIPAKTINVH
                  610     620     630     640     650
cry2ab2_820.   IGNUVASSNSDVFLDINTVLSNGSQFDLMNIMLVPTNISPLY
                  600     610     620     630

```

```

: | : : : ||| ||
C5AA_BACUD LTN---QGSDVFLDRIEIPFSLPIVHGYSNTSGADDVLWSSNNMYDIIVNGQAN
660 670 680 690 700 710

cry2ab2_820.pep
TXN5:C5AC_BACTU

Description: P56955 bacillus thuringiensis. pesticidal crystal protein cry5ac
(insecticidal
Accession/ID: P56955
=====General comments=====
ID C5AC_BACTU STANDARD; PR1; 1220 AA.
AC P56955; . . .

SCORES Initl: 95 Initn: 153 Opt: 194 z-score: 201.2 E(): 2.7e-05
>>TXN5:C5AC_BACTU
Initn: 153 Initl: 95 Opt: 194 z-score: 201.2 expect(): 2.7e-05
Smith-Waterman score: 194; 20.6% identity in 228 aa overlap
(87-300-114-335)

cry2ab2_820. IGVTVASFLLKKVGLVGRILSELRNLIPFGSTNLMQDLIRETEKPLNQRNLTTLAR
60 70 80 90 100 110
cry2ab2_820. VNAELTGLQANVEENRQVDFN-----LNPENRNVPLTSSVNTMQQLFLNLPQF---
120 130 140 150 160
C5AC_BACTU LITLAVPEIGITPTFGIFGLFAALNKHDPAPPNNAKDIFEAMKPAIQEMIDRTLTDAEQTF
90 100 110 120 130 140
cry2ab2_820. LMGISGLQNLARIQSTMDDDIQSHGGFNKVDLSGLIKKFTDEVLSNLSFYDRPLPFIID
150 160 170 180 190 200
C5AC_BACTU
170 180 190 200 210 220
cry2ab2_820. QMOGQYQLLLPLFAQAANLHLSFIRDVLNADEW---GISAAATLRYRDYLNKNTRDYS
210 220 230 240 250 260
C5AC_BACTU NTADRTLLGLPYVAILASMLMLRLDIIITKPTWDSKINFTPDALDSFKDIKNMKILYS
210 220 230 240 250 260
cry2ab2_820. NYCINTQSAFKGLNTRLHDMLEFRTYFMVNFYVYSIWSL--FKYQSLLVSSGANLYAS
230 240 250 260 270 280
C5AC_BACTU KTIYDVQFKGLASYGTP--SDLESFAKKK-----KYIEITHTCLDFARLFFPTFDPLPYT
270 280 290 300 310 320
cry2ab2_820. GSGPQQTQSTFSQDMPELYSLFQVNSNYVLNFGSGARLSNTFNNIVGLPGSTITTHALLAA
290 300 310 320 330 340
C5AC_BACTU GSGDISLQKTRRLSPFIPTAQDGLTNNTSIDTNSPNNTNNGAFNPXPKRILKQFK
320 330 340 350 360 370
cry2ab2_820.pep
TXN5:CCAA_BACTU

Description: Q45754 bacillus thuringiensis. pesticidal crystal protein
CryI2aa (insecticidal
Accession/ID: Q45754
=====General comments=====
ID ID CCAA_BACTU STANDARD; PR1; 1257 AA.
AC Q45754; . . .

```


SCORES Initl: 87 Initn: 87 Opt: 187 z-score: 193.5 E(): 7.1e-05
>TXNS:SCAA_BACTU (1257 aa)
Initn: 87 Opt: 187 z-score: 193.5 expect(): 7.1e-05
Smith-Waterman score: 228; 19.8% identity in 602 aa overlap
(52-632:78-618)

cry2ab2_820. VAAHPFSGFVKSLSLDTVQKTEWKNHSLYPIPIVGVASFLKKGSLVGRKRIUSEL
CCAA_BACTU KGKDLLDVAMTATTEIDEPEVYKSVLTLPEVSTVAS-AASTIVSFYKIFGDK
50 60 70 80 90 100

cry2ab2_820. RNLIFPSSGNTLMQDLRETELKRLNTDGLRVNAELTGLQANVEFNQVDNFINP
CCAA_BACTU PN-----AKNIFELKPOIEALIQDSTNVDAINKKKFSLOKTIINLYVAIDN--ND
110 120 130 140 150

cry2ab2_820. NRNAVPLSITSSVNTMQQLFNLRFQFQMGQYQLLSLDFPQANDKSFADVILNAD
CCAA_BACTU YVTA-----KTQLENLSILTSISIFPEGYETGGUPFYVAVANAHILLRLDVAEAK
160 170 180 190 200

cry2ab2_820. WGISAATLRTYRDLKANYTRDSNYCINTYQSA---PKGLNTRLHDM-LEFRTYMLNVF
CCAA_BACTU LGFSDKEVDTHKKYIKMTIHNHTEAVIKAPFLGLDLPKSLDVNSYKANKYIKGTEML
220 230 240 250 260 270

cry2ab2_820. EYVSIWSLF---KYQSLVSSGANLYAS---GSGPQOTQSTSDQWPFYLSLFOVNSYV
CCAA_BACTU DLVALWPTFDPDHYQKEVEIEFTRITSSPIYQVPKMNQNTSSIVP--SOLFHYQGLV
280 290 300 310 320 330

cry2ab2_820. LNPFSGAR-----LSNTFPNIVGL-----PGS-TTTHALLAARVNYSGGSSGDIASPFNQ
CCAA_BACTU KLEFSTRDNDGLAKIFTGIRNTFYKSPNTHETVYHVDVSYNTQSGNISRGSNPIDIL
340 350 360 370 380 390

cry2ab2_820. NFNCSTFLPPLLITPVRSLDSDREGVAVTVMQTESPETTLGLRSGATARGSNYF
CCAA_BACTU N-----NPIISTCIRNSFYKAI--AGSSVIVNFKD-----GTQGYAFAQAPTGGAW
400 410 420 430

cry2ab2_820. PDYFIRNLISGVLVVRNEDLRPLHYNEIRNIASPTGCGARAYVWSVHRKKNHIAHV
CCAA_BACTU DSHFTES--DGAP-----EGHK--LVNI-----YTSPGDT---LEDFI-----NVYTLI
440 450 460 470

cry2ab2_820. ENGSMIHLAPNDYTGFTISPIHATQVNNQ--TRTIFSEKFGNQGSLRFEQNNTIATYLL
CCAA_BACTU STPTINELSTEKIKGF---PAEKGYIKQOGIMKYGKPEYINGAQVPLENQQLIFEFH
480 490 500 510 520

cry2ab2_820. RGNHNSYLYLRVSSIGNSTIRVTNGRVYATATVNTTINDGVNDNGARFSDINIGNVV
CCAA_BACTU ASKTAQYTIIRIRYASTQGTGKGYFRLDNQELQTLNPTSHNGYVITGNIGNYDLTYIGSYT
550 560 570 580 590 600

cry2ab2_820. ASSNSDVPLDIDINVTLNSGTQFDLNMIMLVPTNISPLY
CCAA_BACTU ITEGNHT-LQIQHNDKNGWILD--RIEFVFKDSLODSDPPPEVHESIITIEDKXSPTIM
590 600 610 620 630 640

CCAA_BACTU SSNKHYSIHILEGYSYTSQGSYPHNLINLHFTDPNRNHTIHNNGMDNMVYDGKDSVAD
650 660 670 680 690 700

cry2ab2_820.pep
TXNS.L07027_1

Description: L07027 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (CryVB) ge
Accession/ID: L07027
=====General comments=====

LOCUS L07027.1 [BACCRYVB]
DEFINITION Bacillus thuringiensis delta-endotoxin (CryVB) gene, 5' end.
SCORES Initl: 87 Initn: 87 Opt: 187 z-score: 193.5 E(): 7.1e-05
>TXNS:L07027_1

Initn: 87 Opt: 187 z-score: 193.5 expect(): 7.1e-05
Smith-Waterman score: 228; 19.8% identity in 602 aa overlap
(52-632:78-618)

cry2ab2_820. VAAHPFSGFVKSLSLDTVQKTEWKNHSLYPIPIVGVASFLKKGSLVGRKRIUSEL
L07027_1 KGKDLLDVAMTATTEIDEPEVYKSVLTLPEVSTVAS-AASTIVSFYKIFGDK
50 60 70 80 90 100

cry2ab2_820. NRNAVPLSITSSVNTMQQLFNLRFQFQMGQYQLLSLDFPQANDKSFADVILNAD
L07027_1 YVTA-----KTQLENLSILTSISIFPEGYETGGUPFYVAVANAHILLRLDVAEAK
160 170 180 190 200 210

cry2ab2_820. WGISAATLRTYRDLKANYTRDSNYCINTYQSA---PKGLNTRLHDM-LEFRTYMLNVF
L07027_1 LGFSDKEVDTHKKYIKMTIHNHTEAVIKAPFLGLDLPKSLDVNSYKANKYIKGTEML
220 230 240 250 260 270

cry2ab2_820. EYVSIWSLF---KYQSLVSSGANLYAS---GSGPQOTQSTSDQWPFYLSLFOVNSYV
L07027_1 DLVALWPTFDPDHYQKEVEIEFTRITSSPIYQVPKMNQNTSSIVP--SOLFHYQGLV
280 290 300 310 320 330

cry2ab2_820. LNPFSGAR-----LSNTFPNIVGL-----PGS-TTTHALLAARVNYSGGSSGDIASPFNQ
L07027_1 KLEFSTRDNDGLAKIFTGIRNTFYKSPNTHETVYHVDVSYNTQSGNISRGSNPIDIL
340 350 360 370 380 390


```
cry2ab2_820. 370 380 390 400 410 420
NFNCSTFLPPLLTFFVRSMLDSCSDREGVATVTVNQTESPEITTLGLRSGAFTARGSNVF
L07027_1 N-----NPISTCTRNSEFYKAI--AGSSVLVNFKD-----GTQVAFQAQAPTGAW
400 410 420 430

cry2ab2_820. 430 440 450 460 470 480
PDYFIRNLSGVPLVRNEDLRPLHYNIRIASPSCPTGGARAYVSVHNRKNNIHAVH
L07027_1 DHSFTES-DGAP-----EGHK--LNVY--YTSFGDT---LRDFI-----NVVTLI
440 450 460 470 480 490

cry2ab2_820. 490 500 510 520 530 540
ENGSMHLAPNDYTGFIISPIHATQNNQ--TRTFISEKFGNQSGLRFEQNNTTARYTL
L07027_1 STFTINELSTEKIKGF---PAEKGYIKNQGIMKYGKPEYINGAQPVNLENOQTILFEFH
480 490 500 510 520 530

cry2ab2_820. 550 560 570 580 590 600
RNGNSYNLYLRVSSIGNSTIRVTINGRVTATVNTVNTTNNQVNDGARGESDINIGNV
L07027_1 ASKTAQYIIRIRYASTQGTGFRIDNQELQTLNIPTSNNGYVTGNGENLDLTIGSYT
530 540 550 560 570 580 590

cry2ab2_820. 610 620 630
ASSNSDVPLDINVLNLSGTQFDLMNIMLVPTNISPLY
L07027_1 ITEGNHT-LQIHNDRKNGMVLQ--RIEFVPKDSLQDSFQDSPPPEVHESTIIFDKSSPTIW
590 600 610 620 630 640

L07027_1 SSNKSYSHIHLEGSYTSQGSYPHLLINLPHPTDPNRNTHIVNNGDMNVYDKDSVAD
650 660 670 680 690 700

cry2ab2_820.pap
TXN5:M12662_1

Description: M12662 Bacillus thuringiensis B.thuringiensis insecticidal
endotoxin gene, compl
Accession/ID: M12662
=====General comments=====
LOCUS M12662_1 [BACMSQB]
DEFINITION B.thuringiensis insecticidal endotoxin gene, complete cd;

SCORES Initl: 69 Initn: 101 Opt: 173 z-score: 183.7 E(): 0.00025
>TXN5:M12662_1
initn: 101 initl: 69 opt: 173 z-score: 183.7 expect(): 0.00025
Smith-Waterman score: 179; 22.8% identity in 232 aa overlap
(55-263:68-296)

cry2ab2_820. 30 40 50 60 70
HDPFSFQHKSLDTVQKEWTKNNHSLYLDPIVGTVASFLKKVGSVLGKR-----
M12662_1 PLKNTNYKDLNVQCQDQNGNAGNFASSETIVGVSAGIIV--VGTMLGAFAPVLAAG
40 50 60 70 80 90

cry2ab2_820. 80 90 100 110 120 130
ILSELRLN-IPFSGS--TNLMQDILRETEKFLNQLRNTDTLARVNAELTGLQANVEFN
M12662_1 IISFGTLPIFWQGSDFPANVWQDLNIGRPI-QEIDKNIIINVLTSIVTPIKNQLDKYQE
100 110 120 130 140 150

cry2ab2_820. 140 150 160 170 180 190
QVDNFLNPNRNPVLSITSSVNTMQQLFLNRLPQFOMOG-YQLLLPLFPAQANLHLSFI
M12662_1 FFDKWEPARTHANAKAVHDLFTLLEPIIDKDLMLKNNASRYRIPTLPAYAQIATWHLNLL
160 170 180 190 200 210

cry2ab2_820. 200 210 220 230 240
RDVILNADEW----GISAAITLRT---YRDYLNKYTRYDSNYCINTYQSAFKGLNTRLH--
M12662_1 KHAATYNIWLQNGINSTFNSSNYQGYLKKKIQEYTDYCIQTYNAGLTMTIRNTNAT
220 230 240 250 260 270

cry2ab2_820. 250 260 270 280 290 300
-DMLE-FRTYMFNLNPFVETVSWLSFKYQSLVSSGANLYASGSGPQQTQSFISQDWPFY
M12662_1 WMYNTYRLMELTIVLDLIAIFPNYDPEKYPVIGKSELIREVYTNVNSDFTFRITTELENG
280 290 300 310 320 330

cry2ab2_820.pap
TXN5:CAAA_BACTI

Description: P09662 bacillus thuringiensis (subsp. israelensis). pesticidal
crystal protein
Accession/ID: P09662
=====General comments=====
ID CAAA_BACTI STANDARD; PRT; 675 AA.
AC P09662;

SCORES Initl: 69 Initn: 101 Opt: 173 z-score: 183.7 E(): 0.00025
>TXN5:CAAA_BACTI
initn: 101 initl: 69 opt: 173 z-score: 183.7 expect(): 0.00025
Smith-Waterman score: 179; 22.8% identity in 232 aa overlap
(55-263:68-296)

cry2ab2_820. 30 40 50 60 70
HDPFSFQHKSLDTVQKEWTKNNHSLYLDPIVGTVASFLKKVGSVLGKR-----
CAAA_BACTI PLKNTNYKDLNVQCQDQNGNAGNFASSETIVGVSAGIIV--VGTMLGAFAPVLAAG
40 50 60 70 80 90

cry2ab2_820. 80 90 100 110 120 130
ILSELRLN-IPFSGS--TNLMQDILRETEKFLNQLRNTDTLARVNAELTGLQANVEFN
CAAA_BACTI IISFGTLPIFWQGSDFPANVWQDLNIGRPI-QEIDKNIIINVLTSIVTPIKNQLDKYQE
100 110 120 130 140 150

cry2ab2_820. 140 150 160 170 180 190
QVDNFLNPNRNPVLSITSSVNTMQQLFLNRLPQFOMOG-YQLLLPLFPAQANLHLSFI
CAAA_BACTI FFDKWEPARTHANAKAVHDLFTLLEPIIDKDLMLKNNASRYRIPTLPAYAQIATWHLNLL
160 170 180 190 200 210

cry2ab2_820. 200 210 220 230 240
RDVILNADEW----GISAAITLRT---YRDYLNKYTRYDSNYCINTYQSAFKGLNTRLH--
CAAA_BACTI KHAATYNIWLQNGINSTFNSSNYQGYLKKKIQEYTDYCIQTYNAGLTMTIRNTNAT
220 230 240 250 260 270

cry2ab2_820. 250 260 270 280 290 300
-DMLE-FRTYMFNLNPFVETVSWLSFKYQSLVSSGANLYASGSGPQQTQSFISQDWPFY
CAAA_BACTI WMYNTYRLMELTIVLDLIAIFPNYDPEKYPVIGKSELIREVYTNVNSDFTFRITTELENG
280 290 300 310 320 330
```

```
cry2ab2_820. 140 150 160 170 180 190
QVDNFLNPNRNPVLSITSSVNTMQQLFLNRLPQFOMOG-YQLLLPLFPAQANLHLSFI
M12662_1 FFDKWEPARTHANAKAVHDLFTLLEPIIDKDLMLKNNASRYRIPTLPAYAQIATWHLNLL
160 170 180 190 200 210

cry2ab2_820. 200 210 220 230 240
RDVILNADEW----GISAAITLRT---YRDYLNKYTRYDSNYCINTYQSAFKGLNTRLH--
M12662_1 KHAATYNIWLQNGINSTFNSSNYQGYLKKKIQEYTDYCIQTYNAGLTMTIRNTNAT
220 230 240 250 260 270

cry2ab2_820. 250 260 270 280 290 300
-DMLE-FRTYMFNLNPFVETVSWLSFKYQSLVSSGANLYASGSGPQQTQSFISQDWPFY
M12662_1 WMYNTYRLMELTIVLDLIAIFPNYDPEKYPVIGKSELIREVYTNVNSDFTFRITTELENG
280 290 300 310 320 330

cry2ab2_820.pap
TXN5:CAAA_BACTI

Description: P09662 bacillus thuringiensis (subsp. israelensis). pesticidal
crystal protein
Accession/ID: P09662
=====General comments=====
ID CAAA_BACTI STANDARD; PRT; 675 AA.
AC P09662;

SCORES Initl: 69 Initn: 101 Opt: 173 z-score: 183.7 E(): 0.00025
>TXN5:CAAA_BACTI
initn: 101 initl: 69 opt: 173 z-score: 183.7 expect(): 0.00025
Smith-Waterman score: 179; 22.8% identity in 232 aa overlap
(55-263:68-296)

cry2ab2_820. 30 40 50 60 70
HDPFSFQHKSLDTVQKEWTKNNHSLYLDPIVGTVASFLKKVGSVLGKR-----
CAAA_BACTI PLKNTNYKDLNVQCQDQNGNAGNFASSETIVGVSAGIIV--VGTMLGAFAPVLAAG
40 50 60 70 80 90

cry2ab2_820. 80 90 100 110 120 130
ILSELRLN-IPFSGS--TNLMQDILRETEKFLNQLRNTDTLARVNAELTGLQANVEFN
CAAA_BACTI IISFGTLPIFWQGSDFPANVWQDLNIGRPI-QEIDKNIIINVLTSIVTPIKNQLDKYQE
100 110 120 130 140 150

cry2ab2_820. 140 150 160 170 180 190
QVDNFLNPNRNPVLSITSSVNTMQQLFLNRLPQFOMOG-YQLLLPLFPAQANLHLSFI
CAAA_BACTI FFDKWEPARTHANAKAVHDLFTLLEPIIDKDLMLKNNASRYRIPTLPAYAQIATWHLNLL
160 170 180 190 200 210

cry2ab2_820. 200 210 220 230 240
RDVILNADEW----GISAAITLRT---YRDYLNKYTRYDSNYCINTYQSAFKGLNTRLH--
CAAA_BACTI KHAATYNIWLQNGINSTFNSSNYQGYLKKKIQEYTDYCIQTYNAGLTMTIRNTNAT
220 230 240 250 260 270

cry2ab2_820. 250 260 270 280 290 300
-DMLE-FRTYMFNLNPFVETVSWLSFKYQSLVSSGANLYASGSGPQQTQSFISQDWPFY
CAAA_BACTI WMYNTYRLMELTIVLDLIAIFPNYDPEKYPVIGKSELIREVYTNVNSDFTFRITTELENG
280 290 300 310 320 330
```


Study No. 06-01-62-01

MSL No. 20307

Page 163 of 361

280	300	310	320	330
-----	-----	-----	-----	-----

Description: X58120 *Bacillus thuringiensis* B. thuringiensis DNA for

=====General comment=====

Handwritten signature

inchi: 127 inchi: 57 op: 167 z-score: 1/2.9 expected: 0.001
Smith-Waterman score: 206. 24 1% identity to 404 overlaps

Year	1950	1955	1960	1965	1970	1975	1980	1985	1990
Population (millions)	150	160	170	180	190	200	210	220	230

Year	1960	1970	1980	1990	2000
Population (millions)	1.2	1.5	1.8	2.1	2.4
GDP (billions of dollars)	100	150	200	250	300
Life expectancy (years)	45	55	65	75	85
Urban population (%)	20	30	40	50	60
Healthcare expenditure (per capita)	10	20	30	40	50
Education expenditure (per capita)	5	10	15	20	25
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (billions of dollars)	0.5	1.0	1.5	2.0	2.5
Trade share (GDP %)	10	15	20	25	30
Immigration (millions)	0.1	0.2	0.3	0.4	0.5
Emigration (millions)	0.1	0.2	0.3	0.4	0.5
Net migration (millions)	0.0	0.0	0.0	0.0	0.0
Population growth rate (%)	1.5	1.8	2.0	2.2	2.4
Urbanization rate (%)	20	30	40	50	60
Healthcare expenditure (GDP %)	1.0	1.5	2.0	2.5	3.0
Education expenditure (GDP %)	0.5	0.8	1.0	1.2	1.5
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (GDP %)	0.5	0.8	1.0	1.2	1.5
Trade share (GDP %)	10	15	20	25	30
Immigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Emigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Net migration (GDP %)	0.0	0.0	0.0	0.0	0.0
Population growth rate (%)	1.5	1.8	2.0	2.2	2.4
Urbanization rate (%)	20	30	40	50	60
Healthcare expenditure (GDP %)	1.0	1.5	2.0	2.5	3.0
Education expenditure (GDP %)	0.5	0.8	1.0	1.2	1.5
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (GDP %)	0.5	0.8	1.0	1.2	1.5
Trade share (GDP %)	10	15	20	25	30
Immigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Emigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Net migration (GDP %)	0.0	0.0	0.0	0.0	0.0
Population growth rate (%)	1.5	1.8	2.0	2.2	2.4
Urbanization rate (%)	20	30	40	50	60
Healthcare expenditure (GDP %)	1.0	1.5	2.0	2.5	3.0
Education expenditure (GDP %)	0.5	0.8	1.0	1.2	1.5
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (GDP %)	0.5	0.8	1.0	1.2	1.5
Trade share (GDP %)	10	15	20	25	30
Immigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Emigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Net migration (GDP %)	0.0	0.0	0.0	0.0	0.0
Population growth rate (%)	1.5	1.8	2.0	2.2	2.4
Urbanization rate (%)	20	30	40	50	60
Healthcare expenditure (GDP %)	1.0	1.5	2.0	2.5	3.0
Education expenditure (GDP %)	0.5	0.8	1.0	1.2	1.5
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (GDP %)	0.5	0.8	1.0	1.2	1.5
Trade share (GDP %)	10	15	20	25	30
Immigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Emigration (GDP %)	0.1	0.2	0.3	0.4	0.5
Net migration (GDP %)	0.0	0.0	0.0	0.0	0.0
Population growth rate (%)	1.5	1.8	2.0	2.2	2.4
Urbanization rate (%)	20	30	40	50	60
Healthcare expenditure (GDP %)	1.0	1.5	2.0	2.5	3.0
Education expenditure (GDP %)	0.5	0.8	1.0	1.2	1.5
Unemployment rate (%)	5	10	15	20	25
Government spending (GDP %)	10	15	20	25	30
Foreign aid (GDP %)	0.5	0.8	1.0	1.2	1.5
Trade share (GDP %)	10	15	20	25	30
Immigration (GDP %)	0.1	0.2			

cy2ab2_820. EWGISAAT-LRTYRDYLKNYTRDYSNYCINTYQSAFKGLNTRLHD--MLEFRTY

X58120 2 LMVI.DIVASSESS1.DITNVPIETDEOISPVITYTDPICEVHRESS1.PCESW-PSE-IN

310	320	330	340	350	360
-----	-----	-----	-----	-----	-----

340	350	360	370	380
-----	-----	-----	-----	-----

cyzabz_820. SIFLPPLLPFVRSWLDGSDREGVATVTNWQTESFETTLGLRSGAF---TARGET

EGYIRT-TGIDNPRVQNTVI.PGENSDTPTPEDYTHI--I.STTINLTCCI PAIV

480	490	500	510	520
-----	-----	-----	-----	-----

500 510 520 530 540

cy2ad2_820. LRFEQNNTTARYTLRGNGNSYNLY-LRVSSIGNSTIRVTINGRVYTAT-NVNTTII

CRY2#b2	820	590	600	610	620	630
	NDNGAPESDINICNVAACSNCSNVDI					
	DIINFTINCSCTEDYMNIMYVDTNYCRY					

Accession/ID:	Q99031
	-----General-----

```

Z-TRANS: CORR_FACTS
initn: 127 initl: 97 opt: 167 Z-score: 172 g expect(): 0 001
(I136 aa)

```

100

C9AA (ACTG ELRTRFRADSEFDRILTRGSLTNGGSLARONAOILLPSFASAAFFHLLLLLRDATRYGT

NY 2362	800	210	220	230	240	250
FIVE STAR - I P T Y B O V I K N V T D P V C N I V C T N T V A C A E R V C T N T T T I D						

220	240	250	260	270
-----	-----	-----	-----	-----

2025-02-20 10:20:00

100

C9AA_BACTG
 DLENAIPNPRPSWFLNNMIISTGSLTLPSPSTDRARVWG--SRDRIT--SPAN-----

370 380 390 400 410 420

390	400	410	420	430	440
-----	-----	-----	-----	-----	-----

020: DIFINISGV--FLVV-----KNEDGRFTHINETRNIASPSGIPGGARAYNVSWIN
:
: :

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 164 of 361

```
cry2ab2_820. 480 490 500 510 520
RKNWTHAVHENGSMHLPNDYTGFTISPIHATGV--NNQTR----TFISERKFGQDS
C9AA_BACTG RSSLS--VMYGWTHKSLARN---TINPDRIQTPLTKVDTRGVSVDNPDGFIGGAL
500 510 520 530 540
cry2ab2_820. 530 540 550 560 570 580
LRFEGNNITARYTLRNGNSYNLY-LRVSSIGNSITRVINGRVYTAI-NVMVTTINNDGV
C9AA_BACTG LORTDHSGLVLRQVPLHRLQOYRIRURVASTINRLSVNGSFGTISQNLPSMTWLGED
550 560 570 580 590 600
cry2ab2_820. 590 600 610 620 630
NDNGARFSDINIGNVASSNSDVPLDINVLNSGTQFDLMNLVFTNISPLY
C9AA_BACTG LRYGSAIREFNTSIRPTASPDQIRLTIEPSFIRQEVYVDRIEFIPVNPTRAKEDLEAA
610 620 630 640 650 660
cry2ab2_820.pcp
TXN5:C4AA_BACTI
Description: P16480 bacillus thuringiensis (subsp. israelensis). pesticidal
crystal protein
Accession/ID: P16480
ID C4AA_BACTI STANDARD; PRT; 1180 AA.
=====
General comments=====
=====
AC P16480; . . .

SCORES Initl: 63 Initn: 199 Opt: 159 z-score: 164.3 E(): 0.003
>TXN5:C4AA_BACTI
Initn: 199 Initl: 63 opt: 159 z-score: 164.3 expect(): 0.003
Smith-Waterman score: 201; 20.8% identity in 630 aa overlap
(57-633:76-681)

cry2ab2_820. 30 40 50 60 70 80
PFSFQHKSLDTVQKEMTKWKNHSLYLDPIVGTV-ASF-LLKKVG-SLVGKELISELRN
C4AA_BACTI DMLNMQOQOYGGDETFIDSGELSAITVVGIVLGTGFTTPLGLALIG---FGLIP
50 60 70 80 90 100

cry2ab2_820. 90 100 110 120 130 140
LIFFS-GSTNIMQDILRETEKFLNQRLNTDLARVNAELTGQAQVBNFRQVDNFLN-P
C4AA_BACTI VLFPQDOSNTWSDFTQTKNIKKKEIASITYISNANKILNRSFNVISYVHNHLKTWENN
110 120 130 140 150 160

cry2ab2_820. 150 160 170 180 190
NRNAVPLSITSSVNTWQQLFLNRLPQF-----OMQGYQLLLPLPQAQANLHLSFI
C4AA_BACTI NPQNTQ-DVRTQQLVHYFQNVIEPVLSVCPNPSDCDYINILVSSYAQAANLHITVL
170 180 190 200 210 220

cry2ab2_820. 200 210 220 230
RDVI-----LNADHWGISATLRTYRDYLNKNTYR---DYSNYCINTYQSAFKGLN-----
C4AA_BACTI NOAVKFEAYLKNRQFDYLEPLFTAIDYVPLTKAIEDYTNVYCVITYK---KGLNLKTTI
230 240 250 260 270

cry2ab2_820. 240 250 260 270 280 290
--TRLHDLMEFTYMLNVPFVSVISWLSLFKYQSILVSSGANLYASGSGPQOT---OSFT
C4AA_BACTI PDSNLDGNINWNTY--NTYRKMTTAVLDLVALFPNYDVGKPIGVQSELTRIIYQVLN
```

```
280 290 300 310 320 330 340
cry2ab2_820. SQDWPLYSLFQWNSYVNLGFGARLSNTFPNIVGL----PGSTTHALLAARVN-YSG
C4AA_BACTI FEESPYYDYFOYQED-----SLTRRPHLFTWLDLNFKEAQTTPNFFTSHYNMPHY
340 350 360 370 380 390
cry2ab2_820. GISSGDIGASPNQNFCSIFLPL-LTFPVRSM LDS--GSDREGVATVNMQTESFETT
C4AA_BACTI TLONISQKSSVFG-NHNVIDKLKSLGLATNIYIFLNLVISLDNKNLYNDNNISKMDFFIT
390 400 410 420 430 440
cry2ab2_820. LGLRSGAFTARGNSYFFDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGGAR
C4AA_BACTI NGTRLLEKELTAGSGQITDYVKNKIIFGLPILAKRRENGNPTLPFTYDNY---SHILSFIK
450 460 470 480 490 500
cry2ab2_820. 470 480 490 500 510 520
AYMVSVHNNKNIHVAHENGSMHLPNDYTGFTISPIHATQVNNQ-TRTFISERKFGQOG
C4AA_BACTI SLSEIPA-TYKTQVYTFAWTHSSVDPKNTIYTHLT-TQIPAVKANSLGTASKVQVQPGHIG
510 520 530 540 550 560
cry2ab2_820. 510 520 530 540 550 560
-DLSRFEON-NTTARYTLRNGNSYNLYLRVSSIGNSITRVIN---GRVYTATNVT
C4AA_BACTI GDLIDFADHFKITCOHS--NPOQSYFIRIRYASNGSANIRAVINLSIPGVAGELGNLPT
570 580 590 600 610 620
cry2ab2_820. 580 590 600 610 620 630
-TNNDGVNDNGARFSDINIGNVA-SNSNDVPLDIN---VTLSGTQFDLMNLMLVPTNI
C4AA_BACTI FSGTDITNLKYDKFOYLEFSNEVKFAPQNISLVFNRSDDVYTNITVLIDKIEFLPTIRSI
630 640 650 660 670 680
cry2ab2_820. SPLY
C4AA_BACTI REDREXQKLETVQQIINTFYANPIKNTLQSELTDYDIDQAAANLVEICISEELXPKEKMLLL
690 700 710 720 730 740
cry2ab2_820.pcp
TXN5:Y00423_1
Description: Y00423 Bacillus thuringiensis Bacillus thuringiensis gene for 130
Kda delta-endo
Accession/ID: Y00423
=====
General comments=====
=====
LOCUS Y00423_1 [BTTOXD1]
DEFINITION Bacillus thuringiensis gene for 130 kDa delta-endotoxin; . . .

SCORES Initl: 63 Initn: 199 Opt: 159 z-score: 164.3 E(): 0.003
>TXN5:Y00423_1
Initn: 199 Initl: 63 opt: 159 z-score: 164.3 expect(): 0.003
Smith-Waterman score: 201; 20.8% identity in 630 aa overlap
(57-633:76-681)

cry2ab2_820. 30 40 50 60 70 80
PFSFQHKSLDTVQKEMTKWKNHSLYLDPIVGTV-ASF-LLKKVG-SLVGKELISELRN
```


Y00423_1 DWLNMQVQQOYGGSEFFIDSGELSAITIVVGTIVLTGFTTPLGLALIG--FGTILP
50 60 70 80 90 100
cry2ab2_820. LIPES GSTNLKQAPSTETKFNGLNLTDLARVNAELTGLQANVEFRQVDNPLN-P
90 100 110 120 130 140
Y00423_1 VLPFAQDSNNSWSDTITOTITIKETIASNTSNANKILNRSFNVISYTHNHLKTWENN
110 120 130 140 150 160
cry2ab2_820. NRNAVPLSITSSVNTMQLFNLPLPQ-----OMQVQDLALPLFAQANLHLSFI
150 160 170 180 190
Y00423_1 NPQNTQ-DVRTQIQLVHVFQNTPEVNSCPKNDGCDYNNILNLSVAQANLHLVL
170 180 190 200 210 220
cry2ab2_820. RDVI-----LNADENGISAATLRTYRDYLNKYN-----DYSNYCINTYQSFKGLN
200 210 220 230
Y00423_1 NOAVKEAYLKNRQFDYLEPLPTAIDYPLVTKAIEKNTNVCYTVN-----LNLIKIT
230 240 250 260
cry2ab2_820. --TELHDMLEFTYMFNLNVFVYSINSLFKYQSLVSSGANLYASGSGQOT---QSET
240 250 260 270 280 290 300 310 320 330 340
Y00423_1 PDSNLGNINWNTY---NIYRTKMTTAVLDVVALPFDVDSKYPIGVQSELRTKTYVLN
280 290 300 310 320 330
cry2ab2_820. SQDMPFLYSLFQVNSYVNLGFCARLSNTFFNIYGL-----PGSTTHALLAARVN-YSG
300 310 320 330 340
Y00423_1 PESPKYKDYDFQVQED-----SLTRPHLFTWLSLNFYKAKQITTPNFFSHYNNMFHY
340 350 360 370 380 390
cry2ab2_820. GISSGDIGASPNQNPNCSTFLPPL-LTPFVRSWLS--GSDREGVATVNWQTESFET
350 360 370 380 390 400
Y00423_1 TLQNIQSSEVFG-NHNVTDKLSGLATNIYIFLLNVLISLNDYNNISKMDFFIT
390 400 410 420 430 440
cry2ab2_820. LGLRSGAFTARGNSVFPDPIRNIISGVPLVVRNEDLRRPLHYNEIRNIASPSGTGGAR
410 420 430 440 450 460
Y00423_1 NGTELLEKELTAGSGQITDYVKNIFGLPILAKERENQGNPTLFTYDNY---SHLLSFIK
450 460 470 480 490 500
cry2ab2_820. AYMVSVHRNNIHAVHENGSMHLPANDYTGFTSPIHATQVNNQ-TRTFISEKFGNQG
470 480 490 500 510 520
Y00423_1 SLGIPA-TYKTOVYTFAMTHSSVDPKNTIYTHLT-TQIPAVKANSLGTASKVVGPGHGT
510 520 530 540 550 560
cry2ab2_820. -DSLRPEQN-NTTARYTLRNGNSYNLYLRVSSIGNSTIRVTIN-----GRVYATNVNT
530 540 550 560 570
Y00423_1 GDLIDFKHFKITCQHS--NFQQSYFIRIRYASNGSNRAVNIPLSPGVAELGWALNPT
570 580 590 600 610 620
cry2ab2_820. -TNNDGVNDGARFSDINIGVVA-SSNSDVPLDIN---VTLNSGTQFDLNMIMLVPTNI
580 590 600 610 620 630
Y00423_1 PSGLDYNLKYKDFQVLEFSNEVFAFNQNISLVFNRSVDVNTVTLIDKIEFLPITASI
630 640 650 660 670 680

cry2ab2_820. SPLX
Y00423_1 REDREKOKLETVOQIINTFYANPIKNTLOSELTDYDIDQAAANLVECISEELYPKKMLLL
690 700 710 720 730 740
cry2ab2_820.pcp
TXNS:CPAA_BACTJ
Description: O87906 bacillus thuringiensis (subsp. jegathesan). pesticidal
crystal protein c
Accession/ID: O87906
=====
ID CPAA_BACTJ STANDARD; PRT; 675 AA.
AC O87906;
SCORES Init1: 72 Initn: 129 Opt: 133 z-score: 141.1 E(): 0.059
>TXNS:CPAA_BACTJ
Initn: 129 Init1: 72 Opt: 133 Z-score: 141.1 expect(): 0.059
Smith-Waterman score: 166; 19.9% identity in 589 aa overlap
(100-636:105-661)
cry2ab2_820. GSLVGRKRLSELNRLFFPGSGTNLMQDILRETKFLNQRLNTDLARVNAELTGLQAN--
70 80 90 100 110 120
CPAA_BACTJ SPSIGDAFALVSSIGYWPETKTSPLSVADVNLRIEALDQNAINRAIRKFNGLMDTYN
80 90 100 110 120 130
cry2ab2_820. --NEEPNRQVDNPL-NPNRNA-VPLSITSSVNTMQLFNLRLP-QFMQGYQLLLPL
140 150 160 170 180
CPAA_BACTJ TVYLANLQVYDRIEIPANQGSQSLREARSLSEEFIEROFKALAGEFAEAGSQIVLLPI
140 150 160 170 180 190
cry2ab2_820. PQAANNLSPFIRDVLNLSDEG-----ISAATLRTYRDYLNKYNTRDYSNYCINTYQ
190 200 210 220 230
CPAA_BACTJ YQAANLHLILKILKQITDGLGRPPGVPIITTSADPPFESEFLRIKKYTDHCSYYD
200 210 220 230 240 250
cry2ab2_820. SAFKGLNTELDH-----MLEEFGNPNVFEYSSIMSLFKYQSLVSSGANL-YASGSG
240 250 260 270 280
CPAA_BACTJ DGLAKIRSGSDGETWENKTRREMILGVYDVALYPIFNINIKYPIQTIELSRVYTD
260 270 280 290 300 310
cry2ab2_820. PQQTQSFTSQDMPFLYSLFQVNSYVNLNRSFARLSNTFFNIYGLPGSTTHALLAARVN
290 300 310 320 330 340
CPAA_BACTJ PVGCFGNKESD---IFS--RLNFDYLENRLRPAEPNPVNLNSVQLFSTFENS
320 330 340 350 360
cry2ab2_820. YSGGISSSDIGASPNQNPNCSTFLPPLLT--PF-VRSW-LSDREGVATVNWQTESFET
350 360 370 380 390
CPAA_BACTJ NNGEVLIRGNLKNIMFEGGVTASRSGDGVTTGTPTFTMDYNSYMGVPRYRVAETSSQV
370 380 390 400 410 420 430
cry2ab2_820. ---TESFETTLGL---RSGAFTARGNSNY-PPDYFIENISGV---PLV-VNED--LRKQ
400 410 420 430 440
CPAA_BACTJ PGLNNSIHVIGVIGDSFRAIGPGGQGDHIFSLPGGDMYDCGKQVINPFLDYRNSDHWISDM
440 450 460 470 480 490 500

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 166 of 361

```

430      440      450      460      470      480
cry2ab2_820. LHYNEIRNIASPGTGGARAYWVSHRKNYIHAVHENGSMIHLAPNDYGTFTLSPIHA
450      460      470      480      490      500
CPAA_BACTJ  MTINOSVLQANPQTQTFASFALSLGMH-----HSSAGNR-----NYYVYDKITQIPA
490      500      510      520
cry2ab2_820. TQVNNQTRTFISEXFGNQGSLRFQONNTIARYTLRGNGS-----YNLYLRVSSIGN
510      520      530      540      550      560      570      580
CPAA_BACTJ  TKTVREHPMIKPGFTG-GDLADLSSNSDILQYDLRSDYDDRLTDEVPFRIRCAIGV
530      540      550      560      570      580
cry2ab2_820. STIRVTINGRYTAINVNTINN-DGVNDNGARFSDINIGNVVASNSDVPLDINVTINS
560      570      580      590      600      610      620      630      640
CPAA_BACTJ  STISVDNMGSSSPQVTVASTAASLDTLKVESQYVVSIP-GNYYFDSAPRIL-----LRQ
590      600      610      620      630      640
cry2ab2_820. GTQFLMIMLMVPINISPLY
620      630
CPAA_BACTJ  PGRLLVDRIEIPVNFPELSEQENKSVDSLFIN
650      660      670
cry2ab2_820.pap
TXN5: BAB35496

Description: Bab35496 escherichia coli o157:h7, hypothetical 48.4 kda protein.
Accession/ID: 000000
ID BAB35496 PRELIMINARY; PRT; 419 AA.
AC BAB35496; . . .

=====General comments=====
>>TXN5: BAB35496
Initn: 94 Initl: 55 Initn: 94 Opt: 111 z-score: 121.6 E(): 0.73
Smith-Waterman score: 133; 23.9% identity in 222 aa overlap
(28-233:152-365)

cry2ab2_820. MQAMDSVLSNGRTTICDAYNVAADHPFSFOHKSLDTVQKWTWKNNHLYLDPINGTVASFLKKVGLVSGKRI--LSELRLNLIFFSGS
10      20      30      40      50
BAB35496 QGRNVSITHSMNNCLRNIDIRLSSITYESAHHKLFVQLESCWLYNLNLSHOLT
130      140      150      160      170      180
cry2ab2_820. DRIVGTVASFLKKVGLVSGKRISELNLIFFPGSGTNLMQD-ILRETEKFLNQLNTDT
60      70      80      90      100      110
BAB35496 DIVTGNKEELLLDLS-----HNKLASLHNLFPNLNTLNNLLSEIRMFYSNFKVQT
190      200      210      220      230
cry2ab2_820. LARVNAELTGLQANVEEFNRQVDNF-LNPNR-NAVPLSITSSVNTMQQ-----FLN
120      130      140      150      160
BAB35496 LNAANNQLEKINLHFTYUSSIKSLRLDNKKITRIDTENTSDIRSLFPIIKKSESLNFLN
240      250      260      270      280      290
cry2ab2_820. RLQFQOMQGYQLLLPLFAQAANLHLSFIRDVILNADEWGISAAITLRTYRDYLNKNT--R
170      180      190      200      210      220
```

```

300      310      320      330      340      350
BAB35496 ISGENNCPITQLMLFNLPSPALKNTGL---ALLSPGAFEDHSDGLVDNE-LFHYTINK
300      310      320      330      340
cry2ab2_820. DYSNYCINTYQSAFGKGLNLRHLMLEFRITYMFLNFVFIWSLFLKYQSLLVSSGANLYA
230      240      250      260      270      280
BAB35496 AYTPYNIHYKTEEVVNQNIKIKNMTLDEINNTYCNNDYYNEAIREEPIDFLDRSFSS
360      370      380      390      400      410
cry2ab2_820.pap
TXN5: Q9EVR2

Description: Q9evr2 bacillus thuringiensis. 81-kda leukemia toxin. 6/2001
Accession/ID: Q9EVR2
ID Q9EVR2 PRELIMINARY; PRT; 723 AA.
AC Q9EVR2;
DT 01-MAR-2001 (TriEBLrel. 16, Created) . . .

=====General comments=====
>>TXN5: Q9EVR2
Initn: 84 Initn: 84 Opt: 112 z-score: 118.2 E(): 1.1
Initn: 84 Initl: 84 Opt: 112 z-score: 118.2 expect(): 1.1
Smith-Waterman score: 233; 20.0% identity in 645 aa overlap
(7-603:87-697)

cry2ab2_820. MQAMDSVLSNGRTTICDAYNVAADHPFSFOHKSLD
60      70      80      90      100      110
Q9EVR2 DNHQHSVDVSNDSINMRNTLCKLPETNNISYDNLRLSTVTVPFSNQDFPIKFLHDIEI
70      80      90      100      110
cry2ab2_820. TVQ-----KWTWKNNHSLYLDPIGTVASFLKKVGLVSGKRI--LSELRLNLIFFSGS
40      50      60      70      80      90
Q9EVR2 AIQTGFSALTQSNWQGTINPML--ISTFF-KVASLLPFLPSSLGALASFVYVTSQ
120      130      140      150      160      170
cry2ab2_820. TNLMDILRETEKFLNQLNTDTLQVNVN---AELTGLQANVEEFNRQVDNFIPLN-RRNA
100      110      120      130      140
Q9EVR2 TGAMANLWRQMVYVEKRIKIDSKILDYHNFIMGAEALANLNASLKEYARVVKIFENDNRMA
180      190      200      210      220      230
cry2ab2_820. VPLS--ITSVNTMQQLFNLPQFMQ-----GYQLLLPLFAQAANLHLSFIRDVIL
150      160      170      180      190
Q9EVR2 EPPSTGVTOFIRLNDNFIKYIAKLFSTNQSDLOQYPVLTLPRAQACVMHMLLKDATT
240      250      260      270      280      290
cry2ab2_820. NADWEG--ISAATLTRYDYKNTYRDYNSYCNITYQSAFGKGLNLRHLMLEFRITYMFLN
200      210      220      230      240      250
Q9EVR2 SV--WQQIDSQQLNGYKAEILRLIKYIVINDVNTYNGLELEKAKPLNYSDEPEYLQAG
300      310      320      330      340      350
cry2ab2_820. VFEVSIWSLFIKYQLLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQVNSNYLNGF
260      270      280      290      300      310
Q9EVR2 RPDISVLNRNFK--EVMKWNFRVAKYKRG-----NAMSALSALALPFTF--GNYPKQAL
360      370      380      390      400
```


Study No. 06-01-62-01

MSL No. 20307

Page 167 of 361

cry2ab2_820. TNLMODILRETEKFNLRNLTDTLVRV-----AETGLQANVEEFNRQVDNFLP-NRRA
 :
 AB031065_1 TGAMANIQMWDYVYVEKRIDSKILDYHNFIMGAEIALALASLEAYARVVVKI-FENDIMRMA
 180 190 200 210 220 230

cry2ab2_820. VPLS--ITSSVNTMOQLFLNRLPOFOMQ-----GYQLLLPLFAOANHLHSFRDVL
 150 160 170 180 190

AB031065_1 EPPSTGVITQFILNDNFPIKYIAKLQFSTNQSDQIQYVTLPLPRAOCVMHMLUKLKDT:
 240 250 260 270 280 290

cry2ab2_820. NADWEG--ISAATLTBYDYLVKNYTRDYSNYCINTYGSAFKGNTLHDLMLEFRMYMFLN
 200 210 220 230 240 250

AB031065_1 SV-WGOQIDSQOLNGHYKAELIRLIKVYNVTNVNTTYOGLEKAKPLNYSPEYLOAQ
 300 310 320 330 340 350

cry2ab2_820. VFEXVISWLFIYQSLLVSSCANLYAGSGPOQTOSTQDWPFYLSLFQVNSNNVLNGF
 260 270 280 290 300 310

AB031065_1 RPDISVLRNFK-EVMKNRWAKYRG------MAMSALSAALEPTF--GENYPKQAL
 360 370 380 390 400

cry2ab2_820. SGAKLSNTPFNIVGUPGSTTHALLAARNVYGGGISDSGDIGASFQNWCNCSFTFLUPLL
 320 330 340 350 360 370

AB031065_1 FVWSQRIFAPVIGIPGITSQ-----DHSGTGSMRFDKVTQIDIALRRLLMELYIQ
 410 420 430 440 450

cry2ab2_820. PFVRSNLB-SQDRGVAIVTNQTSFETTLGLSGAFARGNSVFPDYFIRNISGPV
 380 390 400 410 420 430

AB031065_1 PIKSFVFFVESMTVRYVYVNOYIGKRGSTGLAWGWSSD-----PSVIYTSAUGA
 460 470 480 490 500

cry2ab2_820. LNWMDLRRLPILMPTNTAS-GTFCGARAYMVSVHNRNKHIAHVHGSMHLPAN-
 440 450 460 470 480 490

AB031065_1 GYAENVGVRSLHGSGSTKZGAPVPNTINVA-BEEKEPYGK-LHSVSAVG--LSKADPT
 510 520 530 540 550 560

cry2ab2_820. -DYGTFISPI---HMGNQNPRTIKKS-----NQGSDFEQQN
 500 510 520

AB031065_1 ADSVMFGFRVLLNEANOLLNTRAOIPAEIITVAPAFGRSEENINGQDAIIWESF
 570 580 590 600 610 620 630

cry2ab2_820. TTA---RYTLRG-NGNSNLYLRVSS-IGNSRPLUNGRIYVATVWTYTNWSCUNONG
 540 550 560 570 580 590

AB031065_1 TSGGFYFDVSPOKQKIYIARIANLASVTSUTVNQTTFDLDLN SLDPNGVRGY
 630 640 650 660 670 680

cry2ab2_820. ARFSDINIGNVASSNSDVPLDINVLTNSGTQFDLNMILVPTNISFY
 590 600 610 620 630

AB031065_1 GSYTLVB-GPIIEFGQTNFKLRSQKGFEADSIFSPVS
 690 700 710 720

cry2ab2_820. pep

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 168 of 361

TXN5: BAB35430
Description: Bab35430 escherichia coli o157:h7. putative bigb-like protein.
6/2001
Accession/ID: 000000
ID BAB35430 PRELIMINARY; PRT; 807 AA.
AC BAB35430; . . .
=====General comments=====

SCORES Init1: 55 Initn: 55 Opt: 107 Z-score: 112.0 E(): 2.5
>TXN5: BAB35430
Initn: 55 Init1: 55 Opt: 107 Z-score: 112.0 expect(): 2.5
Smith-Waterman score: 138; 22.2% identity in 356 aa overlap
(276-610:76-418)

cry2ab2_820. LEFRYMFNVFEVSIWLFKYQSLVSSGANLYASGS-GPOQTQSFTSDWPFYLSLF
250 260 270 280 290 300
BAB35430 TVNNSGIASARVNAQGDVFNLLAGSEARKGAILLYNSAVVNNAGTWKWCYQDENNNAGTL
50 60 70 80 90 100

cry2ab2_820. QVNSYVLNGSPGARLNTFPNIVGLPGSTTHALLAARVNSGGISSGD--IGASPFNQ
310 320 330 340 350 360
BAB35430 DDDKSTFNN-SGKLILDNSKNARFQGSNNATL-----YNTGEMTLDALGAGAILY
110 120 130 140 150

cry2ab2_820. NFNCSTFL-PELLTPFVRSLDSDREGVATVNWQTESFETTLGLSGAFTARGSNY
370 380 390 400 410 420
BAB35430 DGCASEFINKGVDAKVTVAVTAGATESDAFL--MNQGGVINFDKNASAVKFTNNY
160 170 180 190 200 210

cry2ab2_820. FP-DYFIRNISGVPLVRNEDLRRLPHYNEIRNIASPSGPGGARVNVSVHNRKNIHA
430 440 450 460 470 480
BAB35430 VALNDGVNITSGNNVAMEGDKNAQLVNNGVNINLTGEGTTDTGLTGMOLDANATAD--A
220 230 240 250 260 270

cry2ab2_820. VHENGSMHLAPNDYGTFTLSPIHATQVNNQTRTFISEKFGN-----QGDLSRFQ-----
490 500 510 520 530
BAB35430 VIENNGTINIFANDSFAFVLTGEGHIVNNGTVVIADGVGTGSLIKQGDVNVVEGVNGNS
280 290 300 310 320 330

cry2ab2_820. -NNTTAR---YTLRGNNGSNVL--YLRVSSIGNST-IRVTINGRVYVATVNTTNNQGV
540 550 560 570 580
BAB35430 GNNTEVHYTDYTLDPDNTYTTSPSETTDSGSDGSSNNLNGYI-VGTVNVDGSAGKLKV
340 350 360 370 380 390

cry2ab2_820. NDNGARFSDINGNVVASNSDVPLDINVLTNGSTQFDLMIMLVPTNISPL
590 600 610 620 630
BAB35430 NNASMNGVINGTGAAGTATTVSFDNVVEGINLTDADATTSVTVWTKAGSTIDASGNDV
400 410 420 430 440 450

cry2ab2_820.pap
TXN5: Q9ZKS9
Description: Q9zks9 helicobacter pylori j99 (campylobacter pylori j99).
putative vacuolating

Accession/ID: Q9ZKS9
=====General comments=====

ID Q9ZKS9 PRELIMINARY; PRT; 2399 AA.
AC Q9ZKS9; . . .

SCORES Init1: 38 Initn: 38 Opt: 113 Z-score: 109.6 E(): 3.4
>TXN5: Q9ZKS9
Initn: 38 Init1: 38 Opt: 113 Z-score: 109.6 expect(): 3.4
Smith-Waterman score: 133; 21.4% identity in 388 aa overlap
(266-634:721-1087)

cry2ab2_820. KGLNRLHDMLEFRTYMFNVFEVSIWLFKYQSLVSSGANLYASGSQPQQTQSFTSQ
240 250 260 270 280 290
Q9ZKS9 TFSAANIYLTNNFKTGEVSNSDGGGANITFKASDNITMDGLNYYNAETVTKMIQTGASQ
700 710 720 730 740 750

cry2ab2_820. DWPLYLQVNSYVLNGSPGARLNTFPNIVGLPGSTTHALLAARVNSGGISSGDI
300 310 320 330 340 350
Q9ZKS9 H---SYITFDANNISVT-----DSDFSDMTWKGFSAKNISFNSAFSGFTNPG--
760 770 780 790

cry2ab2_820. GASPFNQFNCS-TFLPPLLTPFVRSLDSDG---DREGVATV-NWQTESFET---L
360 370 380 390 400
Q9ZKS9 GSSTISTNASLSLSTFDSRLANGGAIYNLQANSLIFNNTQAVNFVLYSRGTSENATQLL
800 810 820 830 840 850

cry2ab2_820. GLSGAFTARGSNYPDYFIRNISGVPLVRNED-LRRLPHYNEIRNIASPSGPGGAR
410 420 430 440 450 460
Q9ZKS9 GNTSFTLSQSLNFGDITLQNNANITLGNKSOAFAFNKSLTDNNSLSDNQSVLNA
860 870 880 890 900 910

cry2ab2_820. AYVSVVHNRKNIHAVHENGSMHLAPNDYGTFTLSPIHATQVNNQTRTFISEKFGNOGD
470 480 490 500 510 520
Q9ZKS9 G--TSAPNQASLNY--NGSQAFSLFNGGTLSLNNASKLNASSFSNNNTINLDD
920 930 940 950 960 970

cry2ab2_820. SLRFEQNNTTARYTLRGNNGSNYLYRVSSIGNSTI-RVTINGRVYVATVNTTNNQGV
530 540 550 560 570 580
Q9ZKS9 SV-LNANNTS---SLNANIN-FQASQADFGGNTTIDTASFNFDSSASSLNFNNLTANGAL
980 990 1000 1010 1020

cry2ab2_820. Y
590 600 610 620 630
Q9ZKS9 NDNGARFS---DINI-GNVVASSNSDVPL-DINV--TLNSGTQFDLMIMLVPTNISPL
1030 1040 1050 1060 1070 1080

cry2ab2_820. Y
590 600 610 620 630
Q9ZKS9 NGVEKILFGMKIQATVSDNNNIQVSWFINPNSQIIQESIKNGDLTIEVNNPNSAS
1090 1100 1110 1120 1130 1140

cry2ab2_820.pap
TXN5: AE001515_3

Description: AE001515 Helicobacter pylori J99 Helicobacter pylori, strain J99
section 76 of 132 of the complete

Accession/ID: AE001515
LOCUS AE001515.3 (AE001515)
DEFINITION Helicobacter pylori, strain J99 section 76 of 132 of the complete
(266-634:721-1087)

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

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

SCORES Init1: 38 Initn: 38 Opt: 113 Z-score: 109.6 E(): 3.4
>>TXNS:AE001515_3
Initn: 38 Init1: 38 Opt: 113 Z-score: 109.6 E(): 3.4
Smith-Waterman score: 133; 21.4% identity in 388 aa overlap
(266-634:721-1087)

cry2ab2_820. KGLNRLHDLMEFRITMFLNVEYVSLSLKYQSSAVSGLANLYASGSGPQSTQSFSG
240 250 260 270 280 290
AE001515_3 TFSAAIYLTNNFKTGTGVNSDGGGANITFASDNLITMDGLNYYNNAATYTKMQLGASQ
700 710 720 730 740 750

cry2ab2_820. DWPFYLSLPQVNSYVINGFSGARLSNTPFNIVGLPGSTTTTLLARVNYSGTSGSDI
300 310 320 330 340 350

AE001515_3 H---SYTFPATNNISVT-----DSDFDMTMGKFSFSAKNISFSAASGFTNAG
760 770 780 790

cry2ab2_820. GASPPNQFNCS-TELPPLLTFFVRSWLDGS---DRGVATVT-NMQTESFTT-L
360 370 380 390 400 410

AE001515_3 GSSTISINASNSLFTDSELNGAGIYNLQANSLSIFNTQAVFNLYVSGTSENFAITQLL
800 810 820 830 840 850

cry2ab2_820. GLRGATFARGNSNYPDFIRINISGVFLVVRNED-LRRPLHYNEIRNIAFSPGTPGGAR
410 420 430 440 450 460

AE001515_3 GNTSFTLSSQSLLNFNGDITLQNNANITLGNKSOAAFKNSLTDNNSNLSLDNQSVLAN
860 870 880 890 900 910

cry2ab2_820. AVVSVHNRKNNHIAVHENGSMHLPNDYTGFTISPIHATOVNNQTRTFISEKFGNQD
470 480 490 500 510 520

AE001515_3 G--TSAPNQAASLNLY--NGSOAFPSLFFNGGTLNANSKLNASASFNNITINLDD
920 930 940 950 960 970

cry2ab2_820. SLRPEQNTTARTYLRGNGSNLYLRVSSIGNSTI-RVYINGRYTATVNTTNNDCV
530 540 550 560 570 580

AE001515_3 SV-LNANNTS---SLNANIN-FOGASQADFGNTIITDASFNFDASSLFNLTANGAL
980 990 1000 1010 1020

cry2ab2_820. NDNGARFS-----DINI-GNVVASSNSDVPL-DINV--TLNSGTQFDLMNMLVPTNISEL
590 600 610 620 630

AE001515_3 NFNGYAPSLTKALMNVSGQFVLNNGDINLSDINIPDNITKSVTYNTLNAAKGIITGISA
1030 1040 1050 1060 1070 1080

cry2ab2_820. Y
1090 1100 1110 1120 1130 1140

AE001515_3 NGYEKILFYGMKIQATYSDNNNIQTWSFINPLNSSLQIOESIKNGDLTIEVLNPNFNAS
1090 1100 1110 1120 1130 1140

cry2ab2_820. pep
1090 1100 1110 1120 1130 1140

TXNS:Q9AM80

Description: Q9am80 bacillus thuringiensis serovar kunthalanags3. insecticidal
crystal protei
Accession/ID: Q9AM80

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

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

ID Q9AM80 PRELIMINARY;
AC Q9AM80: PRT; 1155 AA.

SCORES Init1: 55 Initn: 95 Opt: 106 Z-score: 108.1 E(): 4.1
>>TXNS:Q9AM80

Initn: 95 Init1: 55 Opt: 106 Z-score: 108.1 E(): 4.1
Smith-Waterman score: 108; 20.3% identity in 607 aa overlap
(60-634:41-605)

cry2ab2_820. FQHKSLDTVQKEWTKNNHSLYLDPIVGTVASFLKKVGSVLGKRILSELRLNIFPSG
30 40 50 60 70 80

Q9AM80 IPYNCLSNSEVEVLGGRIETGYTPIDISLSLTQELLSEF--VFGAGFVLGLVDIIMGIF
20 30 40 50 60

cry2ab2_820. STNLMDILRETEKFLNORLNTDTLARVNAELTGLQA--NVESFNQVDNFLNPNRAVP
90 100 110 120 130 140

Q9AM80 GPSQWDAFLVQIEQLINQRIENSLGTPFLDWKAKQSLNLRIFREWEA--DPTNPAIR
70 80 90 100 110 120

cry2ab2_820. LSTISSVNTMQQLFNLQPFQMGQYQLLLPLFAQANLHLSFIR-----DVLNADWE
150 160 170 180 190 200

Q9AM80 EENRIGQARTSALTATPLFAVONTQVELLSVVQAANLMFSTRVQFSSVAVATPGY
130 140 150 160 170 180

cry2ab2_820. GIEATILRY--EDIKNY--TRDYSNYC-----INTYQSAFKGLNRLHDMLE-FRT
210 220 230 240 250

Q9AM80 QSYNKAQCYGAREFLDQVGNIRDKSNFKKEDSKQLCCYLGIFF-LSSYFFKIYKERT
190 200 210 220 230 240

cry2ab2_820. YMF---LNVFVVSIMALE--YQSLNASSNANLYASGSGPOOTQSTSDWPELYS--
250 260 270 280 290 300

Q9AM80 RVYPISEKFSFNKLNLYKPKKSSMVVPEKIRA-----RRKYWSPHLWLYLQDN
250 260 270 280 290

cry2ab2_820. -LQVNSYVINGFSGARLSNTPFNIVGLPGSTTTLLARVNYSGTSGSDI
310 320 330 340 350 360

Q9AM80 HLTDVHRGF--NYWSGHQIIAS-P--VGFQDREFAFFIFGAGNAAPFRLVQLGQGVY
300 310 320 330 340 350

cry2ab2_820. NQNFNCSTFLPPLTTPVRSWLDSDSGREGVATVNNQTESFTTDLGLSGEFTARGNS
370 380 390 400 410 420

Q9AM80 RTL--SSILYEDL---FIR---DKVINTYLFAGSNLLMEPPNIC--HPGRKASVWD
360 370 380 390 400 410

cry2ab2_820. YFPDYFINISGVPLVVRNEDLRRPLHYNEIRNIAFSPGTPGGARVNVVHNNKHA
430 440 450 460 470 480

Q9AM80 SLDELPHQN--NNVP--PROGFSHRLSHVSMFRSGFSNSSV-SIIRAPMFSWLKSAEPNN
410 420 430 440 450

cry2ab2_820. VHENG--SMHLAPNDYTGFTISPIHATQVNNQTRFISEKFGNQGDSLRFEQNNTIARY
510 520 530
Q9AM80 IIPSSQITQIPLTKSTNLGSGTGVVKGFGTGGD--ILRRTSPGQISTLRV--NITAPL
460 470 480 490 500 510
cry2ab2_820. TLRGNGSNLYLRVSSIGNSTIRVTINGRVYATNNTTNNQGVNDGNGARFSDINIGN
540 550 560 570 580 590
Q9AM80 SQR-----YVRIRYASTTNLQFHTSIDGPIINGNFSATMSS-GSNLQSFRTVGFTT
520 530 540 550 560
cry2ab2_820. VVASSNSDVLQINV-TLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630
Q9AM80 PFNFSNGSSVFTLSAHVFNNGNEVYIDRIEFVPAEVTFEAEYDLERAKAVNELFTSSNQ
570 580 590 600 610 620
Q9AM80 IGLKTDVTDVHIDQVSNLVECLSDDEFCLDEKQELSEKVKHAKLSLDERNLLODFNFRGIN
630 640 650 660 670 680
cry2ab2_820.pep
TXN5:AF047028_1
Description: AF047028 Photorhabdus luminescens Photorhabdus luminescens
insecticidal toxin co
Accession/ID: AF047028
=====General comments=====

LOCUS AF047028_1 [AF047028]
DEFINITION Photorhabdus luminescens insecticidal toxin complex proteins TccA
=====General comments=====

SCORES Initl: 48 Initn: 48 Opt: 104 Z-score: 107.4 E(): 4.5
>>TXN5:AF047028_1
initn: 48 initl: 48 opt: 104 Z-score: 107.4 expect(): 4.5
Smith-Waterman score: 104; 28.2% identity in 163 aa overlap
(207-360:196-345)

cry2ab2_820. 180 190 200 210 220 230
AF047028_1 LLPLFAQAANLHLSFIRDVILNADEWGISAAITLRTYRDYLNKNTROYSNYCINTYQSAFK
170 180 190 200 210 220
cry2ab2_820. GLNTRLHDMLEFRTYMFNVFVYSIWSLFKYQSLVSSGA---NLVASGSGPQQTQSF
240 250 260 270 280 290
AF047028_1 EVIPQLQVNEILSKAIQKLSLTDLEAVNARLSITR-YPNNLPHYGHQIQTAQSV--
170 180 190 200 210 220
cry2ab2_820. GLNTRLHDMLEFRTYMFNVFVYSIWSLFKYQSLVSSGA---NLVASGSGPQQTQSF
240 250 260 270 280 290
AF047028_1 LGTILQDITLPTQLDLPQNF-----WATAKGLSDTTASALTRLOIMASQFSPEQKII
230 240 250 260 270
cry2ab2_820. TSQDMPFLYSLFQVNSNYVLNGFSGA-----RLSNTPFNIVGLPGSTTHALLAARVNS
300 310 320 330 340
AF047028_1 TETVQGFYQLNYGDSLSLTNVSFSDMTIMTDRSLTPVQVELMLCSTVG---GSTVVK
280 290 300 310 320 330
cry2ab2_820. GGISSGDIGASPFNQFNCFSTFLPPLTPFVRSWLDGSDREGVATVNWQTESFETTLG
350 360 370 380 390 400
AF047028_1 DNVSSGDTTATPFAYGARFIHAGKPEAITLSRSGAEAHFALTNNLTDDKLDRIINRTVRL
340 350 360 370 380 390
cry2ab2_820. TSQDMPFLYSLFQVNSNYVLNGFSGA-----RLSNTPFNIVGLPGSTTHALLAARVNS
300 310 320 330 340
AF047028_1 TETVQGFYQLNYGDSLSLTNVSFSDMTIMTDRSLTPVQVELMLCSTVG---GSTVVK
280 290 300 310 320 330
cry2ab2_820. GGISSGDIGASPFNQFNCFSTFLPPLTPFVRSWLDGSDREGVATVNWQTESFETTLG
350 360 370 380 390 400
AF047028_1 DNVSSGDTTATPFAYGARFIHAGKPEAITLSRSGAEAHFALTNNLTDDKLDRIINRTVRL
340 350 360 370 380 390

cry2ab2_820.pep
TXN5:O85155
Description: O85155 photorhabdus luminescens (xenorhabdus luminescens).
insecticidal toxin co
Accession/ID: O85155
=====General comments=====

ID O85155 PRELIMINARY; PRT; 965 AA.
AC O85155; . . .

SCORES Initl: 48 Initn: 48 Opt: 104 Z-score: 107.4 E(): 4.5
>>TXN5:O85155
initn: 48 initl: 48 opt: 104 Z-score: 107.4 expect(): 4.5
Smith-Waterman score: 104; 28.2% identity in 163 aa overlap
(207-360:196-345)

cry2ab2_820. 180 190 200 210 220 230
O85155 EVIPQLQVNEILSKAIQKLSLTDLEAVNARLSITR-YPNNLPHYGHQIQTAQSV--
170 180 190 200 210 220
cry2ab2_820. GLNTRLHDMLEFRTYMFNVFVYSIWSLFKYQSLVSSGA---NLVASGSGPQQTQSF
240 250 260 270 280 290
O85155 -LGTILQDITLPTQLDLPQNF-----WATAKGLSDTTASALTRLOIMASQFSPEQKII
230 240 250 260 270
cry2ab2_820. TSQDMPFLYSLFQVNSNYVLNGFSGA-----RLSNTPFNIVGLPGSTTHALLAARVNS
300 310 320 330 340
O85155 TETVQGFYQLNYGDSLSLTNVSFSDMTIMTDRSLTPVQVELMLCSTVG---GSTVVK
280 290 300 310 320 330
cry2ab2_820. GGISSGDIGASPFNQFNCFSTFLPPLTPFVRSWLDGSDREGVATVNWQTESFETTLG
350 360 370 380 390 400
O85155 DNVSSGDTTATPFAYGARFIHAGKPEAITLSRSGAEAHFALTNNLTDDKLDRIINRTVRL
340 350 360 370 380 390
cry2ab2_820.pep
TXN5:BAE34699
Description: Bae34699 escherichia coli o157:h7. putative chaperone protein.
6/2001
Accession/ID: 000000
=====General comments=====

ID BAE34699 PRELIMINARY; PRT; 209 AA.
AC BAE34699; . . .

SCORES Initl: 50 Initn: 50 Opt: 87 Z-score: 101.7 E(): 9.4
>>TXN5:BAE34699
initn: 50 initl: 50 opt: 87 Z-score: 101.7 expect(): 9.4
Smith-Waterman score: 87; 25.2% identity in 111 aa overlap
(482-590:95-202)

cry2ab2_820. RNIASPSGTGGARAYMVSVHNRKNIHAEHENGSMIHLAPNDYTGFTISPIHATQVNNQ
460 470 480 490 500 510
BAE34699 LRIIYNHDFLPQDRESAFLNLYEMPETPHQDPTHLTLAMNTQLKIFYRPKSVMTTQPE
70 80 90 100 110 120

20

BAB34699
 AMRKISWRLGADGSSSYIELNPTF---LNISFTSISIGATKVQQESDMMIKPFSQRRYV
 120 130 140 150 160 170 180

CRY2AB2_820. TATN-VNTTNNNGVNDNGARFSDINIGNVVA~~SSNADVP~~PLDINVTLNSGTQFDLMNIMLV

Start time:	Mon May 1 16:41:58 2006
Completion time:	Mon May 1 16:42:20 2006

```

! Database scan: 0:00:01.8
! Post-scan processing: 0:00:11.6

```

! Output File: cry2ab2_820_toxin5

```
! Output File: cry2ab2_820_toxin5
```


Appendix 5. FASTA sequence alignments of Cry2Ab2 protein
against ALLPEPTIDES database

!!SEQUENCE_LIST 1.0

(Peptide) FASTA of: cry2ab2_820.pep from: 1 to: 637 May 1, 2006 16:50

Cry2Ab2_820

TO: AllPeptides: * Sequences: 3,061,850 Symbols: 1,053,256,873 Word Size: 2

Sequences too short to analyze: 6 (6 symbols)

Databases searched:

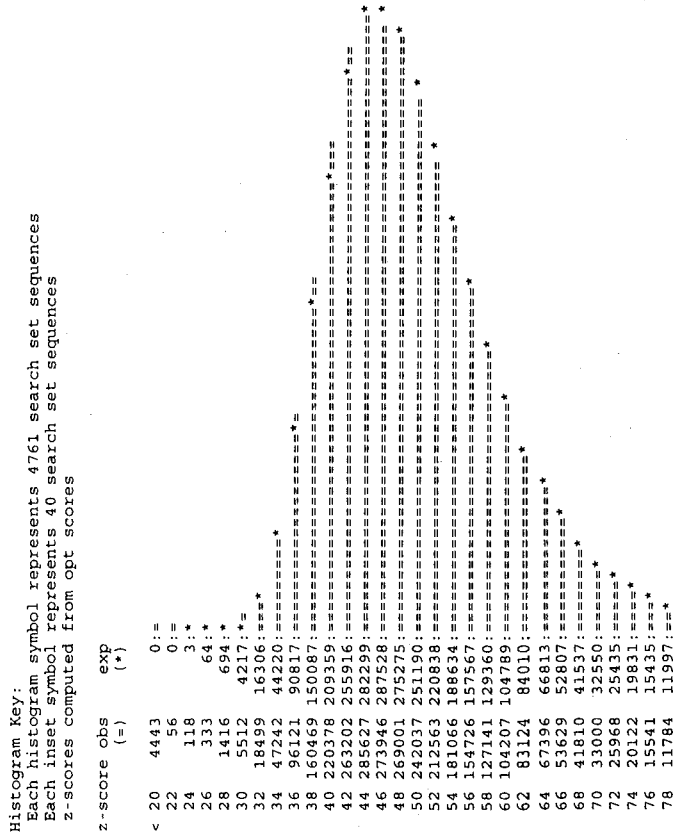
SwissProt, Release 40.0, Released on 4May2005, Formatted on 4May2005

nrnaa, Release 65.0, Released on 24Oct2005, Formatted on 24Oct2005

Scoring matrix: GenFunData:blosum50.cmp

Variable pamfactor used

Gap creation penalty: 12 Gap extension penalty: 2



80	9266	9316:=-*
82	7129	7126:=-*
84	5479	5645:=-*
86	4255	4368:=-*
88	3375	3380:=-*
90	2616	2615:=-*
92	1988	2023:=-*
94	1518	1566:=-*
96	1242	1211:=-*
98	929	937:=-*
100	725	725:=-*
102	584	561:=-*
104	440	434:=-*
106	356	336:=-*
108	266	260:=-*
110	164	201:=-*
112	117	156:=-*
114	132	121:=-*
116	103	93:=-*
118	80	72:=-*
>120	609	56:=-*

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

The best scores are:

	init1	initn	opt	z-sc E(3060967)...
SW:117328	Begin: 2	End: 633		
! description="PESTICIDIAL CRYSTAL PR...	4139	4139	4139	4706.6
NRAA:40312	Begin: 2	End: 633		
! source="GENBANK_PROT" crystal prote...	4139	4139	4139	4706.6
NRAA:33316454	Begin: 2	End: 633		
! source="GENBANK_PROT" Cry2Ab [Bacil...	4128	4128	4128	4694.1
NRAA:27436036	Begin: 2	End: 633		
! source="GENBANK_PROT" crystal delta...	4125	4125	4125	4690.7
NRAA:31872007	Begin: 2	End: 633		
! source="GENBANK_PROT" crystal delta...	4113	4113	4113	4677.0
SW:8927992	Begin: 2	End: 633		
! description="PESTICIDIAL CRYSTAL PR...	3794	3794	3794	4314.2
NRAA:6457578	Begin: 2	End: 633		
! source="GENBANK_PROT" crystal prote...	3794	3794	3794	4314.2
SW:117326	Begin: 2	End: 633		
! description="PESTICIDIAL CRYSTAL PR...	3724	3724	3732	4243.7
NRAA:33314185	Begin: 2	End: 633		
! source="GENBANK_PROT" Cry2aa [Bacil...	3724	3724	3732	4243.7
SW:61221653	Begin: 2	End: 633		
! description="Pesticidal crystal pr...	3724	3724	3732	4243.7
NRAA:47678765	Begin: 2	End: 633		
! source="GENBANK_PROT" insecticidal ...	3720	3720	3728	4239.1
NRAA:27447952	Begin: 2	End: 633		
! source="GENBANK_PROT" insecticidal ...	3719	3719	3727	4238.0
NRAA:4239730	Begin: 2	End: 633		
! source="GENBANK_PROT" Cry2aa protei...	3706	3706	3714	4223.2
NRAA:61252390	Begin: 2	End: 633		
! source="GENBANK_PROT" Pesticidal c...	3713	3713	3713	4222.1
SW:61252390	Begin: 2	End: 633		
! description="Pesticidal crystal pr...	3713	3713	3713	4222.1
NRAA:4239728	Begin: 2	End: 633		
! source="GENBANK_PROT" Cry2aa protei...	3694	3694	3702	4209.6
NRAA:5834516	Begin: 2	End: 551		
! source="GENBANK_PROT" Cry2a protein...	3234	3234	3242	3687.4
NRAA:66734543	Begin: 2	End: 623		
! source="GENBANK_PROT" Cry2ac [Bacil...	1601	2413	2401	2730.1
NRAA:40286	Begin: 2	End: 622		

© 2017

! source="GENBANK_PROT" insecticidal ...	148	148	294	329.3	4.8e-10	! source="GENBANK_PROT" Cry3Aa protei...	114	158	277	314.1	3.4e-09
NRAA:46359604 Begin: 83 End: 300	208	208	286	327.8	5.8e-10	NRAA:45934892 Begin: 47 End: 294	114	158	277	314.1	3.4e-09
! source="GENBANK_PROT" parasporal cr...	159	183	286	320.1	1.6e-09	! source="GENBANK_PROT" insecticidal ...	206	233	281	314.0	3.4e-09
SW:117529 Begin: 54 End: 321	159	183	286	320.1	1.6e-09	SW:61252383 Begin: 68 End: 303	206	233	281	314.0	3.4e-09
! description="PESTICIDIAL CRYSTAL PR...	97	97	282	319.7	1.6e-09	! description="Pesticidial crystal pr...	153	209	280	313.2	3.7e-09
NRAA:40280 Begin: 54 End: 321	97	97	282	319.7	1.6e-09	NRAA:1200002 Begin: 68 End: 303	153	209	280	313.2	3.7e-09
! source="GENBANK_PROT" unnamed prote...	159	183	286	320.1	1.6e-09	! source="GENBANK_PROT" cryIIa2 [bacil...	206	233	281	314.0	3.4e-09
NRAA:40259 Begin: 51 End: 389	159	183	286	320.1	1.6e-09	NRAA:8469142 Begin: 32 End: 598	206	233	281	314.0	3.4e-09
! source="GENBANK_PROT" unnamed prote...	97	97	282	319.7	1.6e-09	! source="GENBANK_PROT" Pesticidial c...	153	209	280	313.2	3.7e-09
SW:117324 Begin: 51 End: 389	97	97	282	319.7	1.6e-09	SW:8469142 Begin: 32 End: 598	153	209	280	313.2	3.7e-09
! description="PESTICIDIAL CRYSTAL PR...	159	226	286	319.7	1.6e-09	! description="PESTICIDIAL CRYSTAL PR...	206	233	280	312.9	3.9e-09
NRAA:15721993 Begin: 39 End: 287	159	226	286	319.7	1.6e-09	SW:61221651 Begin: 68 End: 303	206	233	280	312.9	3.9e-09
! source="GENBANK_PROT" crystal prote...	110	139	283	319.2	1.7e-09	! description="Pesticidial crystal pr...	206	233	280	312.9	3.9e-09
NRAA:51090232 Begin: 12 End: 268	110	139	283	319.2	1.7e-09	NRAA:14486714 Begin: 68 End: 303	206	233	280	312.9	3.9e-09
! source="GENBANK_PROT" cancer cell-k...	110	139	283	319.2	1.7e-09	! source="GENBANK_PROT" CryIba [bacil...	206	233	280	312.9	3.9e-09
NRAA:51090236 Begin: 12 End: 684	110	139	283	319.2	1.7e-09	NRAA:580949 Begin: 68 End: 303	206	233	280	312.9	3.9e-09
! source="GENBANK_PROT" cancer cell-k...	191	191	285	318.9	1.8e-09	! source="GENBANK_PROT" unnamed prote...	206	233	280	312.9	3.9e-09
SW:8469154 Begin: 58 End: 598	191	191	285	318.9	1.8e-09	SW:1345842 Begin: 68 End: 303	206	233	280	312.9	3.9e-09
! description="PESTICIDIAL CRYSTAL PR...	128	168	284	317.9	2.1e-09	! description="PESTICIDIAL CRYSTAL PR...	128	168	278	311.1	4.9e-09
NRAA:8469154 Begin: 58 End: 598	128	168	284	317.9	2.1e-09	NRAA:46409861 Begin: 34 End: 603	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" Pesticidial c...	159	199	284	317.7	2.1e-09	! source="GENBANK_PROT" cryIIA type cr...	128	168	278	311.1	4.9e-09
NRAA:27447986 Begin: 58 End: 598	159	199	284	317.7	2.1e-09	SW:61221643 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" delta-endotox...	114	158	280	317.6	2.1e-09	! description="Pesticidial crystal pr...	128	168	278	311.1	4.9e-09
NRAA:8928012 Begin: 18 End: 651	114	158	280	317.6	2.1e-09	SW:61221650 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" Cry3 delta en...	117	161	280	317.5	2.2e-09	! description="Pesticidial crystal pr...	128	168	278	311.1	4.9e-09
NRAA:52145404 Begin: 47 End: 294	117	161	280	317.5	2.2e-09	SW:117533 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" Cry3Aa protei...	120	160	283	316.6	2.4e-09	! description="PESTICIDIAL CRYSTAL PR...	128	168	278	311.1	4.9e-09
NRAA:8469139 Begin: 41 End: 610	120	160	283	316.6	2.4e-09	NRAA:40273 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" Pesticidial c...	128	168	284	317.9	2.1e-09	! source="GENBANK_PROT" unnamed prote...	128	168	278	311.1	4.9e-09
SW:8469139 Begin: 41 End: 610	128	168	284	317.9	2.1e-09	SW:61221646 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! description="PESTICIDIAL CRYSTAL PR...	114	158	277	314.9	3e-09	! description="Pesticidial crystal pr...	128	168	278	311.1	4.9e-09
NRAA:208155 Begin: 41 End: 610	114	158	277	314.9	3e-09	NRAA:10440886 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" cryIIaA insec...	114	158	277	314.7	3.1e-09	! source="GENBANK_PROT" delta endotox...	128	168	278	311.1	4.9e-09
NRAA:4711281 Begin: 24 End: 239	114	158	277	314.7	3.1e-09	NRAA:40255 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" CryIIIA insec...	114	158	277	314.6	3.2e-09	! source="GENBANK_PROT" unnamed prote...	128	168	278	311.1	4.9e-09
NRAA:40253 Begin: 39 End: 286	114	158	277	314.6	3.2e-09	NRAA:225669 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
! source="GENBANK_PROT" unnamed prote...	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" insect contro...	128	168	278	311.1	4.9e-09
SW:61221657 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" insecticidal ...	128	168	278	311.1	4.9e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	NRAA:143099 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
SW:61221658 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" insecticidal ...	128	168	278	311.1	4.9e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	NRAA:13173238 Begin: 41 End: 610	128	168	278	311.1	4.9e-09
SW:61221658 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" insecticidal ...	128	168	278	311.1	4.9e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	SW:8469147 Begin: 54 End: 321	128	168	278	311.1	4.9e-09
NRAA:143084 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! description="PESTICIDIAL CRYSTAL PR...	152	176	275	307.6	7.7e-09
! source="GENBANK_PROT" insect contro...	114	158	277	314.2	3.3e-09	NRAA:295864 Begin: 54 End: 321	152	176	275	307.6	7.7e-09
SW:117325 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" crystal prote...	152	176	275	307.6	7.7e-09
! description="PESTICIDIAL CRYSTAL PR...	114	158	277	314.2	3.3e-09	NRAA:13899010 Begin: 54 End: 321	152	176	275	307.6	7.7e-09
SW:61221659 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" insecticidal ...	152	176	275	307.6	7.7e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	NRAA:8469144 Begin: 32 End: 597	152	176	275	307.6	7.7e-09
NRAA:61221658 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" Pesticidial c...	150	203	275	307.6	7.7e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	SW:8469144 Begin: 32 End: 597	150	203	275	307.6	7.7e-09
NRAA:143084 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! description="PESTICIDIAL CRYSTAL PR...	150	203	275	307.6	7.7e-09
! source="GENBANK_PROT" insect contro...	114	158	277	314.2	3.3e-09	NRAA:15988322 Begin: 34 End: 538	150	203	275	307.6	7.7e-09
SW:117325 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" Chain A, Crys...	154	192	270	306.9	8.5e-09
! description="PESTICIDIAL CRYSTAL PR...	114	158	277	314.2	3.3e-09	SW:8928007 Begin: 74 End: 648	135	135	270	306.2	9.3e-09
SW:61221659 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! description="PESTICIDIAL CRYSTAL PR...	135	135	270	306.2	9.3e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	NRAA:2624005 Begin: 74 End: 648	135	135	270	306.2	9.3e-09
NRAA:61221658 Begin: 39 End: 286	114	158	277	314.2	3.3e-09	! source="GENBANK_PROT" mosquitoicidal...	135	135	270	306.2	9.3e-09
! description="Pesticidial crystal pr...	114	158	277	314.2	3.3e-09	SW:8469161 Begin: 84 End: 355	135	135	270	306.2	9.3e-09

! description="PESTICIDIAL CRYSTAL PR... NRAA:10288 Begin: 84 End: 355	118	146	270	306.2	9.3e-09	! source="GENBANK_PROT" Cry protein [... SW:8469138 Begin: 12 End: 603	133	170	259	292.0	5.7e-08
! source="GENBANK_PROT" CryIIID [Baci... SW:8469155 Begin: 97 End: 601	118	146	270	306.2	9.3e-09	! description="PESTICIDIAL CRYSTAL PR... NRAA:8469138 Begin: 12 End: 603	189	189	261	291.6	6e-08
! description="PESTICIDIAL CRYSTAL PR... NRAA:8469155 Begin: 97 End: 601	154	192	270	306.1	9.3e-09	! source="GENBANK_PROT" Pesticidal c... NRAA:21239436 Begin: 41 End: 609	189	189	261	291.6	6e-08
! source="GENBANK_PROT" Pesticidal c... NRAA:8469155 Begin: 97 End: 601	154	192	270	306.1	9.3e-09	! source="GENBANK_PROT" crystal prote... NRAA:46359602 Begin: 84 End: 568	128	168	261	291.6	6e-08
! source="GENBANK_PROT" Cxyl type 392... NRAA:1334252 Begin: 51 End: 582	146	192	271	305.9	9.5e-09	! source="GENBANK_PROT" parasporal cr... SW:8469134 Begin: 41 End: 601	117	150	261	290.7	6.7e-08
! source="GENBANK_PROT" delta-endotox... NRAA:19386614 Begin: 68 End: 639	185	246	273	305.4	1e-08	! description="PESTICIDIAL CRYSTAL PR... NRAA:8469134 Begin: 41 End: 601	147	147	260	290.5	6.9e-08
! source="GENBANK_PROT" mosquito toxin... NRAA:56900936 Begin: 41 End: 600	122	155	269	304.9	1.1e-08	! source="GENBANK_PROT" Pesticidal c... NRAA:1942525 Begin: 13 End: 581	147	147	260	290.5	6.9e-08
! source="GENBANK_PROT" CryIAB [Baci... NRAA:14190061 Begin: 41 End: 610	128	168	272	304.2	1.2e-08	! source="GENBANK_PROT" Insecticidal... NRAA:46359600 Begin: 96 End: 324	128	168	255	289.8	7.6e-08
! source="GENBANK_PROT" CryIAB16 [Bac... NRAA:940200 Begin: 97 End: 381	116	156	272	304.2	1.2e-08	! source="GENBANK_PROT" parasporal cr... NRAA:11171233 Begin: 41 End: 609	193	193	260	289.5	7.9e-08
! source="GENBANK_PROT" Cry3Bb2 NRAA:48734426 Begin: 41 End: 610	154	154	268	303.9	1.9e-08	! source="GENBANK_PROT" CryIA(a) NRAA:2982744 Begin: 26 End: 602	128	168	255	289.4	7.9e-08
! source="GENBANK_PROT" parasporal cr... NRAA:8469159 Begin: 87 End: 659	122	162	264	296.7	2.4e-08	! source="GENBANK_PROT" CryINA67-1 [B... SW:8469133 Begin: 26 End: 602	189	216	259	289.4	8e-08
! source="GENBANK_PROT" Pesticidal c... NRAA:41056817 Begin: 87 End: 659	152	152	263	294.0	4.4e-08	! description="PESTICIDIAL CRYSTAL PR... NRAA:6650206 Begin: 26 End: 602	189	216	259	289.4	8e-08
! source="GENBANK_PROT" HBP-1 CryIII... SW:8469159 Begin: 87 End: 659	152	152	263	294.0	4.4e-08	! source="GENBANK_PROT" crystal prote... NRAA:295866 Begin: 26 End: 602	189	216	259	289.4	8e-08
! description="PESTICIDIAL CRYSTAL PR... SW:8469145 Begin: 73 End: 643	152	152	263	294.0	4.4e-08	! source="GENBANK_PROT" crystal prote... NRAA:16231238 Begin: 96 End: 324	189	216	259	289.3	8e-08
! description="PESTICIDIAL CRYSTAL PR... NRAA:8469145 Begin: 73 End: 643	140	140	263	293.5	4.7e-08	! source="GENBANK_PROT" Cryhime1 [Pae... SW:8469143 Begin: 46 End: 260	191	191	259	288.4	9.1e-08
! source="GENBANK_PROT" Pesticidal c... SW:8469153 Begin: 73 End: 652	140	140	263	293.5	4.7e-08	! description="PESTICIDIAL CRYSTAL PR... NRAA:8469143 Begin: 46 End: 260	222	247	256	286.0	1.2e-07
! source="GENBANK_PROT" Pesticidal c... NRAA:22213635 Begin: 73 End: 652	140	164	263	293.5	4.7e-08	! source="GENBANK_PROT" Pesticidal c... NRAA:5901203 Begin: 41 End: 609	222	247	256	286.0	1.2e-07
! source="GENBANK_PROT" CryBII [Baci... SW:8469150 Begin: 73 End: 643	140	164	263	293.5	4.7e-08	! source="GENBANK_PROT" 135 kDa inse... NRAA:533981 Begin: 41 End: 609	128	168	255	284.8	1.4e-07
! description="PESTICIDIAL CRYSTAL PR... NRAA:565394 Begin: 73 End: 643	140	140	263	293.5	4.7e-08	! source="GENBANK_PROT" insecticidal... NRAA:174363 Begin: 41 End: 609	128	168	255	284.8	1.4e-07
! source="GENBANK_PROT" delta-endotox... SW:61252381 Begin: 41 End: 609	140	140	263	293.5	4.7e-08	! source="GENBANK_PROT" leiddoptexan... NRAA:6687073 Begin: 41 End: 609	128	168	255	284.8	1.4e-07
! description="Pesticidal crystal pr... NRAA:61252381 Begin: 41 End: 609	128	168	261	293.3	4.8e-08	! source="GENBANK_PROT" delta-endotox... NRAA:41688283 Begin: 77 End: 608	205	205	251	284.1	1.6e-07
! source="GENBANK_PROT" Pesticidal c... SW:117534 Begin: 41 End: 609	128	168	261	293.3	4.8e-08	! source="GENBANK_PROT" Pesticidal c... NRAA:67089177 Begin: 34 End: 609	128	168	254	283.7	1.6e-07
! description="130 KD CRYSTAL PROTEIN... SW:8927981 Begin: 70 End: 646	128	168	261	293.3	4.8e-08	! source="GENBANK_PROT" Pesticidal c... NRAA:13173240 Begin: 41 End: 600	128	168	253	282.9	1.8e-07
! description="PESTICIDIAL CRYSTAL PR... NRAA:8927981 Begin: 70 End: 646	185	247	259	292.9	5.1e-08	! source="GENBANK_PROT" insecticidal... NRAA:1922253 Begin: 43 End: 259	69	102	248	283.5	2.2e-07
! source="GENBANK_PROT" Pesticidal c... SW:8469148 Begin: 47 End: 261	185	247	259	292.9	5.1e-08	! source="GENBANK_PROT" cbm72 mosquit... SW:10719926 Begin: 43 End: 259	69	102	248	283.5	2.2e-07
! description="PESTICIDIAL CRYSTAL PR... NRAA:296087 Begin: 47 End: 261	224	255	262	292.8	5.2e-08	! description="PESTICIDIAL CRYSTAL-III... NRAA:8469141 Begin: 73 End: 636	148	177	252	281.5	2.2e-07
! source="GENBANK_PROT" crystal prote... NRAA:226053 Begin: 41 End: 609	224	255	262	292.8	5.2e-08	! source="GENBANK_PROT" Pesticidal c... SW:8469141 Begin: 73 End: 636	148	177	252	281.1	2.2e-07
! source="GENBANK_PROT" 135kD insecti... NRAA:32344731 Begin: 41 End: 609	128	168	262	292.7	5.2e-08	! description="PESTICIDIAL CRYSTAL PR... SW:61212640 Begin: 79 End: 609	148	177	252	280.2	2.6e-07
! source="GENBANK_PROT" delta-endotox... SW:61252379 Begin: 41 End: 609	128	168	262	292.7	5.2e-08	! description="Pesticidal crystal pr... NRAA:142765 Begin: 79 End: 609	128	168	251	280.2	2.6e-07
! description="Pesticidal crystal pr... SW:117540 Begin: 41 End: 609	128	168	262	292.7	5.2e-08	! source="GENBANK_PROT" crystal protei... SW:117531 Begin: 79 End: 609	128	168	251	280.2	2.6e-07
! description="135 KD CRYSTAL PROTEIN... NRAA:51090240 Begin: 72 End: 316	128	168	262	292.7	5.2e-08	! description="133 KD CRYSTAL PROTEIN... SW:848967 Begin: 79 End: 609	128	168	251	280.2	2.6e-07
						! description="PESTICIDIAL CRYSTAL PR... NRAA:40267 Begin: 79 End: 609	128	168	251	280.2	2.6e-07

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 176 of 361

! source="GENBANK_PROT" unnamed prote...	128	169	251	280.2	2.6e-07	! source="GENBANK_PROT" hybrid CryIAb...	128	237	268.7	1.1e-06	
SW:61221638 Begin: 79 End: 609						NRAA:50539655 Begin: 22 End: 275					
! description="Pesticidal crystal pr...	128	168	251	280.2	2.6e-07	! source="GENBANK_PROT" delta-endotox...	98	130	268.3	1.2e-06	
SW:8469136 Begin: 41 End: 609						NRAA:40294 Begin: 54 End: 246					
! description="PESTICIDIAL CRYSTAL PR...	151	192	251	280.2	2.6e-07	! source="GENBANK_PROT" unnamed prote...	200	239	266.5	1.5e-06	
NRAA:8469136 Begin: 41 End: 609						SW:61252386 Begin: 54 End: 246					
! source="GENBANK_PROT" Pesticidal c...	151	192	251	280.2	2.6e-07	! description="Pesticidal crystal pr...	200	239	266.5	1.5e-06	
NRAA:1769867 Begin: 54 End: 246						SW:117541 Begin: 11 End: 263					
! source="GENBANK_PROT" delta-endotox...	206	206	245	277.9	3.5e-07	! description="130 KD CRYSTAL PROTEIN...	146	170	238	265.7	1.7e-06
NRAA:11277639 Begin: 54 End: 246						NRAA:216288 Begin: 11 End: 263					
! source="GENBANK_PROT" protoxin Ba...	206	206	245	277.7	3.6e-07	! source="GENBANK_PROT" 130 kDa Insec...	146	170	238	265.7	1.7e-06
NRAA:38231198 Begin: 54 End: 246						NRAA:23344760 Begin: 41 End: 590					
! source="GENBANK_PROT" CryIC [Chloro...	206	206	245	277.6	3.6e-07	! source="GENBANK_PROT" insecticidal ...	128	238	265.4	1.7e-06	
NRAA:143227 Begin: 41 End: 611						NRAA:2584729 Begin: 41 End: 591					
! source="GENBANK_PROT" insecticidal ...	128	168	248	276.9	3.9e-07	! source="GENBANK_PROT" insecticidal ...	128	237	264.3	2e-06	
SW:117542 Begin: 41 End: 611						NRAA:52783575 Begin: 41 End: 591					
! description="131 KD CRYSTAL PROTEIN...	128	168	248	276.9	3.9e-07	! source="GENBANK_PROT" CryIAC [Bacil...	128	237	264.3	2e-06	
NRAA:5669035 Begin: 41 End: 609						SW:117547 Begin: 41 End: 591					
! source="GENBANK_PROT" insecticidal ...	128	160	248	276.8	4e-07	! description="PESTICIDIAL CRYSTAL PR...	128	237	264.3	2e-06	
NRAA:1234884 Begin: 54 End: 246						NRAA:1171235 Begin: 41 End: 590					
! source="GENBANK_PROT" delta-endotox...	206	206	245	276.6	4.1e-07	! source="GENBANK_PROT" CryIA(c)	128	231	262.3	2.6e-06	
NRAA:40356 Begin: 54 End: 246						NRAA:40275 Begin: 41 End: 590					
! source="GENBANK_PROT" unnamed prote...	206	206	245	276.0	4.4e-07	! source="GENBANK_PROT" unnamed prote...	128	231	262.2	2.6e-06	
NRAA:7141141 Begin: 54 End: 246						NRAA:8469152 Begin: 41 End: 609					
! source="GENBANK_PROT" toxin CryICa6...	208	208	247	275.6	4.7e-07	! source="GENBANK_PROT" Pesticidal c...	128	157	235	262.0	2.7e-06
NRAA:37781497 Begin: 41 End: 609						SW:8469152 Begin: 41 End: 609					
! source="GENBANK_PROT" CryIaA [Bacil...	128	168	246	274.5	5.4e-07	! description="PESTICIDIAL CRYSTAL PR...	128	157	235	262.0	2.7e-06
NRAA:61696667 Begin: 54 End: 246						NRAA:17977979 Begin: 52 End: 543					
! source="GENBANK_PROT" insecticidal ...	206	206	245	274.3	5.5e-07	! source="GENBANK_PROT" Cry29Aa prote...	66	231	261.8	2.7e-06	
NRAA:546641 Begin: 41 End: 590						NRAA:5052774 Begin: 41 End: 590					
! source="GENBANK_PROT" insecticidal ...	128	128	242	273.5	6.1e-07	! source="GENBANK_PROT" insecticidal ...	128	231	261.0	3e-06	
NRAA:225472 Begin: 79 End: 609						NRAA:40354 Begin: 11 End: 264					
! source="GENBANK_PROT" endotoxin del...	128	168	245	273.4	6.2e-07	! source="GENBANK_PROT" unnamed prote...	142	166	233	260.0	3.5e-06
NRAA:142750 Begin: 54 End: 246						SW:848969 Begin: 11 End: 264					
! source="GENBANK_PROT" cryIC(b)	206	206	245	273.3	6.3e-07	! description="PESTICIDIAL CRYSTAL PR...	142	166	233	260.0	3.5e-06
NRAA:61252387 Begin: 54 End: 246						NRAA:11493827 Begin: 74 End: 157					
! source="GENBANK_PROT" Pesticidal c...	206	206	245	273.3	6.3e-07	! source="GENBANK_PROT" crystal prote...	193	220	259.6	3.6e-06	
SW:848968 Begin: 54 End: 246						NRAA:40310 Begin: 11 End: 264					
! description="PESTICIDIAL CRYSTAL PR...	206	206	245	273.3	6.3e-07	! source="GENBANK_PROT" unnamed prote...	141	165	232	258.9	4e-06
SW:61252387 Begin: 54 End: 246						NRAA:1669651 Begin: 12 End: 242					
! description="Pesticidal crystal pr...	206	206	245	273.3	6.3e-07	! source="GENBANK_PROT" delta-endotox...	147	171	232	258.6	4.1e-06
NRAA:18913153 Begin: 54 End: 246						SW:8469137 Begin: 50 End: 601					
! source="GENBANK_PROT" delta-endotox...	206	206	245	273.3	6.3e-07	! description="PESTICIDIAL CRYSTAL PR...	134	134	232	258.6	4.1e-06
NRAA:46409857 Begin: 34 End: 583						NRAA:8469137 Begin: 50 End: 601					
! source="GENBANK_PROT" CryIa type cr...	128	128	242	272.9	6.6e-07	! source="GENBANK_PROT" Pesticidal c...	134	134	232	258.6	4.1e-06
NRAA:62548840 Begin: 23 End: 560						NRAA:4574730 Begin: 41 End: 440					
! source="GENBANK_PROT" delta-endotox...	128	128	240	270.8	8.6e-07	! source="GENBANK_PROT" Cry28Aa del...	98	152	231	257.9	4.5e-06
NRAA:295862 Begin: 12 End: 257						SW:8928040 Begin: 41 End: 440					
! source="GENBANK_PROT" crystal prote...	192	192	242	270.0	9.5e-07	! description="PESTICIDIAL CRYSTAL PR...	98	152	231	257.9	4.5e-06
SW:8469146 Begin: 12 End: 257						NRAA:9828610 Begin: 41 End: 229					
! description="PESTICIDIAL CRYSTAL PR...	192	192	242	270.0	9.5e-07	! source="GENBANK_PROT" parasporal in...	98	152	231	257.8	4.6e-06
NRAA:5916230 Begin: 15 End: 565						NRAA:67089175 Begin: 34 End: 583					
! source="GENBANK_PROT" Cry IAC Insec...	128	128	237	269.4	1e-06	! source="GENBANK_PROT" CryIAC [Bacil...	128	128	231	257.5	4.7e-06
NRAA:4090435 Begin: 41 End: 591						NRAA:142742 Begin: 41 End: 590					
! source="GENBANK_PROT" truncated CryIAC	128	128	237	269.0	1.1e-06	! source="GENBANK_PROT" cryIA(c)	128	128	231	257.5	4.8e-06
NRAA:22770982 Begin: 41 End: 591						NRAA:33321716 Begin: 41 End: 590					
! source="GENBANK_PROT" insect toxin ...	128	128	237	269.0	1.1e-06	! source="GENBANK_PROT" CryIAC [Bacil...	128	128	231	257.5	4.8e-06
NRAA:2555147 Begin: 42 End: 592						NRAA:42717976 Begin: 41 End: 591					
! source="GENBANK_PROT" CryIA(c) [syn...	128	128	237	269.0	1.1e-06	! source="GENBANK_PROT" cryIACAT modl...	119	119	227	257.0	5.1e-06
NRAA:2414156 Begin: 41 End: 591						NRAA:3979717 Begin: 41 End: 591					
! source="GENBANK_PROT" delta-endotox...	128	128	237	269.0	1.1e-06	! source="GENBANK_PROT" crystal toxin...	128	128	230	256.3	5.5e-06
NRAA:22415751 Begin: 41 End: 591						NRAA:143126 Begin: 41 End: 591					
! source="GENBANK_PROT" insecticidal ...	128	128	237	269.0	1.1e-06	! source="GENBANK_PROT" [Bacillus thu...	128	128	230	256.3	5.5e-06
NRAA:37993013 Begin: 41 End: 263						NRAA:45387401 Begin: 47 End: 260					

! source="GENBANK_PROT" crystal prote... 103 135 229 255.2 6.4e-06
NRAA:11946622 Begin: 13 End: 576
! source="GENBANK_PROT" Crystal PR... 117 117 227 253.0 8.5e-06
NRAA:17385619 Begin: 13 End: 576
! source="GENBANK_PROT" Crystal PR... 117 117 227 253.0 8.5e-06
NRAA:40282 Begin: 13 End: 576
! source="GENBANK_PROT" crystal prote... 117 117 227 253.0 8.5e-06
SW:8469151 Begin: 13 End: 576
! description="PESTICIDIAL CRYSTAL PR... 117 117 227 253.0 8.5e-06
NRAA:142740 Begin: 41 End: 598
! source="GENBANK_PROT" delta-endotoxin... 128 128 225 250.6 1.1e-05
NRAA:11493829 Begin: 78 End: 158
! source="GENBANK_PROT" crystal prote... 187 187 212 250.4 1.2e-05
NRAA:60308967 Begin: 41 End: 590
! source="GENBANK_PROT" truncated cry... 128 219 219 248.1 1.6e-05
NRAA:66360322 Begin: 8 End: 181
! source="GENBANK_PROT" Chain A, Mosq... 142 142 208 236.7 6.8e-05
NRAA:1246432 Begin: 44 End: 606
! source="GENBANK_PROT" Cbm71 mosquit... 114 114 207 234.9 8.4e-05
SW:10719937 Begin: 44 End: 606
! description="PESTICIDIAL CRYSTAL LI... 114 114 207 234.9 8.4e-05
NRAA:8928008 Begin: 27 End: 631
! source="GENBANK_PROT" Pesticidal c... 101 126 207 233.4 0.0001
SW:8928008 Begin: 27 End: 631
! description="PESTICIDIAL CRYSTAL PR... 101 126 207 233.4 0.0004
NRAA:66800187 Begin: 58 End: 274
! source="GENBANK_PROT" hypothetical ... 79 127 205 232.1 0.00012
NRAA:117385650 Begin: 48 End: 653
! source="GENBANK_PROT" crystal prote... 89 115 202 223.9 0.00034
NRAA:62548293 Begin: 30 End: 126
! source="GENBANK_PROT" CryIA toxin [... 128 128 185 221.1 0.00051
NRAA:8927990 Begin: 114 End: 335
! source="GENBANK_PROT" Pesticidal c... 95 157 196 217.0 0.00086
SW:8927990 Begin: 114 End: 335
! description="PESTICIDIAL CRYSTAL PR... 95 157 196 217.0 0.00086
NRAA:8927991 Begin: 114 End: 669
! source="GENBANK_PROT" Pesticidal c... 95 128 196 216.5 0.00092
SW:8927991 Begin: 114 End: 669
! description="PESTICIDIAL CRYSTAL PR... 95 128 196 216.5 0.00092
NRAA:8927987 Begin: 114 End: 335
! source="GENBANK_PROT" Pesticidal c... 95 153 194 215.1 0.0011
SW:8927987 Begin: 114 End: 335
! description="PESTICIDIAL CRYSTAL PR... 95 153 194 215.1 0.0011
SW:8928024 Begin: 78 End: 618
! description="PESTICIDIAL CRYSTAL PR... 87 87 187 206.9 0.0031
NRAA:8928024 Begin: 78 End: 618
! source="GENBANK_PROT" Pesticidal c... 87 87 187 206.9 0.0031
SW:117338 Begin: 11 End: 263
! description="130 KD CRYSTAL PROTEIN... 103 127 181 200.9 0.0068
NRAA:142738 Begin: 11 End: 263
! source="GENBANK_PROT" mosquitocidal... 103 127 181 200.9 0.0068
NRAA:117329 Begin: 68 End: 296
! source="GENBANK_PROT" Pesticidal c... 69 101 173 195.6 0.013
SW:117329 Begin: 68 End: 296
! description="PESTICIDIAL CRYSTAL PR... 69 101 173 195.6 0.013
NRAA:21685444 Begin: 68 End: 296
! source="GENBANK_PROT" Pesticidal c... 69 101 173 195.6 0.013
NRAA:17385648 Begin: 111 End: 296
! source="GENBANK_PROT" crystal prote... 75 159 172 189.9 0.028
NRAA:17385646 Begin: 63 End: 315
! source="GENBANK_PROT" crystal prote... 110 163 170 187.5 0.038
NRAA:54695305 Begin: 9 End: 611
! source="GENBANK_PROT" Cry30-like [B... 57 91 164 185.2 0.051
NRAA:48880 Begin: 184 End: 602

! source="GENBANK_PROT" crystal prote... 97 127 167 184.8 0.053
SW:8469164 Begin: 184 End: 602
! description="PESTICIDIAL CRYSTAL PR... 97 127 167 184.8 0.053
NRAA:40271 Begin: 184 End: 602
! source="GENBANK_PROT" delta-endotox... 97 127 167 184.8 0.053
NRAA:46132845 Begin: 20 End: 184
! source="GENBANK_PROT" hypothetical ... 92 120 161 184.5 0.056
NRAA:73540082 Begin: 38 End: 202
! source="GENBANK_PROT" Twin-arginine... 92 120 161 184.2 0.058
NRAA:40352 Begin: 76 End: 681
! source="GENBANK_PROT" unnamed prote... 63 199 159 175.6 0.17
NRAA:21685485 Begin: 76 End: 681
! source="GENBANK_PROT" Pesticidal c... 63 199 159 175.6 0.17
SW:117544 Begin: 76 End: 681
! description="PESTICIDIAL CRYSTAL PR... 63 199 159 175.6 0.17
NRAA:17977981 Begin: 86 End: 297
! source="GENBANK_PROT" Cry30Aa prote... 82 122 152 171.5 0.29
NRAA:50285081 Begin: 5 End: 189
! source="GENBANK_PROT" unnamed prote... 37 37 144 167.1 0.51
NRAA:26554239 Begin: 424 End: 831
! source="GENBANK_PROT" hypothetical ... 48 48 147 162.5 0.93
NRAA:66821693 Begin: 261 End: 411
! source="GENBANK_PROT" hypothetical ... 80 105 145 160.1 1.3
NRAA:37527939 Begin: 19 End: 237
! source="GENBANK_PROT" hypothetical ... 43 70 134 154.7 2.5
NRAA:2654204 Begin: 104 End: 334
! source="GENBANK_PROT" putative juve... 91 91 135 154.3 2.7
NRAA:6681253 Begin: 128 End: 269
! source="GENBANK_PROT" hypothetical ... 70 70 136 154.1 2.7
NRAA:50309445 Begin: 31 End: 187
! source="GENBANK_PROT" unnamed prote... 45 45 132 153.2 3.1
NRAA:633735 Begin: 1 End: 259
! source="GENBANK_PROT" Chain A, Cry... 67 67 133 152.4 3.4
NRAA:4101126 Begin: 93 End: 348
! source="GENBANK_PROT" similar to du... 59 59 130 151.1 4
NRAA:66805041 Begin: 91 End: 297
! source="GENBANK_PROT" hypothetical ... 101 128 133 151.0 4.1
NRAA:8928013 Begin: 105 End: 661
! source="GENBANK_PROT" Pesticidal c... 72 129 133 150.1 4.6
SW:8928013 Begin: 105 End: 661
! description="PESTICIDIAL CRYSTAL PR... 72 129 133 150.1 4.6
NRAA:4589753 Begin: 115 End: 444
! source="GENBANK_PROT" Pectate lyase... 49 49 128 149.3 5.1
NRAA:66825667 Begin: 116 End: 572
! source="GENBANK_PROT" hypothetical ... 48 75 133 148.0 6
NRAA:155443 Begin: 476 End: 754
! source="GENBANK_PROT" invasin A (alt... 77 98 133 147.4 6.4
NRAA:155442 Begin: 478 End: 738
! source="GENBANK_PROT" invasin B (alt... 67 98 133 147.4 6.4
NRAA:51596004 Begin: 494 End: 752
! source="GENBANK_PROT" putative inva... 67 98 133 147.3 6.5
SW:55977770 Begin: 494 End: 752
! description="Invasin" library:NA s... 67 98 133 147.3 6.5
SW:124715 Begin: 494 End: 752
! description="INVASIN" library:NA s... 67 98 133 147.3 6.5
NRAA:155441 Begin: 494 End: 752
! source="GENBANK_PROT" invasin A (alt... 67 98 133 147.3 6.5
NRAA:155440 Begin: 495 End: 753
! source="GENBANK_PROT" invasin... 67 98 133 147.3 6.5
NRAA:58042545 Begin: 1 End: 250
! source="GENBANK_PROT" phosphate ABC... 54 54 125 145.4 8.3
NRAA:68350387 Begin: 113 End: 278
! source="GENBANK_PROT" hypothetical ... 80 108 126 144.1 9.9
\\End of List

cry2ab2_820.pep
SW:117328
117328 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AB (INSECTICIDAL DELTA-ENDOTOXIN CRYIIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (71 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis serovar kurstaki" source="swissprot_prot" version=NA type=PR
SCORES Initl: 4139 Initn: 4139 Opt: 4139 z-score: 4706.6 E(): 0
>SW:117328
initn: 4139 initl: 4139 opt: 4139 z-score: 4706.6 expect(): 0
Smith-Waterman score: 4139; 100.0% identity in 632 aa overlap
(6-637:2-633)
cry2ab2_820. MQAMDNSVLNSGRITTCDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLDPIVGT
117328 MNSVLNSGRITTCDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLDPIVGT
cry2ab2_820. VASFLKKVGSVLGKRLSELNLIFFSGSTNLMDILRETEKFLNORLNTDTLARVNAE
117328 VASFLKKVGSVLGKRLSELNLIFFSGSTNLMDILRETEKFLNORLNTDTLARVNAE
cry2ab2_820. LTGLQANVEEFNRQVDNPLPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPL
117328 LTGLQANVEEFNRQVDNPLPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPL
cry2ab2_820. FAQANLHLSFIRDVILNADEWGISAAITLRYDKYLNRYTDSNYCINTYQSAFKGLNT
117328 FAQANLHLSFIRDVILNADEWGISAAITLRYDKYLNRYTDSNYCINTYQSAFKGLNT
cry2ab2_820. RLHDMLEFRITMFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL
117328 RLHDMLEFRITMFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL
cry2ab2_820. YSLFQVNSYLVNPGSGARLSNTFFNIVGLPGSTTHALLAARVNSYGGISGDIASGPF
117328 YSLFQVNSYLVNPGSGARLSNTFFNIVGLPGSTTHALLAARVNSYGGISGDIASGPF
cry2ab2_820. NONFNCSTFLPPLLPFFVRSLDSDGSDREGVATVNTWQTESFETTLGLRSAGFTARGNSN
117328 NONFNCSTFLPPLLPFFVRSLDSDGSDREGVATVNTWQTESFETTLGLRSAGFTARGNSN
cry2ab2_820. YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYVSVNRRKNNIHA
117328 YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYVSVNRRKNNIHA

cry2ab2_820. VHEGSMIHLAPNDYTGFTISPIHATQVNQTRTFISEKFGNQGSLSRFEQNNTTARYTL
117328 VHEGSMIHLAPNDYTGFTISPIHATQVNQTRTFISEKFGNQGSLSRFEQNNTTARYTL
cry2ab2_820. RGNNGSNLYLRVSSIGNSTIRVTINGRVYATNNTTNNNDGVNDNGARFSDINIGNVV
117328 RGNNGSNLYLRVSSIGNSTIRVTINGRVYATNNTTNNNDGVNDNGARFSDINIGNVV
cry2ab2_820. ASSNSDVLPLDINVTLSNGTQFDLMNIMLVPTNISPLY
117328 ASSNSDVLPLDINVTLSNGTQFDLMNIMLVPTNISPLY
cry2ab2_820.pep
NRAA:40312
40312 source="GENBANK PROT" crystal protein CryIIb [Bacillus thuringiensis]gi|11526737|gb|AAG36762.1| Cry2Ab [Bacillus thuringiensis]gi|117328|sp|P21254|CR2AB BACTK Pesticidial crystal protein cry2ab (Insecticidal delta-endotoxin CryIIA(b)) (Crystalline entomocidal protoxin) (71 kDa crystal protein)gi|142748|gb|AAA22342.1| crystal protein B2
SCORES Initl: 4139 Initn: 4139 Opt: 4139 z-score: 4706.6 E(): 0
>NRAA:40312
initn: 4139 initl: 4139 opt: 4139 z-score: 4706.6 expect(): 0
Smith-Waterman score: 4139; 100.0% identity in 632 aa overlap
(6-637:2-633)
cry2ab2_820. MQAMDNSVLNSGRITTCDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLDPIVGT
40312 MNSVLNSGRITTCDAYNVAADHPFQHKSLDTVQKEWTEWKKNNHSLYLDPIVGT
cry2ab2_820. VASFLKKVGSVLGKRLSELNLIFFSGSTNLMDILRETEKFLNORLNTDTLARVNAE
40312 VASFLKKVGSVLGKRLSELNLIFFSGSTNLMDILRETEKFLNORLNTDTLARVNAE
cry2ab2_820. LTGLQANVEEFNRQVDNPLPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPL
40312 LTGLQANVEEFNRQVDNPLPNRNAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPL
cry2ab2_820. FAQANLHLSFIRDVILNADEWGISAAITLRYDKYLNRYTDSNYCINTYQSAFKGLNT
40312 FAQANLHLSFIRDVILNADEWGISAAITLRYDKYLNRYTDSNYCINTYQSAFKGLNT
cry2ab2_820. RLHDMLEFRITMFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL
40312 RLHDMLEFRITMFLNVFEYVSIWSLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLL

©01

```
cry2ab2_820. 240 250 260 270 280 290 300 310 320 330 340 350 360
LTELQANVEEENROVDNLFNPNRNAPVLSITSSVNTMQQLFNLRFQFOMOGYQLLLPL
LTELQANVEEENROVDNLFNPNRNAPVLSITSSVNTMQQLFNLRFQFOMOGYQLLLPL
33316454 120 130 140 150 160 170

cry2ab2_820. 190 200 210 220 230 240
FAQANHLSTIRVILNADMGISAATLRTYRDYLYKNYTRQSYNYCINTYOSAFKGLNT
FAQANHLSTIRVILNADMGISAATLRTYRDYLYKNYTRQSYNYCINTYOSAFKGLNT
33316454 180 190 200 210 220 230

cry2ab2_820. 250 260 270 280 290 300
RLHDMLEFRTYMFNLNVEFYVSWLKFYQSLVSSGANLYASGSGPQQTQSTSDWPFLL
RLHDMLEFRTYMFNLNVEFYVSWLKFYQSLVSSGANLYASGSGPQQTQSTSDWPFLL
33316454 240 250 260 270 280 290

cry2ab2_820. 310 320 330 340 350 360
YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNSGGISGDIASPF
YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNSGGISGDIASPF
33316454 300 310 320 330 340 350

cry2ab2_820. 370 380 390 400 410 420
NQNFNCSTFLPPLTPFVRSWLDSSDREGVATVNTMQTESFETTLGLRSGAFTARGNSN
NQNFNCSTFLPPLTPFVRSWLDSSDREGVATVNTMQTESFETTLGLRSGAFTARGNSN
33316454 360 370 380 390 400 410

cry2ab2_820. 430 440 450 460 470 480
YFDDYFIRNLSGVPLVVRNEDLRPLHNEIRNIASPSGTPGCGARAYWVSHNRKNIHA
YFDDYFIRNLSGVPLVVRNEDLRPLHNEIRNIASPSGTPGCGARAYWVSHNRKNIHA
33316454 420 430 440 450 460 470

cry2ab2_820. 490 500 510 520 530 540
VHENGSMIHLAPNDYTGFTISPIHATOVNQTTFISEKFGNQGDSLRFEQNTTARYTL
VHENGSMIHLAPNDYTGFTISPIHATOVNQTTFISEKFGNQGDSLRFEQNTTARYTL
33316454 480 490 500 510 520 530

cry2ab2_820. 550 560 570 580 590 600
RGNGNSYLYLRVSSISGNTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
RGNGNSYLYLRVSSISGNTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
33316454 540 550 560 570 580 590

cry2ab2_820. 610 620 630
ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY
ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY
33316454 600 610 620 630

cry2ab2_820.pgp
NRAA:33316454

33316454 source="GENBANK_PROT" Cry2ab [Bacillus thuringiensis]

SCORES Initl: 4128 Initn: 4128 Opt: 4128 z-score: 4694.1 E(): 0
>NRAA:33316454
Initn: 4128 Initl: 4128 Opt: 4128 z-score: 4694.1 expect(): 0
Smith-Waterman score: 4128; 99.8% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820. 10 20 30 40 50 60
MQAMDNSVLKSGSTTICDAYNVAADPFSPQHKSLDTQKWTWKKNHSLYLDPIVGT
MQAMDNSVLKSGSTTICDAYNVAADPFSPQHKSLDTQKWTWKKNHSLYLDPIVGT
33316454 10 20 30 40 50 60

cry2ab2_820. 70 80 90 100 110 120
VASFLLKKVSLGVKRIILSELRLNLIFFSGSTNLMQDILRETEKFLNRLNTDILARVNE
VASFLLKKVSLGVKRIILSELRLNLIFFSGSTNLMQDILRETEKFLNRLNTDILARVNE
33316454 60 70 80 90 100 110
```

```
cry2ab2_820. 190 200 210 220 230 240
LTELQANVEEENROVDNLFNPNRNAPVLSITSSVNTMQQLFNLRFQFOMOGYQLLLPL
LTELQANVEEENROVDNLFNPNRNAPVLSITSSVNTMQQLFNLRFQFOMOGYQLLLPL
33316454 120 130 140 150 160 170

cry2ab2_820. 190 200 210 220 230 240
FAQANHLSTIRVILNADMGISAATLRTYRDYLYKNYTRQSYNYCINTYOSAFKGLNT
FAQANHLSTIRVILNADMGISAATLRTYRDYLYKNYTRQSYNYCINTYOSAFKGLNT
33316454 180 190 200 210 220 230

cry2ab2_820. 250 260 270 280 290 300
RLHDMLEFRTYMFNLNVEFYVSWLKFYQSLVSSGANLYASGSGPQQTQSTSDWPFLL
RLHDMLEFRTYMFNLNVEFYVSWLKFYQSLVSSGANLYASGSGPQQTQSTSDWPFLL
33316454 240 250 260 270 280 290

cry2ab2_820. 310 320 330 340 350 360
YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNSGGISGDIASPF
YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNSGGISGDIASPF
33316454 300 310 320 330 340 350

cry2ab2_820. 370 380 390 400 410 420
NQNFNCSTFLPPLTPFVRSWLDSSDREGVATVNTMQTESFETTLGLRSGAFTARGNSN
NQNFNCSTFLPPLTPFVRSWLDSSDREGVATVNTMQTESFETTLGLRSGAFTARGNSN
33316454 360 370 380 390 400 410

cry2ab2_820. 430 440 450 460 470 480
YFDDYFIRNLSGVPLVVRNEDLRPLHNEIRNIASPSGTPGCGARAYWVSHNRKNIHA
YFDDYFIRNLSGVPLVVRNEDLRPLHNEIRNIASPSGTPGCGARAYWVSHNRKNIHA
33316454 420 430 440 450 460 470

cry2ab2_820. 490 500 510 520 530 540
VHENGSMIHLAPNDYTGFTISPIHATOVNQTTFISEKFGNQGDSLRFEQNTTARYTL
VHENGSMIHLAPNDYTGFTISPIHATOVNQTTFISEKFGNQGDSLRFEQNTTARYTL
33316454 480 490 500 510 520 530

cry2ab2_820. 550 560 570 580 590 600
RGNGNSYLYLRVSSISGNTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
RGNGNSYLYLRVSSISGNTIRVTINGRVYATVNTVNTTNDGVNDNGARFSDINIGNV
33316454 540 550 560 570 580 590

cry2ab2_820. 610 620 630
ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY
ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY
33316454 600 610 620 630

cry2ab2_820.pgp
NRAA:27436036

27436036 source="GENBANK_PROT" crystal delta-endotoxin [Bacillus thuringiensis]

SCORES Initl: 4125 Initn: 4125 Opt: 4125 z-score: 4690.7 E(): 0
>NRAA:27436036
Initn: 4125 Initl: 4125 Opt: 4125 z-score: 4690.7 expect(): 0
Smith-Waterman score: 4125; 99.7% identity in 632 aa overlap
```

Information of Monsanto Company

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 180 of 361

(6-637:2-633)

```
cry2ab2_820. MOAMNSVLSGRITTCIDAYNVAADHDPFQHKSLDTVQKWTWKNNHSLYLDPIVGT 10 20 30 40 50 60
27436036 MNSVLNSGRITTCIDAYNVAADHDPFQHKSLDTVQKWTWKNNHSLYLDPIVGT 10 20 30 40 50
cry2ab2_820. VASFLKKVGSVGVKRIILSELRLNLIFFPSGSTNLMDILRETEKFLNORLNTDTLARVNAE 70 80 90 100 110 120
27436036 VASFLKKVGSVGVKRIILSELRLNLIFFPSGSTNLMDILRETEKFLNORLNTDTLARVNAE 70 80 90 100 110
cry2ab2_820. LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 130 140 150 160 170 180
27436036 LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 130 140 150 160 170
cry2ab2_820. LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 120 130 140 150 160 170
27436036 LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 120 130 140 150 160 170
cry2ab2_820. FAQANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAFKGLNT 190 200 210 220 230 240
27436036 FAQANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAFKGLNT 190 200 210 220 230
cry2ab2_820. RLHDMLEFRITMFLNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTOSFTSQDWPF 250 260 270 280 290 300
27436036 RLHDMLEFRITMFLNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTOSFTSQDWPF 250 260 270 280 290
cry2ab2_820. YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 310 320 330 340 350 360
27436036 YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 310 320 330 340 350
cry2ab2_820. YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 300 310 320 330 340 350
27436036 YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 300 310 320 330 340 350
cry2ab2_820. YFPDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA 430 440 450 460 470 480
27436036 YFPDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA 430 440 450 460 470
cry2ab2_820. VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNODSLRFEQNNTIARYTL 490 500 510 520 530 540
27436036 VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNODSLRFEQNNTIARYTL 490 500 510 520 530
cry2ab2_820. RGNNGSNLYLIRVSSIGNSTIRVTINGRVYATNVNTTNDGVNDNGARFSDINIGNV 550 560 570 580 590 600
27436036 RGNNGSNLYLIRVSSIGNSTIRVTINGRVYATNVNTTNDGVNDNGARFSDINIGNV 550 560 570 580 590
cry2ab2_820. ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY 610 620 630
```

```
27436036 ||||| ASSNSDVLIDINVLNSGTQFDLMNIMLVPTNISPLY 600 610 620 630
cry2ab2_820.pcp
NRAA:31872007
31872007 source="GENBANK_PROT" crystal delta-endotoxin Cry2ab-HB [Bacillus
thuringiensis]
SCORES Init1: 4113 Initn: 4113 Opt: 4113 z-score: 4677.0 E(): 0
>NRAA:31872007
Initn: 4113 Init1: 4113 Opt: 4113 z-score: 4677.0 expect(): 0
Smith-Waterman score: 4113; 99.5% identity in 632 aa overlap
(6-637:2-633)
cry2ab2_820. MOAMNSVLSGRITTCIDAYNVAADHDPFQHKSLDTVQKWTWKNNHSLYLDPIVGT 10 20 30 40 50 60
31872007 MNSVLNSGRITTCIDAYNVAADHDPFQHKSLDTVQKWTWKNNHSLYLDPIVGT 10 20 30 40 50
cry2ab2_820. VASFLKKVGSVGVKRIILSELRLNLIFFPSGSTNLMDILRETEKFLNORLNTDTLARVNAE 70 80 90 100 110 120
31872007 VASFLKKVGSVGVKRIILSELRLNLIFFPSGSTNLMDILRETEKFLNORLNTDTLARVNAE 70 80 90 100 110
cry2ab2_820. LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 130 140 150 160 170 180
31872007 LTGLQANVEEFNRQVDNLFNPNRNNAVPLSITSSVNTMQQLFNRLPQFOMQGYQLLLPL 130 140 150 160 170
cry2ab2_820. FAQANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAFKGLNT 190 200 210 220 230 240
31872007 FAQANLHLSFIRDVILNADWEGISAATLRTYRDYLNKYNTRDYSNYCINTYQSAFKGLNT 190 200 210 220 230
cry2ab2_820. RLHDMLEFRITMFLNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTOSFTSQDWPF 250 260 270 280 290 300
31872007 RLHDMLEFRITMFLNVFEVYSIWSLFKYQSLVSSGANLYASGSGPQQTOSFTSQDWPF 250 260 270 280 290
cry2ab2_820. YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 310 320 330 340 350 360
31872007 YSLFQVNSNYVLNGFSGARLSNTFFNIVGLPGSTTHALLAARVNYSGGIGSDIGASPF 310 320 330 340 350
cry2ab2_820. NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNQTESFETTLGLRSGAFTARGNSN 370 380 390 400 410 420
31872007 NONFNCSTFLPPLLTPFVRSWLDGSDREGVATVNNQTESFETTLGLRSGAFTARGNSN 370 380 390 400 410
cry2ab2_820. YFPDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA 430 440 450 460 470 480
31872007 YFPDYFIRNISGVPLVVRNEDLRRLPHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA 430 440 450 460 470
```


Study No. 06-01-62-01

MSL No. 20307

Page 181 of 361

[illegible]

334735Z
 610 620 630
 ASSNSDVEDDINTLNSGTOFDLNNIMLVPETNSPLY
 540 550 560 570 580 590
 KQNSNSINDIURVSSLNSKIRKRVIASNSVNIIINDDNSDINAKFSDINIGNV

[illegible]

6455758 source="GENBANK_PROT" crystal protein Bacillus
thuringiensis [g18927992] (ORMG3) (6220) BACU pesti-
cidial crystal protein (126 kDa) (g18927992) (ORMG3)
cry2Ad (Insecticidal delta-endotoxin crystal (d)) (crystal-
line entomocidal protein) (71 kDa crystal protein)

SCORES Inl1: 3794 Inltn: 3794 Opt: 3794 Z-score: 4314.2 E1: 0
 >>NRRA:6457578
 inltn: 3794 inl1: 3794 opt: 3794 Z-score: 4314.2 E1: 0
 Smith-Waterman score: 3794; 91.0% identity in 632 aa overlap
 (6-632, 2-631)

~~MOAMDNSVLSNGRTTICAYNVAADHPDSFOHKSJLDTVQKWTWCKNHSLXZPA VCT~~

~~MNSVLSNGRATICAYNVVVDPDSFOHKSJLDTIQENWEKKSHSVDKVTGCT~~

```

cry2ab2_820. VASFLKKVGSUGVKRILSERNLIPFGSGTNLMQDILIRTEKFLNQRNTDTLARNAR
70 80 90 100 110 120
VASFLKKVGSUGVKRILSERNLIPFGSGTNLMQDILIRTEKFLNQRNTDTLARNAR
VASFLKKVGSUGVKRILSERNLIPFGSGTNLMQDILIRTEKFLNQRNTDTLARNAR
VASFLKKVGSUGVKRILSERNLIPFGSGTNLMQDILIRTEKFLNQRNTDTLARNAR
6457578

```


Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 182 of 361

```
cry2ab2_820. 130 140 150 160 170 180
>>SW:117326 LTGLQANVEFNRQVDFLNPRNNAVPLSIITSSVNTMQQLFLNRLPQFMQGYQLLLPL
6457578 LTGLQANVEFNRQVDFLNPRNNAVPLSIITSSVNTMQQLFLNRLPQFMQGYQLLLPL
120 130 140 150 160 170

cry2ab2_820. 190 200 210 220 230 240
>>SW:117326 FAQANLHLSFIRDVILNADWGISAATLRTYRDYLNKVTROYSNYCINTYQSAGKGLNT
6457578 FAQANLHLSFIRDVILNADWGISAATLRTYRDYLNKVTROYSNYCINTYQSAGKGLNT
180 190 200 210 220 230

cry2ab2_820. 250 260 270 280 290 300
>>SW:117326 RLHDMLEFRTYMFNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFL
6457578 RLHDMLEFRTYMFNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFL
240 250 260 270 280 290

cry2ab2_820. 310 320 330 340 350 360
>>SW:117326 YSLFQVNSYLVNFGSGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISGDIAGSPF
6457578 YSLFQVNSYLVNFGSGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISGDIAGSPF
300 310 320 330 340 350

cry2ab2_820. 370 380 390 400 410 420
>>SW:117326 NONFNCSTFLPPLLTPEVRSWLDSDREGVATVNWQTESPETTLGLRSGAFTARGNSN
6457578 NONFNCSTFLPPLLTPEVRSWLDSDREGVATVNWQTESPETTLGLRSGAFTARGNSN
360 370 380 390 400 410

cry2ab2_820. 430 440 450 460 470 480
>>SW:117326 YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNNIHA
6457578 YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNNIHA
420 430 440 450 460 470

cry2ab2_820. 490 500 510 520 530 540
>>SW:117326 VHENGSMHLAPNDYTGFTTSPHATQVNNQTRTFISEKFGNQDLSRFEQNTTARYTL
6457578 VHENGSMHLAPNDYTGFTTSPHATQVNNQTRTFISEKFGNQDLSRFEQNTTARYTL
480 490 500 510 520 530

cry2ab2_820. 550 560 570 580 590 600
>>SW:117326 RGNGNSYLVLRVSSISGNTIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVV
6457578 RGNGNSYLVLRVSSISGNTIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVV
540 550 560 570 580 590

cry2ab2_820. 610 620 630
>>SW:117326 ASSNSDVLPLDINTVLTNSGTFQFLNMLVPTNISPLY
6457578 ASSNSDVLPLDINTVLTNSGTFQFLNMLVPTNISPLY
600 610 620 630

cry2ab2_820.pap
SW:117326
```

117326 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AA (INSECTICIDAL DELTA-ENDOTOXIN CRYIIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (71 KDA CRYSTAL PROTEIN) (P2 CRYSTAL PROTEIN) (MOSQUITO FACTOR)." library="NA species="Bacillus thuringiensis setovar kenya" source="swissprot_prot" version="NA type="PRT

```
SCORES Initl: 3724 Initn: 3724 Opt: 3732 Z-score: 4243.7 E(): 0
>>SW:117326 initl: 3724 opt: 3732 Z-score: 4243.7 expect(): 0
Smith-Waterman score: 3732; 87.8% identity in 632 aa overlap
(6-637;2-633)

cry2ab2_820. 10 20 30 40 50 60
>>SW:117326 MQAMDSVNSGRTTICDANNVAADPPFSEFQHSKSLDTVQKENTKKNHSLYLDPIVGT
117326 MNVLSNGRTTICDANNVAADPPFSEFQHSKSLDTVQKENTKKNHSLYLDPIVGT
10 20 30 40 50

cry2ab2_820. 70 80 90 100 110 120
>>SW:117326 VASFLKKVGSVIGKRIILSELRLNLIFFPSGSTNLMODILRETEKFLNQLRNTDTLARVNAE
117326 VSSFLKKVGSVIGKRIILSELRLNLIFFPSGSTNLMODILRETEKFLNQLRNTDTLARVNAE
60 70 80 90 100 110

cry2ab2_820. 130 140 150 160 170 180
>>SW:117326 LTGLQANVEFNRQVDFLNPRNNAVPLSIITSSVNTMQQLFLNRLPQFMQGYQLLLPL
117326 LTGLQANVEFNRQVDFLNPRNNAVPLSIITSSVNTMQQLFLNRLPQFMQGYQLLLPL
120 130 140 150 160 170

cry2ab2_820. 190 200 210 220 230 240
>>SW:117326 FAQANLHLSFIRDVILNADWGISAATLRTYRDYLNKVTROYSNYCINTYQSAGKGLNT
117326 FAQANLHLSFIRDVILNADWGISAATLRTYRDYLNKVTROYSNYCINTYQSAGKGLNT
180 190 200 210 220 230

cry2ab2_820. 250 260 270 280 290 300
>>SW:117326 RLHDMLEFRTYMFNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFL
117326 RLHDMLEFRTYMFNVFEYVSWSLFKYQSLVSSGANLYASGSGPQQTQSTQDWPFL
240 250 260 270 280 290

cry2ab2_820. 310 320 330 340 350 360
>>SW:117326 YSLFQVNSYLVNFGSGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISGDIAGSPF
117326 YSLFQVNSYLVNFGSGARLSNTFPNIVGLPGSTTHALLAARVNYSGGISGDIAGSPF
300 310 320 330 340 350

cry2ab2_820. 370 380 390 400 410 420
>>SW:117326 NONFNCSTFLPPLLTPEVRSWLDSDREGVATVNWQTESPETTLGLRSGAFTARGNSN
117326 NONFNCSTFLPPLLTPEVRSWLDSDREGVATVNWQTESPETTLGLRSGAFTARGNSN
360 370 380 390 400 410

cry2ab2_820. 430 440 450 460 470 480
>>SW:117326 YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNNIHA
117326 YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNNIHA
420 430 440 450 460 470

cry2ab2_820. 490 500 510 520 530 540
>>SW:117326 VHENGSMHLAPNDYTGFTTSPHATQVNNQTRTFISEKFGNQDLSRFEQNTTARYTL
117326 VHENGSMHLAPNDYTGFTTSPHATQVNNQTRTFISEKFGNQDLSRFEQNTTARYTL
480 490 500 510 520 530

cry2ab2_820. 550 560 570 580 590 600
>>SW:117326 RGNGNSYLVLRVSSISGNTIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVV
117326 RGNGNSYLVLRVSSISGNTIRVTINGRVYATNVNTTNDGVNDGARFSDINIGNVV
540 550 560 570 580 590
```


[illegible]


```
cry2ab2_820. 190 200 210 220 230 240
FAQANLHLSFTRDVLNADWEGISAATLRTYRDYLNKNTDRYSNYCINTYQSAFKGLNT
61221653 180 190 200 210 220 230
FAQANMHLSTFTRDVLNADWEGISAATLRTYRDYLNKNTDRYSNYCINTYQTAFRGLNT

cry2ab2_820. 250 260 270 280 290 300
RLHDMLEFRTYMFNLNVEFYVSIWLFKYQSLVSSGANLYASGSGPQQTQSFQSDWPFLL
61221653 240 250 260 270 280 290
RLHDMLEFRTYMFNLNVEFYVSIWLFKYQSLVSSGANLYASGSGPQQTQSFQTAQNWPFLL

cry2ab2_820. 310 320 330 340 350 360
YSLFQVNSYLVNGSFSGARLSNTFPNIVGLPGSTTHALLAARVNYSGSGDIGASFPF
61221653 300 310 320 330 340 350
YSLFQVNSYLVNGSFSGARLSNTFPNIVGLPGSTTHALLAARVNYSGSGDIGATNLL

cry2ab2_820. 370 380 390 400 410 420
NQNFNCSTFLPPLLTPFVRSWLDGSDREGVATVNMOTESFETTLGLRSGAFTARGNSN
61221653 360 370 380 390 400 410
NQNFNCSTFLPPLLTPFVRSWLDGSDREGVATVNMOTESFETTLGLRSGAFTARGNSN

cry2ab2_820. 430 440 450 460 470 480
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA
61221653 420 430 440 450 460 470
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIYA

cry2ab2_820. 490 500 510 520 530 540
VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLSRFPQNNNTARYTL
61221653 480 490 500 510 520 530
ANENGTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLSRFPQNNNTARYTL

cry2ab2_820. 550 560 570 580 590 600
RGNGNSYLVLRVSSIGNSTIRVTINGRVYVTAIVNTTNNNDGVNDNGARFSDINIGVV
61221653 540 550 560 570 580 590
RGNGNSYLVLRVSSIGNSTIRVTINGRVYVTAIVNTTNNNDGVNDNGARFSDINIGIV

cry2ab2_820. 610 620 630
ASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
61221653 600 610 620 630
ASDNTNVTLDINVTLSNGTQFDLMNIMFVPTNLPPLY

cry2ab2_820.pep
NPAA:47678765

47678765 source="GENBANK_PROT" insecticidal crystal protein Cry2Aa [Bacillus
thuringiensis serovar kurstaki]

SCORES Initl: 3720 Initn: 3720 Opt: 3728 z-score: 4239.1 E(): 0
>NPAA:47678765
Initn: 3720 Initl: 3720 Opt: 3728 z-score: 4239.1 expect(): 0
Smith-Waterman score: 3728; 87.7% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820. 10 20 30 40 50 60
MQAMDNVLSNGRTTICDAYNVAAHDPFSEKHSLDTIQKEMWKRTHSLVAVPVGT
```

```
47678765 10 20 30 40 50
MNVVLSNGRTTICDAYNVAAHDPFSEKHSLDTIQKEMWKRTHSLVAVPVGT

cry2ab2_820. 70 80 90 100 110 120
VASFLKKVSGSLVGKILSELNLIIPFSGSTNLMQDILRETEKFLNQRLNIDILARNAE
47678765 60 70 80 90 100 110
VSSFLKKVSGSLVGKILSELNLIIPFSGSTNLMQDILRETEKFLNQRLNIDILARNAE

cry2ab2_820. 130 140 150 160 170 180
LTGLQANVEFPNROVDNFIAPNRAVLSITSSVNTMQQLFLNRLPQFMQGVQLLLPL
47678765 120 130 140 150 160 170
LTGLQANIRFENQOVDNFIAPNRAVLSITSSVNTMQQLFLNRLPQFMQGVQLLLPL

cry2ab2_820. 190 200 210 220 230 240
FAQANLHLSFTRDVLNADWEGISAATLRTYRDYLNKNTDRYSNYCINTYQSAFKGLNT
47678765 180 190 200 210 220 230
FAQANMHLSTFTRDVLNADWEGISAATLRTYRDYLNKNTDRYSNYCINTYQTAFRGLNT

cry2ab2_820. 250 260 270 280 290 300
RLHDMLEFRTYMFNLNVEFYVSIWLFKYQSLVSSGANLYASGSGPQQTQSFQSDWPFLL
47678765 240 250 260 270 280 290
RLHDMLEFRTYMFNLNVEFYVSIWLFKYQSLVSSGANLYASGSGPQQTQSFQTAQNWPFLL

cry2ab2_820. 310 320 330 340 350 360
YSLFQVNSYLVNGSFSGARLSNTFPNIVGLPGSTTHALLAARVNYSGSGDIGASFPF
47678765 300 310 320 330 340 350
YSLFQVNSYLVNGSFSGARLSNTFPNIVGLPGSTTHALLAARVNYSGSGDIGATNLL

cry2ab2_820. 370 380 390 400 410 420
NQNFNCSTFLPPLLTPFVRSWLDGSDREGVATVNMOTESFETTLGLRSGAFTARGNSN
47678765 360 370 380 390 400 410
NQNFNCSTFLPPLLTPFVRSWLDGSDREGVATVNMOTESFETTLGLRSGAFTARGNSN

cry2ab2_820. 430 440 450 460 470 480
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA
47678765 420 430 440 450 460 470
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIYA

cry2ab2_820. 490 500 510 520 530 540
VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLSRFPQNNNTARYTL
47678765 480 490 500 510 520 530
ANENGTMHLAPEDYTGFTISPIHATQVNNQTRTFISEKFGNQDGLSRFPQNNNTARYTL

cry2ab2_820. 550 560 570 580 590 600
RGNGNSYLVLRVSSIGNSTIRVTINGRVYVTAIVNTTNNNDGVNDNGARFSDINIGVV
47678765 540 550 560 570 580 590
RGNGNSYLVLRVSSIGNSTIRVTINGRVYVTAIVNTTNNNDGVNDNGARFSDINIGIV

cry2ab2_820. 610 620 630
ASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
47678765 600 610 620 630
ASDNTNVTLDINVTLSNGTQFDLMNIMFVPTNLPPLY
```


[illegible]


```
cry2ab2_820. 370 380 390 400 410 420
:|||||:|||||:|||||:|||||:|||||:|||||
NHFNCSTVLPPLTPFVRSLDSDREGVATVNWQTESFETTLGLRSGAFTARGNSN
4239730 370 380 390 400 410
:|||||:|||||:|||||:|||||:|||||:|||||
NHFNCSTVLPPLTPFVRSLDSDREGVATVNWQTESFETTLGLRSGAFTARGNSN
360 370 380 390 400 410

cry2ab2_820. 430 440 450 460 470 480
:|||||:|||||:|||||:|||||:|||||:|||||
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNIHA
4239730 430 440 450 460 470 480
:|||||:|||||:|||||:|||||:|||||:|||||
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNIHA
420 430 440 450 460 470 480

cry2ab2_820. 490 500 510 520 530 540
:|||||:|||||:|||||:|||||:|||||:|||||
VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRIFISEKFGNQGDSLRFEQNTTARYTL
4239730 490 500 510 520 530 540
:|||||:|||||:|||||:|||||:|||||:|||||
ANENGTMHLAPEDYTGFTISPIHATQVNNQTRIFISEKFGNQGDSLRFEQNTTARYTL
480 490 500 510 520 530 540

cry2ab2_820. 550 560 570 580 590 600
:|||||:|||||:|||||:|||||:|||||:|||||
RNGNSYNLYLRVSSIGNSTIRVTINGRVTYVSNVNTTNNQDNGDNGARFSDINIGNVV
4239730 550 560 570 580 590 600
:|||||:|||||:|||||:|||||:|||||:|||||
RNGNSYNLYLRVSSIGNSTIRVTINGRVTYVSNVNTTNNQDNGDNGARFSDINIGNV
540 550 560 570 580 590 600

cry2ab2_820. 610 620 630
:|||||:|||||:|||||:|||||:|||||:|||||
ASSNSDVPDLINVLNSGTQFDLMNIMLVPTNISPLY
4239730 610 620 630
:|||||:|||||:|||||:|||||:|||||:|||||
ASDNTNVLDINVLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630

cry2ab2_820.pgp
NRRA:61252390
61252390 source="GENBANK PROT" Pesticidal crystal protein cry2Aa (Insecticidal
delta-endotoxin CryIIA(a)) (Crystalline entomocidal protoxin) (71 kDa crystal
protein) (P2 crystal protein) (Mosquito factor)gi|2921832|gb|AAC04867.1|
insecticidal crystal protein [Bacillus thuringiensis]

SCORES Initl: 3713 Initn: 3713 Opt: 3713 z-score: 4222.1 E(): 0
>>NRRA:61252390
initn: 3713 initl: 3713 opt: 3713 z-score: 4222.1 expect(): 0
Smith-Waterman score: 3713; 87.5% identity in 632 aa overlap
(6-637:2-633)

cry2ab2_820. 70 80 90 100 110 120
:|||||:|||||:|||||:|||||:|||||:|||||
MQAMNSVLSGRITTCIDAYNVAADHPSFOHKSLDITVQKEWTEWKNHSLYLDPIVGT
61252390 70 80 90 100 110 120
:|||||:|||||:|||||:|||||:|||||:|||||
MNSVLSGRITTCIDAYNVAADHPSFOHKSLDITVQKEWTEWKNHSLYLDPIVGT
10 20 30 40 50 60

cry2ab2_820. 130 140 150 160 170 180
:|||||:|||||:|||||:|||||:|||||:|||||
LTGLQANVEEFNRQVDNPLNPNENAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLPL
61252390 130 140 150 160 170 180
:|||||:|||||:|||||:|||||:|||||:|||||
LTGLQANVEEFNRQVDNPLNPNENAVPLSITSSVNTMQQLFLNRLPQFMQGYQLLPL
120 130 140 150 160 170 180
```

```
cry2ab2_820. 190 200 210 220 230 240
:|||||:|||||:|||||:|||||:|||||:|||||
FAQANLHUSFTRDVLNADSWGISAAITLRTDYLKNTYRDYLNKYTDYNYCINTYQSAFKGLNT
61252390 190 200 210 220 230 240
:|||||:|||||:|||||:|||||:|||||:|||||
FAQANLHUSFTRDVLNADSWGISAAITLRTDYLKNTYRDYLNKYTDYNYCINTYQSAFKGLNT
180 190 200 210 220 230 240

cry2ab2_820. 250 260 270 280 290 300
:|||||:|||||:|||||:|||||:|||||:|||||
RLHDMLEFRTYFLNVFEYVSWLSFKYQSLVSSGANLYASGSGPOQTOSTSODWPEL
61252390 250 260 270 280 290 300
:|||||:|||||:|||||:|||||:|||||:|||||
RLHDMLEFRTYFLNVFEYVSWLSFKYQSLVSSGANLYASGSGPOQTOSTSODWPEL
240 250 260 270 280 290 300

cry2ab2_820. 310 320 330 340 350 360
:|||||:|||||:|||||:|||||:|||||:|||||
YSLFQVNSNYLVNLFSGARLNTFPNIVGLPGSTTTTHALLAARVNYSGSISGDIAGSPF
61252390 310 320 330 340 350 360
:|||||:|||||:|||||:|||||:|||||:|||||
YSLFQVNSNYLVNLFSGARLNTFPNIVGLPGSTTTTHALLAARVNYSGSISGDIAGSPF
300 310 320 330 340 350 360

cry2ab2_820. 370 380 390 400 410 420
:|||||:|||||:|||||:|||||:|||||:|||||
NHFNCSTVLPPLTPFVRSLDSDREGVATVNWQTESFETTLGLRSGAFTARGNSN
61252390 370 380 390 400 410 420
:|||||:|||||:|||||:|||||:|||||:|||||
NHFNCSTVLPPLTPFVRSLDSDREGVATVNWQTESFETTLGLRSGAFTARGNSN
360 370 380 390 400 410 420

cry2ab2_820. 430 440 450 460 470 480
:|||||:|||||:|||||:|||||:|||||:|||||
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNIHA
61252390 430 440 450 460 470 480
:|||||:|||||:|||||:|||||:|||||:|||||
YFPDYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNIHA
420 430 440 450 460 470 480

cry2ab2_820. 490 500 510 520 530 540
:|||||:|||||:|||||:|||||:|||||:|||||
VHENGSMIHLAPNDYTGFTISPIHATQVNNQTRIFISEKFGNQGDSLRFEQNTTARYTL
61252390 490 500 510 520 530 540
:|||||:|||||:|||||:|||||:|||||:|||||
ANENGTMHLAPEDYTGFTISPIHATQVNNQTRIFISEKFGNQGDSLRFEQNTTARYTL
480 490 500 510 520 530 540

cry2ab2_820. 550 560 570 580 590 600
:|||||:|||||:|||||:|||||:|||||:|||||
RNGNSYNLYLRVSSIGNSTIRVTINGRVTYVSNVNTTNNQDNGDNGARFSDINIGNVV
61252390 550 560 570 580 590 600
:|||||:|||||:|||||:|||||:|||||:|||||
RNGNSYNLYLRVSSIGNSTIRVTINGRVTYVSNVNTTNNQDNGDNGARFSDINIGNV
540 550 560 570 580 590 600

cry2ab2_820.pgp
SW:61252390
61252390 description="Pesticidal crystal protein cry2Aa (Insecticidal
delta-endotoxin CryIIA(a)) (Crystalline entomocidal protoxin) (71 kDa crystal
protein) (P2 crystal protein) (Mosquito factor)." library=NA species="Bacillus
thuringiensis serovar kenya" source="swissprot_prot" version=NA type=PRF

SCORES Initl: 3713 Initn: 3713 Opt: 3713 z-score: 4222.1 E(): 0
>>SW:61252390
initn: 3713 initl: 3713 opt: 3713 z-score: 4222.1 expect(): 0
Smith-Waterman score: 3713; 87.5% identity in 632 aa overlap
(6-637:2-633)
```


61252390 ASDNVTNVLIDNVLTNGSTFPDMLNIMVFTNMLPPLY 600 610 620 630

crv2ab2_820.pep
NR001:4239728

4239728 source="GENBANK_PROT" Crv2Aa protein [Bacillus thuringiensis]

SCORES Initl: 3694 Initn: 3694 Opt: 3702 2-score: 4209.6 E(): 0
>NR001:4239728
initn: 3694 opt: 3702 2-score: 4209.6 expect(): 0
Smith-Waterman score: 3702; 87.2% identity in 632 aa overlap
(6-637:2-633)

crv2ab2_820. MQAMDSNVLSGRTTICDAYNVAHDPFQFQHSKLDITQKENTWKNHSLYLDPIVGT
4239728 MNVLSRRTSRTICDAYNVAHDPFQFQHSKLDITQKENTWKNHSLYLDPIVGT
10 20 30 40 50
110 120 130 140 150 160 170 180
crv2ab2_820. VASFLKKVGSVLGKRILSELRLNLIFFSGSTNLMODILRETEFLNORLNTDITLARVNAE
4239728 VSSFLKKVGSVLGKRILSELRLNLIFFSGSTNLMODILRETEFLNORLNTDITLARVNAE
60 70 80 90 100 110
120 130 140 150 160 170 180
crv2ab2_820. LELQANVEEFNRQVDNPLNPNRNVPLSITSSVNTMQQLFNRLPFOFQMGYQLLLPL
4239728 LIGQANVEEFNRQVDNPLNPNRNVPLSITSSVNTMQQLFNRLPFOFQMGYQLLLPL
120 130 140 150 160 170
crv2ab2_820. PAFANLHLSFTRIVLNADPWGISAATITRYDVLKNYTRDYSNICYTQSAFQKGT
4239728 PAFANLHLSFTRIVLNADPWGISAATITRYDVLKNYTRDYSNICYTQSAFQKGT
180 190 200 210 220 230 240
crv2ab2_820. RLHDMLESTIRNLFNVAEVSASLKFYSLSLSSGAMLVASGGQQQTQSTQSDMPFL
4239728 RLHDMLESTIRNLFNVAEVSASLKFYSLSLSSGAMLVASGGQQQTQSTQSDMPFL
240 250 260 270 280 290
crv2ab2_820. YSLFOVNSYVLNGFSGARLSNTPNUGGPGITFALLAARVWYSGLSSGSDIGASFP
4239728 YSLFOVNSYVLNGFSGARLSNTPNUGGPGITFALLAARVWYSGLSSGSDIGASFP
300 310 320 330 340 350
crv2ab2_820. NONFNCSCTLPPLLTFFVRSLWDSGSDREGVATVNNQTSSTETLSSGFTARGNSN
4239728 NONFNCSCTLPPLLTFFVRSLWDSGSDREGVATVNNQTSSTETLSSGFTARGNSN
360 370 380 390 400 410 420
crv2ab2_820. YFFDPIRINISGVLVVRNEDLRPLHYNRINIASPSGTPGGARAYVMYSVHNRKNHA
4239728 YFFDPIRINISGVLVVRNEDLRPLHYNRINIASPSGTPGGARAYVMYSVHNRKNHA
420 430 440 450 460 470 480


```

5834516      YSLFOVNSYILSGISGTRLSITFPNIGLPGSTTHSLNSARVNSYGVSSGLIGATNL
              300      310      320      330      340      350
cry2ab2_820.  NQNFNCSTFFPPLLTFFVRSWLDSDGREGVATVNNQTESFETTLGRSGAFTARGNSN
              370      380      390      400      410      420
5834516      NQNFNCSTVLPPLSTFFVRSWLDSDGREGVATVNNQTESFETTLGRSGAFTARGNSN
              360      370      380      390      400      410
cry2ab2_820.  YPFDYFIRNIGSVPLVRNEDLRPLHYNEIRNIASPSGTPGGAAYVWVSHNKNNIHA
              430      440      450      460      470      480
5834516      YPFDYFIRNIGSVPLVRNEDLRPLHYNQIRNIESPSGTPGGAAYLVSHNKNNIYA
              420      430      440      450      460      470
cry2ab2_820.  VHENGSMIHLAPNDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTL
              490      500      510      520      530      540
5834516      ANENGTMIHLAPEDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARHTL
              480      490      500      510      520      530
cry2ab2_820.  RGNNGSNLYLRVSSIGNSTIRVTINGRVTATNVNTTNNQVNDNGARFSDINIGNVV
              550      560      570      580      590      600
5834516      RGNNGSNLYLRVSS
              540      550
cry2ab2_820.pep
NRAA:5834516
66734543 source="GENBANK_PROT" Cry2Ac [Bacillus thuringiensis]

SCORES      Init1: 3234      Initn: 3234      Opt: 3242      Z-score: 3687.4      E(): 4.3e-197
>>NRAA:5834516
      initn: 3234      init1: 3234      opt: 3242      Z-score: 3687.4      expect(): 4.3e-197
Smith-Waterman score: 3242;      87.3% identity in 550 aa overlap
(6-555:2-551)

cry2ab2_820.  MOAMDNSVLSNGRTTICDAYNVAAHDPFSEKSLDTQKEMTEWKNHNSLYLDPVGT
              10      20      30      40      50      60
5834516      MNNVLSNRRTTICDAYNVAAHDPFSEKSLDTQKEMTEWKNHNSLYLDPVGT
              10      20      30      40      50
cry2ab2_820.  VASFLKKVGSVLGKRISELNLIFFPSGSTNLMQDLRETEKFLNQRINTDTLARVNAE
              70      80      90      100      110      120
5834516      VSSFLKKVGSVLGKRISELNLIFFPSGSTNLMQDLRETEKFLNQRINTDTLARVNAE
              60      70      80      90      100      110
cry2ab2_820.  LTGLQANVEEFNRQVDNLFNPNRNVAPLSITSSVNTMQQLFLNLPQFMQGYQLLLPL
              130      140      150      160      170      180
5834516      LTGLQANREFNQVDNLFNPTQNPVLSITSSVNTMQQLFLNLPQFMQGYQLLLPL
              120      130      140      150      160      170
cry2ab2_820.  FAQAANHLHSFIRDVILNADWEGISAATLRDYRLKNTYRDYSNYCINTYQSAFQKGLNT
              190      200      210      220      230      240
5834516      FAQAANHLHSFIRDVILNADWEGISAATLRDYRLKNTYRDYSNYCINTYQSAFQKGLNT
              180      190      200      210      220      230
cry2ab2_820.  RLHDMLEFRYFLNVEYSIWSLFKYQSLVSSGANLYASGGPGQQTQSTFSQDWPFPL
              250      260      270      280      290      300
5834516      RLHDMLEFRYFLNVEYSIWSLFKYQSLVSSGANLYASGGPGQQTQSTFSQDWPFPL
              240      250      260      270      280      290
cry2ab2_820.  YSLFOVNSVNLGFGSARLSNTPFNIVGLPGSTTHALLAARVNSYSGSLSSDGGASFP
              310      320      330      340      350      360

```

```

5834516      YSLFOVNSYILSGISGTRLSITFPNIGLPGSTTHSLNSARVNSYGVSSGLIGATNL
              300      310      320      330      340      350
cry2ab2_820.  NQNFNCSTFFPPLLTFFVRSWLDSDGREGVATVNNQTESFETTLGRSGAFTARGNSN
              370      380      390      400      410      420
5834516      NQNFNCSTVLPPLSTFFVRSWLDSDGREGVATVNNQTESFETTLGRSGAFTARGNSN
              360      370      380      390      400      410
cry2ab2_820.  YPFDYFIRNIGSVPLVRNEDLRPLHYNEIRNIASPSGTPGGAAYVWVSHNKNNIHA
              430      440      450      460      470      480
5834516      YPFDYFIRNIGSVPLVRNEDLRPLHYNQIRNIESPSGTPGGAAYLVSHNKNNIYA
              420      430      440      450      460      470
cry2ab2_820.  VHENGSMIHLAPNDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARYTL
              490      500      510      520      530      540
5834516      ANENGTMIHLAPEDYTGFTISPIHATQVNNOTRTFISEKFGQDGLRFEQNTTARHTL
              480      490      500      510      520      530
cry2ab2_820.  RGNNGSNLYLRVSSIGNSTIRVTINGRVTATNVNTTNNQVNDNGARFSDINIGNVV
              550      560      570      580      590      600
5834516      RGNNGSNLYLRVSS
              540      550
cry2ab2_820.pep
NRAA:66734543
66734543 source="GENBANK_PROT" Cry2Ac [Bacillus thuringiensis]

SCORES      Init1: 1601      Initn: 2413      Opt: 2401      Z-score: 2730.1      E(): 9e-144
>>NRAA:66734543
      initn: 2413      init1: 1601      opt: 2401      Z-score: 2730.1      expect(): 9e-144
Smith-Waterman score: 3324;      80.1% identity in 632 aa overlap
(6-637:2-623)

cry2ab2_820.  MOAMDNSVLSNGRTTICDAYNVAAHDPFSEKSLDTQKEMTEWKNHNSLYLDPVGT
              10      20      30      40      50      60
66734543      MNTVLNNGRNTTCHAHNVVAHDPFSEKSLNTIEKEMKWKRTDHSLYVAPVGT
              10      20      30      40      50
cry2ab2_820.  VASFLKKVGSVLGKRISELNLIFFPSGSTNLMQDLRETEKFLNQRINTDTLARVNAE
              70      80      90      100      110      120
66734543      VGSFLKKVGSVLGKRISELNLIFFPSGSTNLMQDLRETEKFLNQRINTDTLARVNAE
              60      70      80      90      100      110
cry2ab2_820.  LTGLQANVEEFNRQVDNLFNPNRNVAPLSITSSVNTMQQLFLNLPQFMQGYQLLLPL
              130      140      150      160      170      180
66734543      LAGLQANVAEENRQVDNLFNPNQNPVLAIDSNLTQQLFLSRPQFMQGYQLLLPL
              120      130      140      150      160      170
cry2ab2_820.  FAQAANHLHSFIRDVILNADWEGISAATLRDYRLKNTYRDYSNYCINTYQSAFQKGLNT
              190      200      210      220      230      240
66734543      FAQAANHLHSFIRDVILNADWEGISAATLRDYRLKNTYRDYSNYCINTYQSAFQKGLNT
              180      190      200      210      220      230

```


©01 **Product Characterization**

CRY2AB2_820. RLHDLMEFTYMLNVEFVSWLSFKYQSLVSSGANLYASGSGPQQTQSTQSDWPFLL
66734543. RLHDLMEFTYMLNVEFVSWLSFKYQSLVSSGANLYASGSGP--TQSTFAQNWPFLL
CRY2AB2_820. YSLFOVNSVYLVNGFSGCARLSNTFENIUGLP--GSTTHALLAARVNSGGISSGSDIGAS
66734543. YSLFOVNSVYLVNGFSGCARLSNTFENIUGLP--GSTTHALLAARVNSGGISSGSDIGAS
CRY2AB2_820. NONFNCSTFLPPLTPFVRSWLSGSDREGVATVNTNNDGVNDGARFSDINIGNVV
66734543. NONFNCSTFLPPLTPFVRSWLSGSDREGVATVNTNNDGVNDGARFSDINIGNVV
CRY2AB2_820. YHNGMSVYLVSSGSGSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
66734543. YHNGMSVYLVSSGSGSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
CRY2AB2_820. ASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
66734543. ASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
CRY2AB2_820. pep
NR2A:40286

40286 source="GENBANK_PROT" CRYIIC delta-endotoxin [Bacillus
thuringiensis]gi|18469156|sp|Q45743|CR2AC_BACTU pesticidal crystal protein
CRY2AC (Insecticidal delta-endotoxin CryIIA(c)) (Crystalline entomocidal
protoxin) (70 kDa crystal protein)gi|228281|prf||1802281A delta endotoxin

SCORES Initl: 1548 Initn: 2654 Opt: 2294 Z-score: 2608.4 E(): 5.4e-137
->NR2A:40286
initn: 2654 initl: 1548 opt: 2294 Z-score: 2608.4 expect(): 5.4e-137
Smith-Waterman score: 3211; 77.8% identity in 634 aa overlap
(6-637:2-622)

CRY2AB2_820. MQAMDSVLSGRITTCIDAYNVAADPFQHKSLDITVQKWEKTEWKNKNSLYLDPDPIGT
40286. MNTVLNNGENTTCHAHNVVAHDFEFSEKSLNTEKEKWEKTEWKNKNSLYLDPDPIGT

CRY2AB2_820. VASFLKKVSLVGKILSELNRLIFFSGSTNLMQDILRETEKFLNQSLNTDTLARVNAE
40286. VGSFLKKVSLVGKILSELNRLIFFSGSIDLMQELRAEQFQINORLNADTLGRVNAE
CRY2AB2_820. LTGLQANVEFNRQVNFNPNNNAVPLSISSVNTMWOOLFNLRLPOFOMOGVOLLPL
40286. LAGLANVAEFNRQVNFNPNNNAVPLSISSVNTMWOOLFNLRLPOFOMOGVOLLPL
CRY2AB2_820. FQAANLHLSFIRDVILNADWGISAAATLRTYRDYLNKVTYRYSNYCINTYQSFAKGLNT
40286. FQAANLHLSFIRDVILNADWGISAAATLRTYRDYLNKVTYRYSNYCINTYQSFAKGLNT
CRY2AB2_820. RLHDLMEFTYMLNVEFVSWLSFKYQSLVSSGANLYASGSGPQQTQSTQSDWPFLL
40286. RLHDLMEFTYMLNVEFVSWLSFKYQSLVSSGANLYASGSGP--TQSTFAQNWPFLL
CRY2AB2_820. YSLFOVNSVYLVNGFSGCARLSNTFENIUGLP--GSTTHALLAARVNSGGISSGSDIGAS
40286. YSLFOVNSVYLVNGFSGCARLSNTFENIUGLP--GSTTHALLAARVNSGGISSGSDIGAS
CRY2AB2_820. PFWQNFSTFLPPLTPFVRSWLSGSDREGVATVNTNNDGVNDGARFSDINIGNVV
40286. PFWQNFSTFLPPLTPFVRSWLSGSDREGVATVNTNNDGVNDGARFSDINIGNVV
CRY2AB2_820. YHNGMSVYLVSSGSGSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
40286. YHNGMSVYLVSSGSGSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
CRY2AB2_820. ASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
40286. ASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
CRY2AB2_820. HAVHENGSMTHLAPNDYTFPNSPIHACQNNQIRTFISEKYNQDGLRFLSNPTARY
40286. YDTHENGSMTHLAPNDYTFPNSPIHACQNNQIRTFISEKYNQDGLRFLSNPTARY
CRY2AB2_820. TLRGNGSNLYLRFVSSIGNSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
40286. TLRGNGSNLYLRFVSSIGNSTIRVTINGRVVTA--NYNTITNDGVNDGARFSDINIGNVV
CRY2AB2_820. VVASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
40286. VVASSNSDVPLDINVTLSGTQFDLMNIMLVPTNISPLY
CRY2AB2_820. pep
SW:8469156

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 190 of 361

8469156 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AC (INSECTICIDAL DELTA-ENDOTOXIN CRYIIA(C)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (70 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 1548 Initn: 2654 Opt: 2294 z-score: 2608.4 E(): 5.4e-137
>>SW:8469156
initn: 2654 initl: 1548 opt: 2294 z-score: 2608.4 expect(): 5.4e-137
Smith-Waterman score: 3211; 77.8% identity in 634 aa overlap
(6-637;2-622)

cry2ab2_820. MQAMNSVLNNGRTTICDAYNVAADHDFSFQHKSLDTQKTEWKKNHSLYLDPIVGT
8469156 MNTVLNNGRTTICAHNVVAADHDFSFQHKSLDTQKTEWKKNHSLYLDPIVGT
10 20 30 40 50
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

cry2ab2_820. VASFLKKVGSILVGRILSELRLNLFPSGSTNLMDILRETEKFLNQRINTTLARVNAE
8469156 VGSFLKKVGSILVGRILSELRLNLFPSGSTNLMDILRETEKFLNQRINTTLARVNAE
70 80 90 100 110 120
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

cry2ab2_820. LTGLQANVEEFNRQVDNPLNPNNAVPLSITSSVNTMQQLFLNRLPQFQMGYQLLLPL
8469156 LAGLQANVAENRQVDNPLNPNNAVPLSITSSVNTMQQLFLNRLPQFQMGYQLLLPL
130 140 150 160 170 180
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

cry2ab2_820. FAQANLHLSFIRVILNADEWGISATLRTYRDLKYNTRDYSNICYNTYQSAFKGLNT
8469156 FAQANLHLSFIRVILNADEWGISATLRTYRDLKYNTRDYSNICYNTYQSAFKGLNT
190 200 210 220 230 240
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

cry2ab2_820. RLHDMLEFETMFLNVEYVINSLEKYQSLVSSGANLYASGSGQQTQSTQSDNFFL
8469156 RLHDMLEFETMFLNVEYVINSLEKYQSLVSSGANLYASGSGQQTQSTQSDNFFL
250 260 270 280 290 300
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

cry2ab2_820. YSLFQVNSVNLGPFSGARLNTFFNIVGLP--GSTTHALLAARVNYSGGSDIGAS
8469156 YSLFQVNSVNLGPFSGARLNTFFNIVGLP--GSTTHALLAARVNYSGGSDIGAS
310 320 330 340 350
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

cry2ab2_820. PFNQPNCSFTPLPPLTFVRSLDSDREGVATVNTWQSFETTLGLRSGATTARGN
8469156 NLNQPNCSFTPLPPLTFVRSLDSDREGVATVNTWQSFETTLGLRSGATTARGN
360 370 380 390 400 410
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

cry2ab2_820. SNFPDYFIRNLSGVLVWNEOLRPLHYNEIRINIASPSTGCGARAWSVHNRKNI
8469156 SNFPDYFIRNLSGVLVWNEOLRPLHYNEIRINIASPSTGCGARAWSVHNRKNI
420 430 440 450 460 470
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

cry2ab2_820. HAVHENGSIHLAPNDYTGFTISPIHATOVNNTQRTFSEKFGNQDGLRFEONNTIARY
8469156 HAVHENGSIHLAPNDYTGFTISPIHATOVNNTQRTFSEKFGNQDGLRFEONNTIARY
480 490 500 510 520 530
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

cry2ab2_820. TLRNGNSYNLYRVSSIGSTIRVTINGRVYTAIVNTTNNNDGVNDGARFSDINIGN
8469156 TLRNGNSYNLYRVSSIGSTIRVTINGRVYTAIVNTTNNNDGVNDGARFSDINIGN
540 550 560 570 580 590
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

cry2ab2_820. VVASNSDVLDINVTLSGTFQDLNMLVPTNISPLY
8469156 VVASNSDVLDINVTLSGTFQDLNMLVPTNISPLY
600 610 620 630
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

cry2ab2_820.pep
SW:10719936

10719936 description="PARASPORAL CRYSTAL PROTEIN CRY18AA (PARASPORAL DELTA-ENDOTOXIN CRYXVIII(A)) (CRYSTALLINE PARASPORAL PROTOXIN) (79 KDA CRYSTAL PROTEIN)." library=NA species="Paenibacillus popilliae" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 725 Initn: 1195 Opt: 1032 z-score: 1172.2 E(): 5.4e-57
>>SW:10719936
initn: 1195 initl: 725 opt: 1032 z-score: 1172.2 expect(): 5.4e-57
Smith-Waterman score: 1364; 38.8% identity in 665 aa overlap
(1-637;72-706)

cry2ab2_820. MQAMNSVLNNGRTTICDAYNVAADHDFSF
10719936 DGISDDLICCLDPIYNNNDNDAICDELGLTIDNNTICSTDTF---PINVVRTDFF--
50 60 70 80 90 10
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

cry2ab2_820. QHKSIDTVQKTEWKKNHSLYLDPIVGTVASFLKKVGSILVGRILSELRLNLFPSGS
10719936 RKKSQELTREWTEWKENSPLFTFAIVGVVTSFLQSLKQATSFLLKTLTDLFFNNS
100 110 120 130 140 150
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

cry2ab2_820. TNLMDILRETEKFLNQRINTTLARVNAELTGLQANVEEFNRQVDNPLNPNNAVPLSI
10719936 SILTMEELRATEQYVOERLDTIDTANRVSQELVGLKNNLTTFNDQVEDFLQNRVYGLSLAI
160 170 180 190 200 210
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

cry2ab2_820. TSSVNTMQQLFLNRLPQFQMGYQLLLPLFAQANLHLSFIRVILNADEWGISATLR
10719936 IDSINTMQQLFLNRLPQFQMGYQLLLPLFAQANLHLSFIRVILNADEWGISATLR
160 170 180 190 200 210
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

cry2ab2_820. TYRDLKNYTRDYSNICYNTYQSAFKG-LNTR--LHDMLEFETMFLNVEYVINSLEPK
10719936 TYRDLKNYTRDYSNICYNTYQSAFKG-LNTR--LHDMLEFETMFLNVEYVINSLEPK
220 230 240 250 260 270
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

cry2ab2_820. YGSLVAGANLYASGSGQQTQSTQSDNFFLQSLVSSGANLYASGSGARLNTFPNI
10719936 YGSLVAGANLYASGSGQQTQSTQSDNFFLQSLVSSGANLYASGSGARLNTFPNI
270 280 290 300 310 320
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

©01 Proprietary Information of Monsanto Company

```
cry2ab2_820 330 340 350 360 370 380 390
VGLPGSTTHALLAARVNSGSSG-DIGASPN-----QNFNCSTFL
10719936 400 410 420 430 440 450
LSRYHDDLKNITVWGTOGPNGVSTTDELKQOQATDSLVDQFFTLNCWL

cry2ab2_820 380 390 400 410 420
P-PLTLP-FVRSWLDSC-SDREGVATVNMOTESFETTLGLRS-GAFTARGNSNYFPDYF
10719936 460 470 480 490 500
ENPITAPYFATSLYESRASSGGYLRSVFKSE--DSTCGLGNPGAWTS-----YPDY

cry2ab2_820 430 440 450 460 470 480
IRNLSG-VPLVVRNEDLRPHYNEIRNLSASGTPGARGAYMVSVHNRKNIHANG
10719936 510 520 530 540 550 560
ITNISATVQINGENTDTT-PLYFKENRPTSTNGV---NKVIAVYNRKANIAGTNG

cry2ab2_820 490 500 510 520 530 540 550 560
SMILAPNDYTGFTISPIHATOVANNQRTFISEKFGNCGDSLNEQONTTARTILSNG-
10719936 570 580 590 600 610 620 630
TMIHQAPDGTGFTVSPHPSA--NTITSYIKENYGNCGDSLHLKGOVL-HYMLSGNGO

cry2ab2_820 550 560 570 580 590 600 610 620 630
NSYNLYRVSSIGNSTIRVTINGRVYTATVNTTNNGVNDNGARFSDINIGVASSN
10719936 620 630 640 650 660 670
DRYLVRLSAGAN--QIKLQSPPTTSIYAFDTSTNNEGIDNNGSKFDFAF-----STP

cry2ab2_820 610 620 630
SDVPLDINVTLN-SGT-QFDLMNIMLVPTNISPLY
10719936 680 690 700
FVPEQKEIVLYFEGVGSGLDLNLIFLPADDTPLY

cry2ab2_820 pep
NRAA:1429252

1429252 source="GENBANK PROT" parasporal crystal protein [Paenibacillus
popilliae]gi|10719936|sp|Q45358|C18AA_PAEPP Parasporal crystal protein cry18aa
(Parasporal delta-endotoxin CryAVIIIa(a)) (Crystalline parasporal protoxin) (79
kDa crystal protein)

SCORES Initl: 725 Initn: 1195 Opt: 1032 z-score: 1172.2 E(): 5.4e-57
>NRAA:1429252
Initn: 1195 Initl: 725 Opt: 1032 z-score: 1172.2 expect(): 5.4e-57
Smith-Waterman score: 1364; 38.8% identity in 665 aa overlap
(1-637/72-706)

cry2ab2_820. 10 20 30
MQAMNSVLSGRTTCIDANVAADPFSP
1429252 DGI5DDLICLDPIYNNNDNAICDELGLTIDNTCTDET---PINVVRTDFF--
50 60 70 80 90

cry2ab2_820. 40 50 60 70 80 90
QHKSLDVTQEWKWKNNHSLYLDPIVGTVASFLKKGVLGKRLSERNLIFPSGS
1429252 RKXSTQELTREWTEWKENSPLFTFAIVGVVTSFLLQSLKQATSFLLKTLTOLLFPNNS
```

```
cry2ab2_820 100 110 120 130 140 150
TNLMODILRETEKFLNORLNTDTLARVNAELTGLQANVEEFNRQVDNENRNVAPLSI
1429252 160 170 180 190 200 210
SLTMEIILRATEQVQERLDTDTANRVSQELVGLKNNLITFNDQVEDFLQNRVGSPLAI

cry2ab2_820 160 170 180 190 200 210
TSSVNTMOQLFNRLPQFMQOQYQLLLPLFAQANLHLSFIRDVILNADWEGISAATLR
1429252 220 230 240 250 260 270
IDSINTMOQLFNRLPQFMQOQYQLLLPLFAQATLHLTFRDVIINADWENIPTAQLN

cry2ab2_820 220 230 240 250 260
TYRDYLNKTYRDISNYCINTYQSAFKG-LNTR--LHDMLEFRITYMELNVFEYVSIWLSFK
1429252 280 290 300 310 320 330
TYTRYFKEYIAEYNSVALSTYDDGFRTFYPRNTEMDMFOFKTFMLNALDLVSIWLSLLK

cry2ab2_820 270 280 290 300 310 320
YOSLLVSSGANLYASGSGPOQTQSFSTQDWPFLYSLFQVNSNYVLNFGSGARLSNTFPNI
1429252 340 350 360 370 380 390
YUNLVYTSANLYNIGDNKNVNGAYPISVGPFENSYIQTKSNYVLGSGVSGIGARTYSTV

cry2ab2_820 330 340 350 360 370 380 390
VGLPGSTTHALLAARVNSGSSG-DIGASPN-----QNFNCSTFL
1429252 400 410 420 430 440 450
LSRYHDDLKNITVWGTOGPNGVSTTDELKQOQATDSLVDQFFTLNCWL

cry2ab2_820 430 440 450 460 470 480
P-PLTLP-FVRSWLDSC-SDREGVATVNMOTESFETTLGLRS-GAFTARGNSNYFPDYF
1429252 460 470 480 490 500 510
ENPITAPYFATSLYESRASSGGYLRSVFKSE--DSTCGLGNPGAWTS-----YPDY

cry2ab2_820 430 440 450 460 470 480
IRNLSG-VPLVVRNEDLRPHYNEIRNLSASGTPGARGAYMVSVHNRKNIHANG
1429252 510 520 530 540 550 560
ITNISATVQINGENTDTT-PLYFKENRPTSTNGV---NKVIAVYNRKANIAGTNG

cry2ab2_820 490 500 510 520 530 540 550 560
SMILAPNDYTGFTISPIHATOVANNQRTFISEKFGNCGDSLNEQONTTARTILSNG-
1429252 570 580 590 600 610 620 630
TMIHQAPDGTGFTVSPHPSA--NTITSYIKENYGNCGDSLHLKGOVL-HYMLSGNGO

cry2ab2_820 550 560 570 580 590 600 610 620 630
NSYNLYRVSSIGNSTIRVTINGRVYTATVNTTNNGVNDNGARFSDINIGVASSN
1429252 620 630 640 650 660 670
DRYLVRLSAGAN--QIKLQSPPTTSIYAFDTSTNNEGIDNNGSKFDFAF-----STP

cry2ab2_820 pep
NRAA:1429252
```


Study No. 06-01-62-01
MSL No. 20307
Page 192 of 361

9622200 source="GENBANK PROT" parasporel crystal protein Cry18Ca1 [Paenibacillus popilliae|gi|10719930|sp|P57092|C18Ca PHEPP Parasporel crystal protein cry18Ca (Parasporel delta-endotoxin CryXVIIIc(a)) (Crystalline parasporel protoxin) (78 kDa crystal protein)]

crv2ab2 820.
MOAMDNVLSGRTTICDAYNVAADPFSE
10 20 30

820. civ2ab2 OHKSI DTVOKEFWTEWKKNHSHIYI DPVTGTVASEFLI KKVGSIVGKRILISELRNLIFFPSGS

820. *ctv2ab2* 100 110 120 130 140 150
TNLMODILRETEKFINORINTDTLARVNAELTGLQANVEEFNRVDNFI PNENAVPLSI

chr2ab2 820. TSSVNTMOOFLNRLPQFOMQGYOLLILPLFAOANLHLSFIRDVITNADEWGISAAATLR
160 170 180 190 200 210

crv2ab2 820. TYRDYLYKNYPTDYSNYCINTYQSAFKG-LNTR--LHDMLEFRTYMFELNVFEYVSTWSLFLK

270 280 290 300 310 320
 civ2ab2 820. YOSLLVSSGANLYASGGPQOTQSTSDMPFLYSLFOVNSNVXVNGESGARLNTFPNI

cry2ab2 820. VGLPGSTTHALLAARVNYSGGISSGDIGAS-----P--FNO-NFNC
330 340 350 360

civ2ab2 820. STFLPPLITPEVRSWLDSGDREGVATVNW-OTESF---ETVLGRSGAFTAFGNSNYF

civ2ab2 820. PDYFIRNISSG-VPLVVRNEDLRRLHYNEIRNIASPSGTPGGARAYMVSVHNRKNNIHA-
430 440 450 460 470 480

10719930
TYKRLDQVAGQNTALSTYEEAFARFYPRNTVENMLFEKFTMLNVLVDLSMSLLK
280 290 300 310
cry2ab2_820. VSLDSSGALLDSSGPOOTOSTSDMPFLYSLFQVNSVNLVNGSGARLSNTFPNI
280 290 300 310 320
10719930 VNLVNTSLNLTGNNLWNGEYSLSNPEENTYIOTKSNVLSGVSGYARWSYTN-
320 330 340 350 360
cry2ab2_820. VGLPGSTITALLAARNYSGLSSGIGS-----P-FNQ-NFNC
330 340 350
10719930 -PFFGEYIQDHLNITASVIGQNGSQIQQLSELDQLVQCARAPVDFDTQIPINC
370 380 390 400 410 420
cry2ab2_820. STEFLPPLITPPVRSLDSSDREGVATVNW-STESF-ETTLGRSAFTAGSNVF
370 380 390 400 410 420
10719930 -TLRNPLEVPIYATRFNELTSL-GTAGVGGEVRSDVPLNSVCGL GTVSSGQT-PL
430 440 450 460 470 480
cry2ab2_820. PDYFRNFSG-VPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYM-SVNRKNNTIA
430 440 450 460 470 480
10719930 PDYITNISATVQVNGTNTDIS-PLYFGENRAITSGNV-----NKVIATVYNTKNDDF
490 500 510 520 530
cry2ab2_820. VHNGSMHILAPNDYTGFTISPIHATQVNNOTRTFISEKFGNGQSLRPEQNNIATRYLL
490 500 510 520 530 540
10719930 TNIRGTIVHEAPDTSIGFTISPLHDTVNIINSYLIQENYGNNGSLRV-INRAIIKYRL
540 550 560 570 580 590
cry2ab2_820. RGNGNS-VNLYLRVSSISGNTIRVTINGRVYATVNTVNTDNGVNDGAFSDINIGV
550 560 570 580 590
10719930 SAARSVIYRLVLRVSGTASSIVAIENYPVGSANQINTGDNREGVIDNDSKFIDLIENIP
600 610 620 630 640 650
cry2ab2_820. VASSNSDVPIDINVTLNSGTQFDLMNIMLVPTNISPLY
600 610 620 630
10719930 FVSGTARELQLOVSGATTSSPLDIMNIIILIPINDVPLY
660 670 680 690
cry2ab2_820.pep
NRAA:9622198
popilliaae|g|10719929|sp|P57091|C18BA.PAEPF Parasporeal crystal protein cry18Ba
(Parasporeal delta-endotoxin CryVIIIa) (Crystalline parasporeal protoxin) (76
kDa crystal protein)
SCORES Init1: 693 Initn: 1213 Opt: 965 z-score: 1096.3 E(): 9e-53
>>NRAA:9622198
Initn: 1213 Initl: 693 Opt: 965 z-score: 1096.3 expect(): 9e-53
Smith-Waterman score: 1388; 38.4% identity in 670 aa overlap
(1-637:30-675)
cry2ab2_820. MQAMDSVLNS-GFTTICDAYNVAADPFPS
10 20 30

9622198 MNNGNALSRALTPTTNKVIKSGDLVTNGLPIDNNIICSGFWPI-----NVIRKQPF--
10 20 30 40 50
cry2ab2_820. QHKSLLDTQKEMTKNNHSLYLDPIVGTIVASFLKKVKSLSVKGRIILSELNLIFFSGS
40 50 60 70 80 90
9622198 RKRTTEFIRETWKENSFLTAPIVGVVSTLLEALKKQVQSRLLLMTNLLFPNNS
60 70 80 90 100 110
cry2ab2_820. TNLNQDILRETEKFLNORLMTDLARVNAELTGLQANVEFNQVDNFLNPNNAVPLSI
100 110 120 130 140 150
9622198 TSTMEEILRATEQYVQQLDVTWNVRVSOELEGKNNLRTFNQIDDFLQNRVEISPTAM
120 130 140 150 160 170
cry2ab2_820. TSSVNTMQQLFLNRLPQFOMQGYQLLLPLFAQANLHLSFIRDVILNADENGISAATLR
160 170 180 190 200 210
9622198 IDSINTMQQVFNRLPQFQQLDSDYQLLLPLFAQATLHIFIRDVILNADENGISAATLR
180 190 200 210 220 230
cry2ab2_820. TYRDYLNKTRDYSNYCINTYQAFKGL---NTRLHDMLEFRTVMFNVEYVSWSLFK
220 230 240 250 260
9622198 TCKRYLKQVVAQYSNYALSTVEGAFRPFYPRATLENMLQFKFTMLNVLVDLSWSLLK
240 250 260 270 280 290
cry2ab2_820. YMLYITANLYNTGNNKNGEYISYWPFPFNYSYIOTKSNVLSGVSGYAIRWYLYNT
300 310 320 330 340 350
cry2ab2_820. VGEFTTTHALDARLNNYSGGISGSDIGAS-----PF---NONFNC
330 340 350 360
9622198 -PFGKIQDNLNLIASVQSNVNGPKIGVQLSTTELDKQIKQOARAGWFTGLDLSFNC
360 370 380 390 400 410
cry2ab2_820. STEFLPPLITPPVRSLDSSDREGVATVNW-STESF-ETTLGRSAFTAGSNVF
370 380 390 400 410 420
9622198 -TLRNPLEVPIYATRFNELTSL-GTAGVGGEVRSDVPLNSVCGL GTVSSGQT-PL
420 430 440 450 460
cry2ab2_820. HENGSMHILAPNDYTGFTISPIHATQVNNOTRTFISEKFGNGQSLRPEQNNIATRYLL
430 440 450 460 470 480
9622198 PDYITNISATVQVNGTNTDIS-PLYFGENRAITSGNV-----NKVIATVYNTKNDDF
470 480 490 500 510 520
cry2ab2_820. HENGSMHILAPNDYTGFTISPIHATQVNNOTRTFISEKFGNGQSLRPEQNNIATRYLL
490 500 510 520 530 540
9622198 NQNGTMIHQAPNDGTGFTIVSLHLASFTHPSHAHQENYGNNSLTLTGPIVAFVMS
530 540 550 560 570 580
cry2ab2_820. GNGNS-VNLYLRVSS-IGNSTIRVTINGRVYATVNTVNTDNGVNDGAFSDINIGV
550 560 570 580
9622198 GDGRTIYKLVLRVSGVITRIATAKVRGNSIGYLEY-INTVDNNQGITDNGSKFQDFEFTAT
590 600 610 620 630 640

[illegible]

```

SCORES      Initi: 149      Intn: 251      Opt: 371      z-score: 420.0 E(): 4.2e-15
>>SW:8928042
      Initi: 251      Opt: 371      2-score: 420.0 expect(): 4.2e-15
      Smith-Waterman score: 403;      22.3% identity in 619 aa overlap
      (58-629;35-633)

      30      40      50      60      70      80
cry2ab2_820.  FSPQHSKSLDTQVKEWTWKNNKNSLYLDPIGVTSVFLKKVQSVLGVKRLSELRLNLPF
8928042      SFNVLANNNMSSFPFLNFKSPSPSIAPALIAVAPATLAKALWAKGFKAKLKEISFF
      10      20      30      40      50      60

      90      100      110      120      130      140
cry2ab2_820.  SGSTNLMMQDILRETEKFLNQRKLNFTDLKAVNAELTGLQANVEFNQVDVFNLPNRRNVP
8928042      GNETATMEKVRULEVOTILNQTDRAVTLKAEYEGFHLGKGVFTDYVQ-----STTPP
      70      80      90      100      110      120

      150      160      170      180      190      200
cry2ab2_820.  LSITSSVNTMQQLFNLPQFMQGYQLLLFLPFAQAANHLHFSFRIDVLNADWEGISAA
8928042      ATAKTHPLNNMNLILQRLPQEIAGYEGVISLFTQMCTHLGLKDLGLADWGFPTPE
      120      130      140      150      160      170

```


©01 PROTECTIVE INFORMATION

```
cry2ab2_820. TLRTYRDYLNKTRDYNSVCINTYOSAF-KGLNTRLDHMLEFRTYMFELNVFVYSWLSF
8928042. DKSLLICQFNRYVNEWTMMGLYSIEFGRLAKNLNLFNMCSLYVFPFSEAWLL

cry2ab2_820. KYQSLVSSCANLYASGSGPOQTQSFTSDWP-FLYSLFQVNSYVLNG--FSGARLSNT
8928042. RVEGKLENTLSLW-NFVG-EDIGGILHNDMGKALYKLLMGATNORLANVRFNYSYFSDT

cry2ab2_820. FNVIVLPGSTTTTHALLAARVNSYSGISGDCG-ASPPNQNFCSELPPLLPFVRSW
8928042. -OGTTHRENILGAHTPYNGEQPTGNGNGLGRFAPYVRLLEITKVEOEI-----TY

cry2ab2_820. LSGSDREGVATVNMQTESFETTLGRSGAF--TARGNSNYFPD--YFIRNI-----
8928042. NNKGDSNSIVPA-NTRNEILLATVITADPFKATADINNKWTSGLYGVGKIKIDRVI

cry2ab2_820. --SGVPLVVRNEDLRRLPHNEIRNI-ASPSGTP-GGARAYMVSVNHRKNNHAVHENG
8928042. LNSRVPGGIPSNRLEYDGY--IRAVSACPRNVLNSYHNHLYLTNLEADYDAPTON-I

cry2ab2_820. MTHLAPNDYTGFTISPIHATOVNNOTRTFISEKFGNOG-----SIRFEON
8928042. IVGFSPNNTKSFYARNSHYLSATNDAYVIPALQFATVSDRSFLEDPDQATGSGIKETET

cry2ab2_820. --NTTARYTLRGNSYNLYLRVSSI--GNSTIRVTINGRYVYATNVNT-----TNN
8928042. VLNGEAKYSIRLN-TGFNTATRYRLVIRFKATARLAAGIRVRSQNSGNNRLLGGIPVEGN

cry2ab2_820. DG-VNDNGARFSDINIGNVASSNSDVPDLNVLNLSGTQFDLMNMLVPTNISPLY
8928042. SGWVDYITDSTFNDLGIITASTINAFSSIDSD-GVNASQOWYLSKLILVKDFVNNSGRFN

cry2ab2_820. QVPLAPYVIARCPNFTFVNSNTSSGYEQGYNDYNQNTSSGYEQGYNDYNQNTSSGYEQ
8928042. 650 660 670 680 690 700

cry2ab2_820.pep
NRAA:8928042
```

8928042 source="GENBANK, PROT" Pesticidal crystal protein cry1Bb (Insecticidal delta-endotoxin CryXIb(b)) (Crystalline entomocidal protoxin) (84 kDa crystal protein)gi|4033727|gs|AAC97162.1| d-endotoxin [Bacillus thuringiensis]

SCORES Init1: 149 Initn: 251 Opt: 371 Z-score: 420.0 E(): 4.2e-15
>NRAA:8928042
Initn: 251 Initl: 149 Opt: 371 Z-score: 420.0 expect(): 4.2e-15
Smith-Waterman score: 403; 22.3% identity in 619 aa overlap

(58-629;35-633)

```
cry2ab2_820. FSPQHSKSLDVTQKEWTEWKKNHSLYLDPIVGTVASFLKKVGLSKRLSELNLTTP
8928042. SFNVLANNNSSFPFLPNSKIEPSTAPALIAPIAKIATATAKALKQGFAGKKEIIPP

cry2ab2_820. SGSTNLMDQILRETEKFNLRLPQOMOGYQLLLPLFAQAANLHLSFIRVILNADWGISAA
8928042. ATAKTHFLMNSLLIQLRLOPEIAGYEGVISLSLFTQMCTHLGLKDLGILAGSDMGFTPE

cry2ab2_820. TLRTYRDYLNKTRDYNSVCINTYOSAF-KGLNTRLDHMLEFRTYMFELNVFVYSWLSF
8928042. DKSLLICQFNRYVNEWTMMGLYSIEFGRLAKNLNLFNMCSLYVFPFSEAWLL

cry2ab2_820. KYQSLVSSCANLYASGSGPOQTQSFTSDWP-FLYSLFQVNSYVLNG--FSGARLSNT
8928042. RVEGKLENTLSLW-NFVG-EDIGGILHNDMGKALYKLLMGATNORLANVRFNYSYFSDT

cry2ab2_820. FNVIVLPGSTTTTHALLAARVNSYSGISGDCG-ASPPNQNFCSELPPLLPFVRSW
8928042. LNSRVPGGIPSNRLEYDGY--IRAVSACPRNVLNSYHNHLYLTNLEADYDAPTON-I

cry2ab2_820. MTHLAPNDYTGFTISPIHATOVNNOTRTFISEKFGNOG-----SIRFEON
8928042. IVGFSPNNTKSFYARNSHYLSATNDAYVIPALQFATVSDRSFLEDPDQATGSGIKETET

cry2ab2_820. --NTTARYTLRGNSYNLYLRVSSI--GNSTIRVTINGRYVYATNVNT-----TNN
8928042. VLNGEAKYSIRLN-TGFNTATRYRLVIRFKATARLAAGIRVRSQNSGNNRLLGGIPVEGN

cry2ab2_820. DG-VNDNGARFSDINIGNVASSNSDVPDLNVLNLSGTQFDLMNMLVPTNISPLY
8928042. SGWVDYITDSTFNDLGIITASTINAFSSIDSD-GVNASQOWYLSKLILVKDFVNNSGRFN

cry2ab2_820. QVPLAPYVIARCPNFTFVNSNTSSGYEQGYNDYNQNTSSGYEQGYNDYNQNTSSGYEQ
8928042. 650 660 670 680 690 700

cry2ab2_820.pep
NRAA:8928042
```


[illegible]

©01 Popr. kolekt. 1980

```
crv2ab2_820 270 280 290 300 310 320
KYQSLVSSGALNYASGPGTQSTSDWP-FLYSILFQVNGVNYVLNG--FSGARLSNT
8928023 240 250 260 270 280 290
EYESTKLENTLQWVNFVG-ESSNN-SPNDKCALYKLLGAGNQRNLNNVFNYSYFSDT

crv2ab2_820 330 340 350 360 370 380
PFTNVGLPGSTTTHALLAAVNTSGIS-SGDIGASFPNQ-NFNCSTFPLPLLPVFRSW
8928023 300 310 320 330 340 350
QATI---HRENIHQMLFV--YNGEPLTCHIGNGRSGSG-SPPCSNELEITKIKQEITY

crv2ab2_820 390 400 410 420 430
LDGSGDREGVAVTNWQTESFETLSRCAF--PARGVNYF-PD-VFIRMI-----
8928023 360 370 380 390 400 410
NDKGGNFSSIVPAAT-RNEILTATVPTSDPFFKADINMKVSPGLYSGMNTKFDPTVT

crv2ab2_820 440 450 460 470 480 490
--SGVPLVFNEDLRPLHYNEIRNI-ASPSCTPGCARAYNVSNKNKNKAYHEVQSM
8928023 410 420 430 440 450 460
LKSRVPSIIPSNILKYDDY--IRAVSACPKGVSUAYNHDFLLITTKKNDAPTSNTV

crv2ab2_820 500 510 520 530 540 550
IHLAPNDYTGTFTISPHATOVNNTRTFTSEKFGNQGSLRFEON----NTTARYSLRG
8928023 470 480 490 500 510 520
VGFSPDNTKSFYRSNSHYLSLTDDAVVIALOFSTVSDRSFLEDTPDQATGSIKFTDTV

crv2ab2_820 550 560 570 580 590
NGNSYNLYLRVSSIGNSTIR---VTINGRVYVATNVTNTTNDGVNDN-GARFSDINIG
8928023 530 540 550 560 570 580
LGNEAKYSIRLNTGNTATRYLLRIIFKAPARLAAGIRVRSOISGNNKLLGGIPVEGNSG

crv2ab2_820 600 610 620 630 640 650
NVVASSNSDVPDLNDINTVNSGTQFDLMNLVFTNISPLY
8928023 570 600 610 620 630 640
WIDYITDSFTFDLGIITTSSTNAPFSDSDGVNASQWYLSKLILVKESSTFTQIPLKPY

crv2ab2_820.pgp
NRAA:21685428

21685428 source="GENBANK_PROT" pesticidal crystal protein crv11AA (Bacillus
thuringiensis serovar israelensis)gi|117327|sp|T21256|C11AA BACTI Pesticidal
crystal protein crv11AA (Insecticidal delta-endotoxin CrvXIA(a)) (Crystalline
entomocidal protoxin) (72 kDa crystal protein)gi|142763|gb|AAA22352.1|
mosquito-toxic crystal protein

SCORES Initl: 147 Inltn: 315 Opt: 361 Z-score: 409.7 E(): 1.6e-14
>>NRAA:21685428
initl: 315 inltn: 147 opt: 361 Z-score: 409.7 expect(): 1.6e-14
Smith-Waterman score: 422; 25.2% identity in 636 aa overlap
(58-636;35-641)

crv2ab2_820 30 40 50 60 70 80
FSPQHKSLDVTQKQETWKKNNHSLYLDPIVGTVASFLKKVKVSLGVKRIELSELNLIFF
21685428 SLDTLSIVNETDPLPYNNYVTEFTIAPALAVAPIQAYLATIAGKAAKAAFAFSKVLISLIFF
```

[illegible]

[illegible]

8928011
SDFSLGKSTVLLSYASRANLHLLLRDAVYKELGYPSTDFVEFYNEQYKTEKYSN
180 190 200 210 220 230

cry2ab2_820.
YSNNQSAFKLWYH----DMLEFRTVMELNVPEVSVWSLAFKQSLVSSGANLYA
240 250 260 270 280
8928011
YCVNTYAS--GLESKKQIGWDFNRYRREMLSLDLVALFELYD--TGLYPSKDGKIHV
240 250 260 270 280 290

cry2ab2_820.
SGSGPQQTOSFTSDQW---PEFLYSLFQVNSNV---LNGFSGARL--SNTFPNIVG
290 300 310 320
8928011
KAEITREIYSDVINOHVGLMWVI--SFEHAEISLYTRPHAFTHWKGFRFVINSMTF
300 310 320 330 340 350

cry2ab2_820.
LPGSTTHALLAR--VNYSGGSSGDI---GASPFQVNSNV---LNGFSGARL--SNTFPNIVG
330 340 350 360 370 380
8928011
LSGGENRYFLTHGEGTIYNGPFGQDTGYGTSYID--SNNSSIYN--SNTKNEYIYPTW
360 370 380 390 400 410

cry2ab2_820.
DSGSDREGVATNMOTESFETTLGL--RSGAFTAGNSNYPDFYFIRMISGFLVVRNED
390 400 410 420 430 440
8928011
DPVNTIKNFSIID--NSNSSESIYGAERMKPIVTRDFN-----FLNLRAGNRTTN--D
420 430 440 450 460 470

cry2ab2_820.
LRRLPHYNEIRNIASPSGTPGARAYMVSVHNRKNHIAVHENGSMIHLAPNDYTGFTI-
450 460 470 480 490 500
8928011
YNHILSYMLINGETFGOKRGYGFATHTSSVDVNTI--VPDKISVQRAVKTMK--SNTFI
470 480 490 500 510 520

cry2ab2_820.
-SPIHATQVNNQTRTFISEKFGNQGDSLRPEQ--NNTARTYLRNGN--SYNLYRVSISG
510 520 530 540 550
8928011
KPGGHT---GGDLLKLEVERFL---SLRIKLIASMTFRIRIRYASNISGQMINIGYON
530 540 550 560 570

cry2ab2_820.
NSTIRVT--INGRYVYATN-----VNTT---TNNDGVNDGARFSDINIGNVVASNSDV
560 570 580 590 600
8928011
PTYENIIPTSRDYTELKFEQFQVADTSYIYSGSPSSISNTLMDNFSNGPVLIDKIEFI
580 590 600 610 620 630

cry2ab2_820.
PLDINVLINGTGTFDMLNMLVPTNISPLY
610 620 630
8928011
PLGI--TLNQAQGYDITYDONANGMYHQNSGNYNQENYTYQSVNN
640 650 660 670 680

cry2ab2_820.pap
SW:8928011

8928011 description="PESTICIDIAL CRYSTAL PROTEIN CRY19BA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIXB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (78 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar higo"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 194 Initn: 240 Opt: 357 z-score: 404.7 E(): 3e-14
>>SW:8928011 (682 aa)

initn: 240 initl: 194 opt: 357 z-score: 404.7 expect(): 3e-14
Smith-Waterman score: 364; 23.7% identity in 667 aa overlap
(8-625:12-651)

cry2ab2_820.
MQAMDSVLSNGRTTICDAYVAADPFSP--QHKSLDTVQKEWTKNNHLSYL
10 20 30 40 50
8928011
MNSYQNKNEVEILLDAKENT--CHMSNCYPKYELANDQMYLRNTHYKDWINCEASVASS
10 20 30 40 50

cry2ab2_820.
DP-----IVGTVASFLKVLKGVKRLSELRLNLPFS--GSTNIMQDILRETEKELNQ
60 70 80 90 100
8928011
GPSQLFKVGGSVIAKILGMPF--VGP--LLSMWVSLFWPTTEKNTVWEDMIKYVANLLKQ
60 70 80 90 100 110

cry2ab2_820.
RLNTOTLARVNAELTGLQANVEFNRQVDNF--LNPENAVPLSITSSVNTWQOLFANRLP
110 120 130 140 150 160
8928011
ELTNDILNRATSNLSGSLNLSIYNARALAAWKQNNFASGELIRSYINDLHLIFTRDIQ
120 130 140 150 160 170

cry2ab2_820.
Q-FOMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGISAATLRTYRDYKNTDRYSN
170 180 190 200 210 220
8928011
SDFSLGKSTVLLSYASRANLHLLLRDAVYKELGYPSTDFVEFYNEQYKTEKYSN
180 190 200 210 220 230

cry2ab2_820.
YSNTYQSAFKLWYH----DMLEFRTVMELNVPEVSVWSLAFKQSLVSSGANLYA
230 240 250 260 270 280
8928011
YCVNTYAS--GLESKKQIGWDFNRYRREMLSLDLVALFELYD--TGLYPSKDGKIHV
240 250 260 270 280 290

cry2ab2_820.
SGSGPQQTOSFTSDQW---PEFLYSLFQVNSNV---LNGFSGARL--SNTFPNIVG
290 300 310 320
8928011
KAEITREIYSDVINOHVGLMWVI--SFEHAEISLYTRPHAFTHWKGFRFVINSMTF
300 310 320 330 340 350

cry2ab2_820.
LPGSTTHALLAR--VNYSGGSSGDI---GASPFQVNSNV---LNGFSGARL--SNTFPNIVG
330 340 350 360 370 380
8928011
LSGGENRYFLTHGEGTIYNGPFGQDTGYGTSYID--SNNSSIYN--SNTKNEYIYPTW
360 370 380 390 400 410

cry2ab2_820.
DSGSDREGVATNMOTESFETTLGL--RSGAFTAGNSNYPDFYFIRMISGFLVVRNED
390 400 410 420 430 440
8928011
DPVNTIKNFSIID--NSNSSESIYGAERMKPIVTRDFN-----FLNLRAGNRTTN--D
420 430 440 450 460 470

cry2ab2_820.
LRRLPHYNEIRNIASPSGTPGARAYMVSVHNRKNHIAVHENGSMIHLAPNDYTGFTI-
450 460 470 480 490 500
8928011
YNHILSYMLINGETFGOKRGYGFATHTSSVDVNTI--VPDKISVQRAVKTMK--SNTFI
470 480 490 500 510 520

cry2ab2_820.
-SPIHATQVNNQTRTFISEKFGNQGDSLRPEQ--NNTARTYLRNGN--SYNLYRVSISG
510 520 530 540 550
8928011
KPGGHT---GGDLLKLEVERFL---SLRIKLIASMTFRIRIRYASNISGQMINIGYON
530 540 550 560 570

[illegible]

```

cry2ab2_820. LPFLLTFVRSWLDGSGREGVATVINMQTESFETLL-----GLRGAFTARG--NSNYFFP
      ||| :||:::||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:|
547556 --GLITT-TRATINPGVD--GTNRIESTAVD-FRLALIGIVGNRASFPVGCLFNQITSP
      400          410          420          430          440          450
cry2ab2_820. -----DYFRNRISGVPLVVNRDLDRPLPHYNEIRNIASFGTGGARAYMVSVNRRKN
      430          440          450          460          470          480
547556 ANGGRDLYDTNDDELPPDESTGSSTRKLSHVTFSSFOTNQAGSIANAGSVPYIYNVRD-
      450          460          470          480          490          500
cry2ab2_820. IHAVHENGSMIHLPANDYTGFTSPIAHQTVMNQRTRFISEKGNGDSLRPEQNNTIAR
      480          490          500          510          520          530
547556 ---VOLNNTI---TPNRIQTQLPL--VKASAPVSGTTVLKGPGETG-GGLIRTINGTGFG-
      510          520          530          540          550          560
cry2ab2_820. YILRGNGS-----YNLRLRVSSIGNSTIRVTINGRVVIATNVNTINNVDNGDGARFS
      540          550          560          570          580          590
547556 -TLAVTVSNPLTOQRSLVARVFASFNFSRILVRGVSICGDVLRGSTMNRGQELYESFFT
      560          570          580          590          600          610
cry2ab2_820. DINIGNVVAASSSDVPLDNVLTNSGTQFDLMNMILVPTNISPLY
      600          610          620          630
547556 REFTTIGPNPFPTTQAQBILTVNAAEGYSTGEYYIDRIEIVPVNPAREAEEDLEAKK
      620          630          640          650          660          670
cry2ab2_820.pcp
SW:8469160
8469160 description="PESTICIDIAL CRYSTALL PROTEIN CRYP9A (INSECTICIDAL DELTA-ENDOTOXIN CRYIXC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (I30 KDA CRYSTALL PROTEIN)." library=NA species=Bacillus thuringiensis serovar tolworthii source=swissprot_prot version=NA type=PRT
SCORES   Initl: 148    Inltnt: 178    Opt: 344    Z-score: 386.1 E(): 3.3e-13
>>SW:8469160
Initl: 178 Initi: 148 Opt: 344 Z-score: 386.1 expect(): 3.3e-13
Smith-Waterman score: 344; 25.1% identity in 558 aa overlap
(60-580.75-600)
cry2ab2_820. FOHKSLTDVOKEWTEWKNNHSYLDPDIVGTVASFLKKYGSLVGKRILSE---LRNLIF
      30           40           50           60           70           80
8469160 YLQMDEDITYDSINYPSLSTSGRDVAQTALTAVGRILLGALGVFPQSIVSFVQLLNLTW
      50           60           70           80           90         100
cry2ab2_820. PMSGTNMLODIRRETKFLNORINTDTLARVNAELTGLQAVEEFNOVDNFLAPRNNAV
      90          100          110          120          130          140
8469160 PVNTLATWEAFPROVEELLVMOOITEFARNQALARLOGLGDSFVIVORSIQNWLAADRMNR
      110          120          130          140          150          160
cry2ab2_820. PLST-SSENTMWOOLFNLRLPOFMOGYOQLLLLPLFAQANHLISRIRDVINADEGIS
      150          160          170          180          190          200
8469160 NLSVVRAQFTALDDLFVNAIPFAVNGQQOVPLL SVYACVANHLHLLKDKASLFGEGWGFI
      170          180          190          200          210          220

```


Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 201 of 361

©01
cry2ab2_820. AATLRYDYKNTIRDSNYC---INTYQAFKGLNT---RLHDMLEPRTYMLNVEE
8469160 AGEISTYVAGLELAKYNYCNWYNTGLDRGNTESMLRVH---QFRREMTLAVLD
cry2ab2_820. YVSTWISRYKLYVSSGAYTASGGPQNTQSTQ---DWPFLLYSLVQVNSNVLVNG
8469160 VVA---LFYYDYV---RLVYGSNOUTREVDPVFNPNANVGLCKRWGNTPNYNT
cry2ab2_820. FSGARLNTF---PMIVG-LFGSTTHALLAAQSCGISGDSGASRENON-FNCSTF
8469160 FS---ELENAFIRPPHLPDELANSLTSSNFPSSNFMVWVSHLRSYNDSDVOEDSY
cry2ab2_820. LPPLLTFFVRSMLDSSDREGVATVNMOTESPETTLA---GURSGANARGNSNYFP
8469160 --GLITT-TRATINPGVD--GTNRIESTAVID-FRSALIGIVGVARAFVPGGAFNOSP
cry2ab2_820. ---DYFIRNISGVPLVVRNEDLRPLHYNEIRNIASPSGTGGARAYVWSVNRKON
8469160 ANGCRDLXTDNDLPEPDESGTSHLSHTVTFSPQNTQAGSIANAGSVTYVWTRRD
cry2ab2_820. IHAHENGSMIHLAPNDYGTFTISPIHATQVNNOTRTFSEKFGNQDSLRFFQNNNTAR
8469160 ---VDLNNITI---TPNRITQLEPL--VKASAPVSGTIVLKGFCFTG-GGILRRITNGTFFG-
cry2ab2_820. YTLRGNGS-----YNLYLRVSSIGNSTIRVTINGRVYTAIVNNTTNDNDVNDGARFS
8469160 -TLRVTVNSPLTQOYRLRVRFVASTGNFSIRVLRGGVSGIDVRLAGSTWNRGQELTYESFFT
cry2ab2_820. DINIGNVASSNSDVPDLINVLNSGTQFDLMIMLVPTNISPLY
8469160 REFTTGGFPNPPFTTQAOEILTVAAGVSTGGEYVIDRIEIVPVNPARAEEDLEAAKK
cry2ab2_820.pap
NRAA:32260894
32260894 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis serovar
kurstaki]
SCORES Initl: 205 Initn: 267 Opt: 336 z-score: 380.5 E(): 6.7e-13
>NRAA:32260894
Initn: 267 Initl: 205 Opt: 336 z-score: 380.5 expect(): 6.7e-13
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820. PFSQHKSLDTQKWEWKNNHSLYLDIPVIGTVASFLLKKVSLGVCKILSELNLNLF

32260894 EDCMKSEYENVEPFVSASTIQTGIGIAGKILGTGVFPAGQVASYLS-FILGEL---W
cry2ab2_820. PGGSNLMODILRETEKFNORLNTDTLARVNAELTGLQANVEEFNRQVDNPLNPNNAV
32260894 PKGK-NQWEIFMEIVEEINOKISYARKKALTDLKGGLDALAVHDSLESWGVGNRRNIR
cry2ab2_820. PLSIT-SSVNTMOOLFNLRLPQFOMQGYQLLLPLFAQANLHLFSIRDVINADENGIS
32260894 ARSVKSOYIALELMFVOKLPSPFAVSGEEVLLPIYAQANLHLLLLRDASIFGKEWGLS
cry2ab2_820. AATLRYDYKNTIRDSNYCINTYQAFKGL-NTLRHDMLE---EFRIYMLNVEFYS
32260894 SSEITFYNRQVERAGSDYCHCVKYSTGLANLREGTNAESWVRYNQFRDMLVLDLVA
cry2ab2_820. IWSLEKYQSLVSSGANL---YASGSGPQOTO-SFTSQDWPELYSLFOVNSNYLVNGFS
32260894 LFPSYDTOMYPIKITAQLIREVYTAIGTVHPHPSFTITW---YN---NNAPSFAIE
cry2ab2_820. GASLNTFFNIVGLPGSTTHALLA---ARVNYSGG--ISSGDIGAS-PFNQNFNCST
32260894 AAVNEN-PHLLDELEVITYLSLRWSNTQVMWGGHKLPLERTIGGTLNISTQSGTINT
cry2ab2_820. FUPLLPFFVSWNSDREGVATVNMOTESF-ETTLGRSGAFTARGNSNFPDYFI
32260894 SANPVTNFTSRDYRTESAGGLFLTPQVNGVPRVDFHWKEVTHPTIASDNFYPGY--
cry2ab2_820. RNISGVPLVVRNEDLRPLHYNEIRNIASPSGTGGARAYVWSVNRKNNIHA-VHENG
32260894 ---AGIGTQLOQDSNEDPEATGQFNSYSYSHRL-SHIGLISASHVXKALYVSWTHRSAD
cry2ab2_820. MIH-LAPNDYGTFTISPIHATQVNNOTRTFSEKFGNQDSLRFFQNNNTAR
32260894 RNTTIEPNSITQIPL--VKAFNLSSGAAWIRGSGFTG-GGILR--RTNTISFGAIRVININ
cry2ab2_820. S-----YNLYLRVSSIGNSTIRVTINGRVYTAIVNNTTNDNDVNDGARFS
32260894 PPAQRYRVRIRYASITDLOFHTSINGKAINOGNSATMNR-CEGLDYKTFR--GGLT
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLMIMLVPTNISPLY
32260894 PFSFLDVOSTTIGTANFSSGNEVIDRIEIVPVNPARAEEDLEAAKK
cry2ab2_820. PFSFLDVOSTTIGTANFSSGNEVIDRIEIVPVNPARAEEDLEAAKK

32250894	RGUKTDVKDYHDQVSNLVESLDEFDYLDKRELFKVKVQKAIHIERNM	670	680	690	700	710
cry2ab2_820.pep						
SW:8469140						
8469140	description="PESTICIDIAL CRYSTAL PROTEIN CRYIIB (INSECTICIDAL DELTA-ENDOTOXIN CRVII(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis serovar entomocidus" source="swissprot_prot" version=NA type=PRT					
SCORES	Init1: 225	Inith: 287	Opt: 336	z-score: 380.5	E(): 6.7e-13	
>>SW:8469140					(719 aa)	
initn: 287	init1: 225	opt: 336	z-score: 380.5	expect(): 6.7e-13		
Smith-Waterman score: 333;				21.9% identity in 607 aa overlap		
(57-634:70-646)						
cry2ab2_820.	30	40	50	60	70	80
8469140	PFSGHKSJLDTVQKEMTKNNHSLYLDPIVGTVASFLKKVGLGKRLISELRNLIF					
	EDYLRMSGHESIDPFVSASTIQTGIGAKILGTLPVPFAGQIASLYS-FILGEL----	W				
	40	50	60	70	80	90
cry2ab2_820.	90	100	110	120	130	140
8469140	PGSNLMQDLIRETEKFLNQLRNTDITLARVNAELTGLQANVEEFNRQVDFLNPNNNAV					
	PKGSKQ-WEIFMEHVEEIIKILYARNAKSLDRGLGDALAVYHESLESWEVNRNTR					
	100	110	120	130	140	150
cry2ab2_820.	150	160	170	180	190	200
8469140	PLSIT-SSVNTMOQLFLNRLPOFOMOGYQVOLLPLPFAQANHLHLSFIRDVLNADWGIS					
	ARSVVKQVIALELMFVKQLPFAVSGEVFLPIYAQAANHLHLLDASIFKKEGLS					
	160	170	180	190	200	210
cry2ab2_820.	210	220	230	240	250	260
8469140	AATLTYRDYLNKTYRDYSDNYCI---NTYQSAFKGLNTR-LHDMLEFRTYVFLNVEFYS					
	ASEISTFYNRQVERTDYSDHCHIKWNTGLNLRGTNAKSWRYNQFRKDTLWLDLVA					
	220	230	240	250	260	270
cry2ab2_820.	270	280	290	300	310	
8469140	IWSLFKQSVLLVSSGANL----YASGSP-QCTQSTSDWPFLLYSFPQNSNYVLNFGS					
	LPFSYDYLVPKITSQLTREYVDYDAIGTVPNQAFSTW---YN---NNAPSFSAIE					
	280	300	310	320		
cry2ab2_820.	320	330	340	350	360	
8469140	GARLSTFPNIVLPGSTTHALLA---ARNYSSG--ISSGDIG-APFPNQFNCT					
	AAVIRS--PHLLDFLEKVIYLSLRNSNTQYNMGGHRESRPIGGLANTSTQGSTNT					
	330	340	350	360	370	380
cry2ab2_820.	370	380	390	400	410	420
8469140	FLPPLPFPVRSWLDGSDREGVATVNTWQTESF-ETTLGRSGAFTARNVYFDFYI					
	SINPVTLQFTSRDYTESLAGLNLFLTPQVNGVPRVDFHWKFTPLPIASDNFYLYG--					
	390	400	410	420	430	440
cry2ab2_820.	430	440	450	460	470	480
8469140	RNIGSVFLVNRNEDLRPLHNYNEIRNTIASPSGTPGGRARYMVSVHNRKNIHA--VHENG					
	480	490	500	510	520	530
cry2ab2_820.	530	540	550	560	570	580
8469140	PPAQRYRRIYASTIDLOFHISINGKAINQGNFSATMNR-GEGLDYKTFR--TIGFTT					
	580	590	600	610	620	630
cry2ab2_820.	630	640	650	660	670	680
8469140	RGUKTDVKDYHDQVSNLVESLDEFDYLDKRELFKVKVQKAIHIERNM					
	680	690	700	710		
cry2ab2_820.pep						
SW:8469149						
8469149	description="PESTICIDIAL CRYSTAL PROTEIN CRYIIA (INSECTICIDAL DELTA-ENDOTOXIN CRVII(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis serovar kurstaki" source="swissprot_prot" version=NA type=PRT					
SCORES	Init1: 205	Inith: 267	Opt: 336	z-score: 380.5	E(): 6.7e-13	
>>SW:8469149					(719 aa)	
initn: 267	init1: 205	opt: 336	z-score: 380.5	expect(): 6.7e-13		
Smith-Waterman score: 365;				21.7% identity in 607 aa overlap		
(57-634:70-646)						
cry2ab2_820.	30	40	50	60	70	80
8469149	EDCLKMSEYENVEPFVSASTIQTGIGAKILGTLPVPFAGQVASLYS-FILGEL----					
	40	50	60	70	80	90
cry2ab2_820.	90	100	110	120	130	140
8469149	PGSNLMQDLIRETEKFLNQLRNTDITLARVNAELTGLQANVEEFNRQVDFLNPNNNAV					
	PKGK-NOEIFMEHVEEIIKILYARNAKSLDRGLGDALAVYHDSLESWGVRNTR					
	100	110	120	130	140	150
cry2ab2_820.	150	160	1			

[illegible]

```

SCORES   Init1: 205      Initn: 267      Opt: 336      Z-score: 380.5 E(): 6.7e-13
>>NRAA:32709126
initn: 267      init1: 205      opt: 336      Z-score: 380.5      expect(): 6.7e-13
Smith-Waterman score: 365;      21.% identity in 607 aa overlap
(57-634;70-646)

```

cry2ab2_820. PFSQHKSLDIVQKEWTKNNHSLYLDPIVGTVASFLKKVGS�VGRKILSELRLNLF


```
670      680      690      700      710

cry2ab2_820.pep
NRAA:1621216

1621216 source="GENBANK_PROT" Bt toxin [Bacillus thuringiensis]

SCORES   Init1: 205   Initn: 267   Opt: 336   z-score: 380.5 E(): 6.7e-13
>>NRAA:1621216
Initn: 267 Init1: 205 opt: 336 z-score: 380.5 expect(): 6.7e-13
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820. PFSQHKSLDTVQKEWTEMKNNHSLYLDPIVGTVASFLKKVGLGKRLSELNLF
1621216 EDCWKSEYENVEPFVSASTIQTGIGIAGKILGTLGVPPAGQVASIYS-FILGEL---W
30 40 50 60 70 80
1621216 90 100 110 120 130 140
cry2ab2_820. PGSTNLMQDLIRETEKFLNQRLNTDTLARVNAELTGLQANVEEFNRQVDFLNPNNAV
1621216 PKGK-NQWEIFMEHVEEIIQKISTYARKALTDLKGGLDALAVHDSLESWSGVRNNRTR
100 110 120 130 140 150
cry2ab2_820. AATLRTYRDYLNKYNTRYNYCINTYQSAFKGL-NTRLHDML---EFTYMFNVFVYS
1621216 SSEISTFYNRQVERAGDYSDDHCVKWYSTGLNLRGTNAESWVRYNQFRDWTLMVLVLA
210 220 230 240 250 260 270
cry2ab2_820. IWSLFKYQSLVSSGANL---YASGSGPQQTQ-SFTSQDWPFYLSLFQVNSNYLVNGFS
1621216 LFPSYDTQMPYIKTQALTRVYTDAGTVHPHPSFTTITW---YN---NNAPSFSAIE
280 290 300 310 320
cry2ab2_820. GARLNTFPNIVGLPGSTTTHALLA---ARVNSYGG---ISSGDIGAS-PFNQNFNCST
1621216 AAVRN---PHLLDFLEQVITYLSLRSWNTQYMMWGGHKLPEFTIGTLNISTQGSINT
330 340 350 360 370 380
cry2ab2_820. FLPLPLTFVRSWLDGSGREGVATVNWQTESF-ETTLGLRSGAFTARGNSYFPDYFI
1621216 SINPVTLPFTSRDVRTESLAGNLFLTPQVNGVPRVDPHWKFVTHPIASDNFYPGY--
390 400 410 420 430 440
cry2ab2_820. RNISGVPLVNRDLRPLHYNEIRNIASPSGTFGGARAYMVSVNRKNNIHA-VHENG
1621216 ---AGIGTQLQDSENELPPEATQPNYESYSHRL--SHIGLISASHVKALVYSWTHRSAD
450 460 470 480 490
490 500 510 520 530 540

cry2ab2_820. MIH-LAPNDYTGTTISPIHATQVNNOTRIFISEKFGNOGDSLRFQONNTTARYTLRGNGN
1621216 RTNTEFNSITQIPL--VKAFLUSSGAARVGRPGFTG-GDILR--RINTGTGDIRVNN
500 510 520 530 540 550
cry2ab2_820. S-----YNLYLRVSSIGNSTIRVINGRVYVATNNTTINNDGVNDNGARFSDINGNV
1621216 PPAQAQYRVIRYASVTTLQPHSINGKALNQGNFSATMNR-GEGLDYKTFR--TVGFTT
560 570 580 590 600
cry2ab2_820. ASSNSDVPLDINV---TLNSGTQFDLMNMLVPTNISPLY
1621216 PFSFLDVQSTFTTIGAMNFSNGVEYIDRIEFVFEVVEYAEYDFEKAQEKVTALETSTNP
610 620 630 640 650 660
1621216 RGLKTDVKDYHIDQVSNLVESLSDSEFYLDDEKRELFEIVKYANELHIERNN
670 680 690 700 710

cry2ab2_820.pep
NRAA:8469140

8469140 source="GENBANK_PROT" Pesticidal crystal protein cryIIb (Insecticidal
delta-endotoxin CryII(b)) (Crystalline entomocidal protoxin) (81 kDa crystal
protein)gi|467235|gb|AAA82114.1| cryV465 gene product

SCORES   Init1: 225   Initn: 287   Opt: 336   z-score: 380.5 E(): 6.7e-13
>>NRAA:8469140
Initn: 287 Init1: 225 opt: 336 z-score: 380.5 expect(): 6.7e-13
Smith-Waterman score: 353; 21.9% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820. PFSQHKSLDTVQKEWTEMKNNHSLYLDPIVGTVASFLKKVGLGKRLSELNLF
8469140 EDYLRMSEHESIDPFVSASTIQTGIGIAGKILGTLGVPPAGQIASIYS-FILGEL---W
30 40 50 60 70 80
cry2ab2_820. PGSTNLMQDLIRETEKFLNQRLNTDTLARVNAELTGLQANVEEFNRQVDFLNPNNAV
8469140 PKGKSO-WEIFMEHVEEIIQKILTYARNKALSDLRGLDALAVYHESLESWVENRNTNR
90 100 110 120 130 140 150
cry2ab2_820. PLSIT-SSVNTMQQLFLNRLPQOMQGYQLLLPLFAQAANLHLSFTRDVLNADENGIS
8469140 ARSVVKNQVIALELMFVQKLPFAVSGEEVPLPIYAQAANLHLLLRDASIFGKEWGLS
160 170 180 190 200 210
cry2ab2_820. AATLRTYRDYLNKYNTRYDYSNYCI---NTVQSAFKGLNTR-LHDMLEBFTYMFNVFVYS
8469140 ASEISFYNRQVERAGDYSDDHCWKWYSTGLNLRGTNAESWVRYNQFRDWTLMVLVLA
220 230 240 250 260 270
cry2ab2_820. IWSLFKYQSLVSSGANL---YASGSGP-QQTQSTQDWPFYLSLFQVNSNYLVNGFS
8469140 LFPSYDTLPYPIKTKTSOLTREYTDAGTVHPHPSFTTITW---YN---NNAPSFSAIE
280 290 300 310 320
```


Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 205 of 361

©01

cry2ab2_820. GARLNTFNTVGLPGSTTHALLA-----ARVNSGG--ISSGDIG-ASPFNQFNCS
8469140. AAVRS--PHLDPLEQVITYSLLSRWSNTQYMMMGHKLFRITIGGTLNISTQGSTNT
330 340 350 360 370 380
cry2ab2_820. AATLTYDYDKNTIDYNYCINTYQSAFKGL-NTRLHDML---EFRTYMLNVFEYVS
8469140. SINFVLOFTSRDVTSTESLAGNLNLPFGVGVPRVPHKFTFLFIASDNFYLYG--
390 400 410 420 430 440
cry2ab2_820. RNISGVPLVVRNEDLRRLHYNEIRNIASGTPGQQAAMVSVHNRKNNIHA-VHENG
8469140. ---AGVGTOLQDSENELPETTGQPNYESYSHRL--SHIGLISASHVVALVYSWTHRSAD
450 460 470 480 490
cry2ab2_820. MIH-LAPNDYTGFTPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNITARYTLRNGN
8469140. RNTIENSTIOTIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RNTGTGDIRVIN
500 510 520 530 540 550
cry2ab2_820. S-----YNLYRVSSIGNSTIRVTINGRVYATNNTTINNDGNDNGARFSDINIGNV
8469140. PPFQRYVRIRYASTITDLPHTSINGKAINQGNFSATMNR--GBDLYDKTFR--TIGFTT
560 570 580 590 600
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLMNIMVPTNISPL
8469140. PFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTLFTSINP
610 620 630 640 650 660
8469140. RGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM
670 680 690 700 710
cry2ab2_820.pcp
NRAA:55583756
55583756 source="GENBANK_PROT" delta endotoxin [Bacillus thuringiensis]
SCORES Initl: 205 Initn: 267 Opt: 336 z-score: 380.5 E(): 6.7e-13
>NRAA:55583756
initn: 267 initl: 205 opt: 336 z-score: 380.5 expect(): 6.7e-13
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820. PFSQHSKSLDTQKQEWKNNHSLYLDPIVGTVASFLKKVGSIVKXKILSELNLIF
30 40 50 60 70 80
55583756. EDCIKMSEYENVEPVFSASTIQTIGTIGAKILGTLPFGAGQVSLYS-FILGEL----W
40 50 60 70 80 90
cry2ab2_820. PSGSTNLMQDILIRETEKFLNORLNTDTLAFVNAELTGLQANVEFNFQVNDNPNRNV
90 100 110 120 130 140
55583756. PKGR-NOWEIFMEHVEELINOKISTYARNVALDILKGLGDALVYHOSLESWGVNENR
100 110 120 130 140 150

cry2ab2_820. PLSIT-SSVNTMQQLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVILNADWGIS
150 160 170 180 190 200
55583756. ARSVRSQYALELMFVQKLPFAVSGEVEVLLPIVAQANLHLLLRDASIFGKEMGLS
160 170 180 190 200 210
cry2ab2_820. AATLTYDYDKNTIDYNYCINTYQSAFKGL-NTRLHDML---EFRTYMLNVFEYVS
210 220 230 240 250 260
55583756. SSEITFTNROVERAGDYDHCWKYISGLNLRGNTAESVWRYNQFRDMLMVLVLA
220 230 240 250 260 270
cry2ab2_820. IWSLFKYQSLLVSGANL---YASGSGPOOTO-SFTSQDWPFPLYSLFQVNSVYLVNGFS
270 280 290 300 310 320
55583756. LFPSYDTOMYPIKTKTQLTREVTDAIGTVHPHPSFTSTW---YN---NNAPSFAIE
280 290 300 310 320 330
cry2ab2_820. GARLNTFNTVGLPGSTTHALLA-----ARVNSGG--ISSGDIGAS-PFNQFNCS
320 330 340 350 360
55583756. AAVRS--PHLDPLEQVITYSLLSRWSNTQYMMMGHKLFRITIGGTLNISTQGSTNT
330 340 350 360 370 380
cry2ab2_820. FLPPLLTFFVRWLDGSGREGVAIVTNMQTESF-ETTLGASGAGTARGNSNFPDYFI
370 380 390 400 410 420
55583756. GINPVLFTSRDVTSTESLAGNLNLPFGVGVPRVPHKFTFLFIASDNFYLYG--
390 400 410 420 430 440
cry2ab2_820. RNISGVPLVVRNEDLRRLHYNEIRNIASGTPGQQAAMVSVHNRKNNIHA-VHENG
430 440 450 460 470 480
55583756. ---AGVGTOLQDSENELPETTGQPNYESYSHRL--SHIGLISASHVVALVYSWTHRSAD
430 440 450 460 470 480 490
cry2ab2_820. MIH-LAPNDYTGFTPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNITARYTLRNGN
490 500 510 520 530 540
55583756. RNTIENSTIOTIPL--VKAFNLSSGAAVVRGPGFTG-GDILR--RNTGTGDIRVIN
500 510 520 530 540 550
cry2ab2_820. S-----YNLYRVSSIGNSTIRVTINGRVYATNNTTINNDGNDNGARFSDINIGNV
490 500 510 520 530 540
55583756. PPFQRYVRIRYASTITDLPHTSINGKAINQGNFSATMNR--GBDLYDKTFR--TVGFTT
500 510 520 530 540 550
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLMNIMVPTNISPL
550 560 570 580 590 600
55583756. PPFQRYVRIRYASTITDLPHTSINGKAINQGNFSATMNR--GBDLYDKTFR--TVGFTT
560 570 580 590 600 610
cry2ab2_820. ASSNSDVPDLINV---TLNSGTQFDLMNIMVPTNISPL
610 620 630 640 650 660
55583756. PFSFDVQSTFTIGAWNFSSGNEVYIDRIEFVPEVTEYAEYDFEKAQEKVTLFTSINP
610 620 630 640 650 660
55583756. RGLKTDVKYHIDQVSNLVESLSDEFYLDKRELFVYKAKQIHIERNM
670 680 690 700 710
cry2ab2_820.pcp
NRAA:55583756
33326396 source="GENBANK_PROT" CryIIa [Bacillus thuringiensis]

Study No. 06-01-62-01

MSL No. 20307

Page 206 of 361

```

33326396  PPAQRVVRVIRVASTDLDQFHTSINKAINQGNFSATMNR--GEDLDYKIFR--TVGTFT
          560   570   580   590   600
cry2ab2_820. ASSNSDVPFLDINV---TLNSGTQFDLMNIMLVPTNISPLY
          610   620   630
33326396  PFSFLDQVSTFTIGAWNFSSGNEVVIDRIEFVPEVVEAEVDFEKAQEKVLTALFTSTNP
          610   620   630   640   650   660
33326396  RGLKTDVVDKHIDQVSNLVESLSDEFVLDKRELFVUYAKQVHIERNMP
          670   680   690   700   710   720
cry2ab2_820.pep
NRAA:33325407
33325407 source="GENBANK_PROT" CryIIa [Bacillus thuringiensis]

SCORES      Init1: 205      Initn: 267      Opt: 336      z-score: 380.2 E(): 7e-13
>NRAA:33325407
Initn: 267 Init1: 205 Opt: 336 Z-score: 380.2 expect(): 7e-13
Smith-Waterman score: 365; 21.7% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820. PFSFQHSKSLDVQKEWTEWKKNNHSLYLDPIVGTVASFLKKVSGSLVCKILSELNLIFF
          30   40   50   60   70   80
33325407  EDCLKMSYENVEFFVSASTIGTGIGIAGKILGTGLGVPFAQGVASLYS--FILGEL-----W
          40   50   60   70   80   90
33325407  PKGK-NQWEIFMEHVEEIQKISTYARNKALDILAGKLDALAVYHDSLESWGVRNENRTR
          100  110  120  130  140  150
cry2ab2_820. PGGSNLMODILRETEKFLNQLRNTDITLARVNAELGLQANVEEFNQVDNFNINRAV
          90  100  110  120  130  140
33325407  PKGK-NQWEIFMEHVEEIQKISTYARNKALDILAGKLDALAVYHDSLESWGVRNENRTR
          100  110  120  130  140  150
cry2ab2_820. PLSIT-SSVNTMOQLFNRLPQFMQGVQLLLPLPFAQANLHLHSFIRDVLNADGWGIS
          150  160  170  180  190  200
33325407  ARSVVKSQYIALELMFVQKLPSPFASVSGEVEPLPIYQAQANLHLLLRDASIFGKEMGLS
          160  170  180  190  200  210
cry2ab2_820. AAILTRDYKLKNYTRDYSNYCINYSQAFKGL-NTRLHDLM---EERTYFNLVNPVYS
          210  220  230  240  250  260
33325407  SSEISTFYNRQVRAGDYSDDHCWKYVSTGLNLRGLRTNAESWVRYNQFRDMDIMLIDLVA
          220  230  240  250  260  270
cry2ab2_820. IWSLFKYSGLLVSSGANL---YASGSGPQQTQ-SFTSQDMPFYSYLFQVNSYVLNGFS
          270  280  290  300  310
33325407  LPFSYDQMPFKITIAQLTREVIDYDILAGTVRHPSPSTITW---IN---NNAPSFSALE
          280  290  300  310  320
cry2ab2_820. GARLSTFPNPIVGLPGSTTHALIA-----ARVNYSGG--TSSGDIGAS-PFNQFNCGST
          320  330  340  350  360
33325407  AAVVEN--PHLLDFLEQVTVIYSLSRWSKNTQYNNWGGHKLFEFTIGTGLNISTGOSTNT
          330  340  350  360  370  380
cry2ab2_820. FLPPLLTVPKRSMLDGSREGVATVNTWQTESF--ETTLGRSGAFTARNGSYPPDYFI
          370  380  390  400  410  420

```


[illegible]

8928019 cry2ab2_820. pep 610 620 630
 580 590 600 610 620 630
 8928019 QRLSIGIGQINTNL-FILNTEFIPVDETETPLEAAKAVNLFNTNTKGLQPGVTDY 640 650 660 670 680 690
 610 620 630
 8928019 cry2ab2_820. pep 610 620 630
 580 590 600 610 620 630
 8928019 NR2A..8928019
 8928019 source="GENBANK_PROT" Pesticidial crystal protein cry8Ba (Insecticidal
 delta-endotoxin CryVIIIb(a)) (Crystalline entomocidal protoxin) 130 kDa crystal
 protein|gi|436835|gb|AAA21118.1| CryVIII delta-endotoxin

03200112 640 650 660 670 680 690

cry2ab2_820.pep
NR044:8928019

delta-endotoxin CryIIIB(A) | Crystaline entomocidal protoxin | 139 kDa Crystallin
protein|q1|436835|cb|AA021118.1| CryIII delta-endotoxin.

```

SCORES      Init1: 209   Initn: 251   Opt: 338   z-score: 379.2   E1: 0.000000
>>NRAA:8928019
initn: 251   init1: 209   Opt: 338   z-score: 379.2   expect(): 7.9e-13
Smith-Waterman score: 338;   21.3% identity in 596 aa overlap
(57-632;76-658)

```


Study No. 06-01-62-01
MSL No. 20307
Page 208 of 361

[illegible]

©01 PROOF INFORMATION

```
12003323  DRVTNENSIQDRL--VKAFNUSGAAVVRGPGTGG--GDILR--RINTGTGDIRVNI
508 510 520 530 540
cry2ab2_820_  NS---YNLYKVSIGNSIRVIRVYATVNTTNDGVDNGARFSDINIGNV
550 560 570 580 590
12003323  NPPFAQRYRIRYASTTDLQFHTSINGKAINCFNSATMNR--GEDLDYKTFR--TVGFT
560 570 580 590 600
cry2ab2_820_  VASNSDVLDINV---TLNSGTQDLMNIMLVPTNISPLY
600 610 620 630
12003323  TPFSSFDVQSTFTIGAMNFSGSEYVDRIEFVPEVYEAEDYFKAQEKVTLFTSTN
610 620 630 640 650
12003323  PRGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM
670 680 690 700 710
cry2ab2_820.pep
NRAA:1261624
1261624 source="GENBANK_PROT" CGCrYV gene product
SCORES  Initl: 205  Initn: 267  Opt: 334  z-score: 378.2 E(): 9e-13
Initn: 267  Initl: 205  Opt: 334  z-score: 378.2 expect(): 9e-13
Smith-Waterman score: 363; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820_  PFSFQHSKSLDTVQKEWTEMKNNHSLYLDPIVGTASVFLKLVGSLVKRILSELRLNLF
30 40 50 60 70 80
1261624  EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTGVPAGQVASLYS--FILGEL---W
40 50 60 70 80
cry2ab2_820_  PSGSTNLMQDILRETEKFLNQRLNTDTLARVNAELTGLQANVEEFNRQVNFNPRNAV
90 100 110 120 130 140
1261624  PKGK-NQWEIMEFMEHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLSLESWYGNRNTR
100 110 120 130 140 150
cry2ab2_820_  PLSIT-SSVNTMQOLFNLRLPOFOMQGVQLLLPLFAQAAANHLHSFIRDVILNADWGLS
150 160 170 180 190 200
1261624  ARSVVKSOYIALELMEVOKLPSFAVSGEEVPLPIFYAQAANHLHLLEDASIFGKRGUS
160 170 180 190 200 210
cry2ab2_820_  AATLRTYRDLKNTYRDSNYCINTYQSAFKGL-NTRLHML---EFRTYMLNVEFYVS
210 220 230 240 250 260
1261624  SSEISTFYNRQVERAGDYSDHCVKWYSTGLNLRGYNABSVRVNQFRDRLMLVLDLVA
220 230 240 250 260 270
cry2ab2_820_  IWSLFYQSLLVSSGANL----YASGSGPOQTQ-SPTSODMFFLYSIFQVNSYVNLNGFS
270 280 290 300 310
1261624  LFPSTYDQMTYPIKTAQLTREYTDAGTGVHPHPSFTSTM---YN----NNAPSFSAIE
280 290 300 310 320
cry2ab2_820_  GARLSNTFPNIVGLPGSTTTHALLA----ARVNYSGG--ISSGDIGAS-PFNQNFNCST
320 330 340 350 360
```

```
1261624  AAVVRN--PHLLDLEQVITLYLSLSRWSNTQYMMNMGWGHKLEFRITGGTLNISTQGSTNT
330 340 350 360 370 380
cry2ab2_820_  FLPPLLTPVRSWLDSDSGDEGVATVNMQTESF--ETTLGLRSGAFTARGNSNYPDPYFI
370 380 390 400 410 420
1261624  SINPVLPTSDRDYRVTESLAGLNLELTOPVNGVRVDVFWKFTVHPHPIASDNFYYPGV-
390 400 410 420 430 440
cry2ab2_820_  RNISGVLVVRNEOLRPLHNEIRNIASPSGTPGAGARATMVSVHNRKNNIHA--VHENG
430 440 450 460 470 480
1261624  ---GIGTQLODSENELPPEATQPNYESYSHRL--SHIGLISASHVKALVYSWTHRSAD
450 460 470 480 490
cry2ab2_820_  MIH-LAPNDYTGFTISIHATQNTQTRTFISEKFGQSGSLRFEQNNTIARYTLRGNG
490 500 510 520 530 540
1261624  RTNTIEFNSITQIPL--VKAFNUSGAAVVRGPGTGG--GDILR--RINTGTGDIRVNI
500 510 520 530 540 550
cry2ab2_820_  S-----YNLYKVSIGNSIRVIRVYATVNTTNDGVDNGARFSDINIGNV
550 560 570 580 590 600
1261624  PPFQORYRIRYASTTDLQFHTSINGKAINCFNSATMNR--GEDLDYKTFR--TVGFTT
560 570 580 590 600
cry2ab2_820_  ASNSDVLDINV---TLNSGTQDLMNIMLVPTNISPLY
610 620 630
1261624  PFSFSDVQSTFTIGAMNFSGSEYVDRIEFVPEVYEAEDYFKAQEKVTLFTSTNP
630 640 650 660
1261624  RGLKTDVKDYHIDQVSNLVESLSDEFYLDKRELFEIVKYAKOLHIERNM
670 680 690 700 710
cry2ab2_820.pep
NRAA:14537812
14537812 source="GENBANK_PROT" Cry2a (Bacillus thuringiensis)
SCORES  Initl: 205  Initn: 267  Opt: 333  z-score: 378.2 E(): 9e-13
Initn: 267  Initl: 205  Opt: 333  z-score: 378.2 expect(): 9e-13
Smith-Waterman score: 363; 21.7% identity in 607 aa overlap
(57-634:70-646)
cry2ab2_820_  PFSFQHSKSLDTVQKEWTEMKNNHSLYLDPIVGTASVFLKLVGSLVKRILSELRLNLF
30 40 50 60 70 80
14537812  EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTGVPAGQVASLYS--FILGEL---W
40 50 60 70 80
cry2ab2_820_  PSGSTNLMQDILRETEKFLNQRLNTDTLARVNAELTGLQANVEEFNRQVNFNPRNAV
90 100 110 120 130 140
14537812  PKGK-NQWEIMEFMEHVEEIIINQKISTYARNKALTDLKGDLAVYHDSLSLESWYGNRNTR
100 110 120 130 140 150
cry2ab2_820_  PLSIT-SSVNTMQOLFNLRLPOFOMQGVQLLLPLFAQAAANHLHSFIRDVILNADWGLS
150 160 170 180 190 200
```


Study No. 06-01-62-01
MSL No. 20307
Page 210 of 361

```
>>NRAA:3329593
Smith: 267 init1: 205 opt: 333 Z-score: 377.1 expect(): 1e-12
Smith-Waterman score: 362; 21.6% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820. PFSQHSKSLDTQCKEWTWKNNHSLYLDPIVGTVASFLKKYKGSVGVGRKILSELNRNIF
30 40 50 60 70 80
cry2ab2_820. EDCLKMSEYENVEPFSVASTITQIGIGIAKGLTGLGVFPFAGQVASLYS-FLIGEL-
40 50 60 70 80 90
cry2ab2_820. FSGTNLMQDILRETEKFLINQRLTDTLARVNAELTGLQANVVEFPNQVDNLFNPNRNV
90 100 110 120 130 140
cry2ab2_820. PKGK-NOWEIFMEHVEETINQKISTYARNKALTDLKGLGDALAVYHDSLESWGVRNNRNT
100 110 120 130 140 150
cry2ab2_820. PLUUIT-SVNTMQLPLNRLPQFQMGYQVLLLPFAQAANLHLSFIRDVILNADGWS
150 160 170 180 190 200
cry2ab2_820. ARSVYSQYIALELMPVQKLPSPFVAGEEVLPIYAAQANLHLLLRDASIFGKWEGLS
160 170 180 190 200 210
cry2ab2_820. AATLTIRYDKYKNTRDYSNICYTQSAFKGD-NTRLHML-EPFTYMFILNVFVYS
210 220 230 240 250 260
cry2ab2_820. SSETSPNQVERAGDYDHCVMKYSTGLNLRGTAESVWRVNOFRDMLTMLDLVA
220 230 240 250 260 270
cry2ab2_820. IWSLFKQSLVSGANL---YASGSGPQQTQ-SFTSQDWPFLYSFQVNSNYVINGFS
270 280 290 300 310
cry2ab2_820. LFPSTQMPYPIKNTAQLTREVYDAIGTVHPHPSFTISW---YN---NNAPSFSIAE
280 290 300 310 320
cry2ab2_820. 320 330 340 350 360
cry2ab2_820. GARLSTFPNIVGLPGSTTHALIA-----ARVNSGG-SSGDIQAS-PPNQNFNST
320 330 340 350 360
cry2ab2_820. AAVRN--PHLLDFLEQVTIYSLLSRWSNTQYNNMGHGLEFTIGTGLNTISTQGSTNT
330 340 350 360 370 380
cry2ab2_820. 370 380 390 400 410 420
cry2ab2_820. FLPLLTFFVRSMLDSSGDEQVATVNTMOTESF-ETTLGRSGAFTARGSNYPDPYFI
390 400 410 420 430 440
cry2ab2_820. SINPTLFTSRDYYTESLAGENLFIQTPVGVPRVDFHKKFVTHPIASDNFYIPGY-
430 440 450 460 470 480
cry2ab2_820. RNISGVLVVRNDELRRPLHNYNEIRNIASPSPGPGARAYVSVHNEKNHIA-VHENG
430 440 450 460 470 480
cry2ab2_820. ---AGIGTQLQDSENELPPEATQGPVNESYSHRL--SHIGLISASHVKALVYSWTHSRSD
450 460 470 480 490
cry2ab2_820. 490 500 510 520 530 540
cry2ab2_820. MTH-LAPNDVYGTFTSPHATQVNNQTRTIFSEKFGNGDSLRPEQNNTTARTYLRGN--
510 520 530 540 550 560
cry2ab2_820. RNTNTEPNSITQIPL--VKAFMLSGAAVVRGPGFTG-GDILR--RTNTGTGDIRVNIK
500 510 520 530 540 550
cry2ab2_820. 550 560 570 580 590 600
cry2ab2_820. ---GNSYMLYRVSSIGNSTIRVTINGRVYATVNTVNTINDGVNDNGAFSGDINGV
560 570 580 590 600
cry2ab2_820. PPFQGRVVRVYASTDQLQFHTSINGKALNQGNFATMNR-GEDLDYKTFTR--TVGFTFI
560 570 580 590 600
```


©01 Proprietary Information of Monsanto Company

```
cry2ab2_820 310 620 630
>NRAA:540282 ASSNSDVPDLINV---TNSGTFDLMNMLVPTNISPLY
initn: 263 Inittl: 201 Opt: 263 Z-score: 375.9 E(): 1.2e-12
Smith-Waterman score: 361; 21.7% identity in 607 aa overlap
(57-634:70-646)

3329593 610 620 630 640 650 660
PFSFLDVQSTFTTIGAMWFFSGNEVYDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP
610 620 630 640 650 660
RGLKTDVQDYHIDQVSNLVSLSDEFYLDKELFEIVKVANELHIERNM
670 680 690 700 710

3329593 670 680 690 700 710
cry2ab2_820_820 pep
NRAA:540282

540282 source="GENBANK_PROT" insecticidal protein cryI - Bacillus thuringiensis
insecticidal protein cryI - Bacillus thuringiensis

SCORES Inittl: 201 Inittl: 263 Opt: 263 Z-score: 375.9 E(): 1.2e-12
>NRAA:540282
initn: 263 Inittl: 201 Opt: 332 Z-score: 375.9 expect(): 1.2e-12
Smith-Waterman score: 361; 21.7% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820 30 40 50 60 70 80
PFSFQKSLDVTQKWTWKNNHSLYLDPIVGVASFLFKKVLGKRLISELRNLF
60 70 80 90 100 110 120 130 140
EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTILGVFPAGQVASLYS-FILGEL---W
40 50 60 70 80 90

cry2ab2_820 90 100 110 120 130 140
PGSTNLMDILIRETEKFLNQLNTDILARVNAELTGLQANVEEFNRQVDNLPNNAV
140 150 160 170 180 190 200
PKGK-NQWEIFMEHVEEIIINQKISTYARKALTDLKGGLDALAVYHDSLESWGNRNT
100 110 120 130 140 150

cry2ab2_820 150 160 170 180 190 200
PLSIT-SSVNTMQQLFLNLPQFMQGYQLLLPLFAQANLHLFIRDVILNDEWGIS
160 170 180 190 200
ARSVKSYQIATLELMFVKLPSPFAVSGEEVPLLPPIYAAQANLHLLLDASIFKRWGLS
160 170 180 190 200 210

cry2ab2_820 210 220 230 240 250 260
AATLTYRDYLNKYTRDYSNYCINTYQSAFKGL-NTRLHDM---EFTYMFNAVFEYVS
220 230 240 250 260
SSEISITFYNRQVERAGDYSYHCVKYSTGLNLRGTNAESWRYNQFRDMLVLDLVA
220 230 240 250 260 270

cry2ab2_820 270 280 290 300 310
IWSLPKYSQSLVSSGANL---YASGSGFQQTQ-SFTSQDWPLFLYSLFQVNSNYLVNGFS
280 290 300 310
LFPSTYDQMPYIKITTAQLTREVYTDAGTVHPHPSFTTWT---YN---NNAPSFAIE
280 290 300 310 320

cry2ab2_820 320 330 340 350 360
CARLSNTEPNVIGLPGSTTHALLA----ARVNYSGG-ISSGDIGAS-FPNQFNCS
330 340 350 360
AAVVRN--PHLDLEQVITYISLLSRWNTQYMMWGGHKLKLEPRTIGTLNISTQGSTNT
330 340 350 360 370 380

cry2ab2_820 370 380 390 400 410 420
FPLPILTFVRSWLDGSDREGVATVNWOTESF-ETTLGLRSGAFTARGNSNFPDYFI
380 390 400 410 420
SINPVLFTSRDVRYESLAGLNLFLQTPVNGVPRVDFHWKVFVTHPIASDNFYPGY--
380 390 400 410 420
```

```
cry2ab2_820 430 440 450 460 470 480
>NRAA:540282 RNTSGVPLVRNEDLRPLRPHYNIRNIASPGTGGARAYMVSHNRKNIHA-VHENG
430 440 450 460 470 480
540282 ---AGITQLOQSENELPPATQPNYESYSHRL--SHIGLISASHVKALVYSWTHRSAD
450 460 470 480 490

cry2ab2_820 490 500 510 520 530 540
MIH-LAPNDYTGFTLSPHATQVNNQTRTFISEKFGNQGSLRPEQNNTIARYTLRNGN
490 500 510 520 530 540
540282 RTNTEPNSITQIPL--VKAPNLSGGAAVVRGPGFTG-GDILR--RTNIGTFGDIRVIN
500 510 520 530 540 550

cry2ab2_820 550 560 570 580 590 600
S-----YNLYRVSSSIGNSTRVINGRVYATNVNITTNDGVNDNGARFSDIINIGNV
550 560 570 580 590 600
540282 PPFQAQRYVRIRYASTTDLQPHYSINGKAINQGNFSATMNR-GEDLDYKTR--TVGFTT
560 570 580 590 600

cry2ab2_820 610 620 630
ASSNSDVPDLINV---TNSGTFDLMNMLVPTNISPLY
610 620 630
540282 PFSFLDVQSTFTTIGAMWFFSGNEVYDRIEFVPEVTEAEYDFEKAQEKVTAFTSTNP
610 620 630 640 650 660

540282 RGLKTDVQDYHIDQVSNLVSLSDEFYLDKELFEIVKVANELHIERNM
670 680 690 700 710

cry2ab2_820_820 pep
NRAA:540282

40290 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
delta-endotoxin [Bacillus thuringiensis]

SCORES Inittl: 201 Inittl: 263 Opt: 332 Z-score: 375.9 E(): 1.2e-12
>NRAA:40290
initn: 263 Inittl: 201 Opt: 332 Z-score: 375.9 expect(): 1.2e-12
Smith-Waterman score: 361; 21.7% identity in 607 aa overlap
(57-634:70-646)

cry2ab2_820 30 40 50 60 70 80
PFSFQKSLDVTQKWTWKNNHSLYLDPIVGVASFLFKKVLGKRLISELRNLF
60 70 80 90 100 110 120 130 140
EDCLKMSEYENVEPFVSASTIQTGIGIAGKILGTILGVFPAGQVASLYS-FILGEL---W
40 50 60 70 80 90

40290 90 100 110 120 130 140
PGSTNLMDILIRETEKFLNQLNTDILARVNAELTGLQANVEEFNRQVDNLPNNAV
140 150 160 170 180 190 200
PKGK-NQWEIFMEHVEEIIINQKISTYARKALTDLKGGLDALAVYHDSLESWGNRNT
100 110 120 130 140 150

cry2ab2_820 150 160 170 180 190 200
PLSIT-SSVNTMQQLFLNLPQFMQGYQLLLPLFAQANLHLFIRDVILNDEWGIS
160 170 180 190 200
ARSVKSYQIATLELMFVKLPSPFAVSGEEVPLLPPIYAAQANLHLLLDASIFKRWGLS
160 170 180 190 200 210

cry2ab2_820 210 220 230 240 250 260
AATLTYRDYLNKYTRDYSNYCINTYQSAFKGL-NTRLHDM---EFTYMFNAVFEYVS
220 230 240 250 260
SSEISITFYNRQVERAGDYSYHCVKYSTGLNLRGTNAESWRYNQFRDMLVLDLVA
220 230 240 250 260 270

cry2ab2_820 270 280 290 300 310
IWSLPKYSQSLVSSGANL---YASGSGFQQTQ-SFTSQDWPLFLYSLFQVNSNYLVNGFS
280 290 300 310
LFPSTYDQMPYIKITTAQLTREVYTDAGTVHPHPSFTTWT---YN---NNAPSFAIE
280 290 300 310 320

cry2ab2_820 320 330 340 350 360
CARLSNTEPNVIGLPGSTTHALLA----ARVNYSGG-ISSGDIGAS-FPNQFNCS
330 340 350 360
AAVVRN--PHLDLEQVITYISLLSRWNTQYMMWGGHKLKLEPRTIGTLNISTQGSTNT
330 340 350 360 370 380

cry2ab2_820 370 380 390 400 410 420
FPLPILTFVRSWLDGSDREGVATVNWOTESF-ETTLGLRSGAFTARGNSNFPDYFI
380 390 400 410 420
SINPVLFTSRDVRYESLAGLNLFLQTPVNGVPRVDFHWKVFVTHPIASDNFYPGY--
380 390 400 410 420
```


Study No. 06-01-62-01
MSL No. 20307
Page 212 of 361

	50	60	70	80	90	100
crv2ab2_820.	90	100	110	120	130	140
62288327	110	120	130	140	150	160
	170	180	190	200	210	220
crv2ab2_820.	150	160	170	180	190	200
62288327	170	180	190	200	210	220
	230	240	250	260	270	280
crv2ab2_820.	210	220	230	240	250	260
62288327	230	240	250	260	270	280
	290	300	310	320	330	340
crv2ab2_820.	270	280	290	300	310	320
62288327	290	300	310	320	330	340
	350	360	370	380	390	400
crv2ab2_820.	330	340	350	360	370	380
62288327	350	360	370	380	390	400
	410	420	430	440	450	460
crv2ab2_820.	430	440	450	460	470	480
62288327	450	460	470	480	490	500
	510	520	530	540	550	560
crv2ab2_820.	490	500	510	520	530	540
62288327	510	520	530	540	550	560
	570	580	590	600	610	620
crv2ab2_820.	550	560	570	580	590	600
62288327	570	580	590	600	610	620
	630	640	650	660	670	680
crv2ab2_820.pgp	610	620	630	640	650	660
NRAA:21665941	630	640	650	660	670	680
21665941 source="GENBANK_PROT" Cry [Bacillus thuringiensis]	650	660	670	680	690	700

SCORES	Init1: 205	Initn: 267	Opt: 329	z-score: 372.5 E(): 1.9e-12
--------	------------	------------	----------	-----------------------------

Monsanto Company

~~Final Report~~

~~Product Characterization Center~~

[illegible]

```

cry2ab2_820      600          610          620          630
>>SW:9087134
: ||| :: :||:: |::|::
TFPSFSQVSTFTIGAWNFSSGNEVYDRIFRVFVEVTEAEYDFEKAQEKVALTFTSTN
211665941      610          620          630          640          650
PGGLKNTVTEVHIDQVSNLVESLSLSEFYDDEKRELFELVKYAKQLHTGRNM
211665941      670          680          690          700          710
cry2ab2_820.pep
>>SW:9087134
9087134 description=PESTICIDIAL CRYSTAL PROTEIN CRY7AB (INSECTICIDAL
DELTA-ENDOTOXIN CRVYIIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar dakota"
source="swissprot_prot" version=NA type=PRT

SCORES   Initl: 242   Inltn: 271   Opt: 331   z-score: 371.4 E(): 2.1e-12
>>SW:9087134
inltn: 271 initl: 242 opt: 331 z-score: 371.4 expect(): 2.1e-12
Smith-Waterman score: 331;    26.5% identity in 215 aa overlap
(57-266:65-277)

cry2ab2_820     30       40       50       60       70       80
PFSFQHSLSDTVQKEWTKKNHSLYLDIVGTVASFLKKYGVSLVGKRILSELRLNLI
9087134         MNQDFLSITEROEPALASGNVAINTVSVTGAILSGALGVFGASFTIFYL-KITGLLW
              90       100      110      120      130      140
PSGSTNLMLDLRTEKFNLRNLTDLARVNAELTGLQANVEFNFRVDNELN-PNRNA
cry2ab2_820     100      110      120      130      140      150
PHNKRWDEFTMTVELTEQIEGYARNKAALEGISNNLLTYQQAALEDWLNNPDPA
9087134         100      110      120      130      140      150
cry2ab2_820     160      170      180      190      200
VPSPITSVNTMOOHLRALPOFQMGHOLLPLFAQAANLHLSFIRVLNADEWGIS
9087134         TITRIDRIEDALEFSGMSTRVAGYESPLNTVYAQAANLHALLRDSTLYGDKGFT
              160      170      180      190      200      210
cry2ab2_820     210      220      230      240      250      260
AATLRFDYDLKNVTDRDNVNYNIYOSGGIANTRLHML--EFRTYMFNVFEVVS
9087134         QNNHIENYNROKKKHISEYNHCWKVYNGLSRLMSKSGEOWINTNFEREMILMVLDIAA
              220      230      240      250      260      270
cry2ab2_820     270      280      290      300      310      320
IWSLFKYGSLLVSSGANLVASGSGPQOTQFTSQMPYLFIQVNSVLAANGFSGARS
9087134         : : :
VFPIIDPRMYSMETSTQTIREVYTDPITSLGISNPDIQSFPSCMENTALTIPIHVIDLEL
              280      290      300      310      320      330
cry2ab2_820.pep
NRRA:9087134
9087134 source="GENBANK_PROT". Pesticidal crystal protein cry7Ab (Insecticidal
delta-endotoxin in CrvYIIA(b)) (Crystalline entomocidial protoxin) (130 kDa Crystal
protein)[gi|436839|gb|AAA21120.1] CrvYII delta-endotoxin

```

Study No. 06-01-62-01
MSL No. 20307
Page 213 of 361

Study No. 06-01-62-01
MSL No. 20307
Page 214 of 361

[illegible]

```
cry2ab2_820_AATLRTYRDLKYNRYDSNYC--INTVSQFKNGLR-LHDMLEPFTMYLNVEFYXV
      : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
8927997 ESEISTYNQQSQQTQEVS DYCSWYNTGTLRLTGTAESWVRNQFRDMLTMDVLVA
      220   230   240   250   260   270
```

```

cry2ab2_820..TWSLFKQSLVSSGANL-----YASGGSP-QQTQGTSDMPFYSLFQNSYNVLNGFS
:: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
8927997..LPFSYDRMYPIPTSAQLTREYYDAGTGTVHNPASFSTTW---YN---NNAPESFTIE
280 290 300 310 320

```

```

320 330 340 350 360 370 380
cry2ab2_820. GARLSTFNNIIVGELSTTHALLA-----ARVNTVSGG--TSSGDIGASGFQNFQNCST-
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8927997 AAVRN--PHLLDFEQTIVTISLSRMSNTQYNNMWGCHKLEFFITGCT-LNTSTQGSTN
330 340 350 360 370 380

```

cy2ab2_820...-FLPPLTTPRSDWSSDREGVATVNNQTESF-ETTLGLRSGATARTAGNSVNPYPFY
8927997 TSINPVLPTISRDVYRTESLAGNLNLTQVNGVPRVDFHWKFVTHPIASDNFYPGY-

[illegible]

cry2ab2_820. SMIHLPNDYGTGISIHATQVNNQTRTFISEFGNQDGLAFEQNNTTARYTLRNGN

8527537
DRAINLINS-SIQIFUWNRNERSGASVVRGPFIS-QULT-QRINIGI,POGLARVNI
500 510 520 530 540 550

```

8927999/      560      570      580      590      600      610
FFAQRRLKRTASTTINETHFSLNGKAHQNGNSATMNR-GULLDTRAKFLVGFITIP
CRY2ab2_820..ASSNSDVLDINV-TLNSGTQFDLMNMLVPTNISPLY
|||:: : :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::

```

8927997	LKNTVTDCHIDQVSNLIVESLSDFYLDKELFETVKKVAKQINERNM	680	690	700	710	620	630	640	650	660	670
---------	--	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

8927997 description="PESTICIDIAL CRYSTAL PROTEIN CRYLID (INSECTICIDAL DELTA-**ENDOTOXIN** CRYII (D) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL CRYZABZ_820.pep
SW:8927997

892/99/ description= "PESTICIDIAL CRYSTAL PROTEIN CRYIID (INSECTICIDAL DELTA-ENDOTOXIN CRYII (D)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (81 KDA CRYSTAL

PROTAIN("Library:NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PR

SCORES Init1: 206 Init2: 267 Opt: 328 z-score: 371.4 E(): 2.2e-12
>>SM:8927997
initn: 267 initn: 266 opt: 328 z-score: 371.4 expect(): 2.2e-12
Smith-Waterman score: 366; 114 identity in 605 aa overlap
(57-634:70-646)

cry2ab2_820. PFSQKSLDTVKQKWKNNHSLDPTGTVASFLKKGSLVKGKRLSELRNLI
8927997 EDCKMSEYSEVPEFVSSTIQRGIVAGKTLQNTVVFAGOVASLYS-FILGEL---W
40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. PFGSTNLMODILRETEKFLNORLNTDILARVNAELGLQANVEEFNQNELNENANA
8927997 PKGSKQ-WELFHEVHEELINQKISTYARNKALADLKG-GDMAYVHSELESWEHNNIT
100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. VPSITSSVNTMOQLNRLPFQFMQGYQLLLPLFAQAANLHLSFTDVIYNADEWIS
8927997 VRSVKNQVIALELMFVQKLPFAVSGEEVPLLPYQAQAANLHLLLRDASITGKENGSL
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. AATLRYRDYLNKVDYSNYC---INTQSAFKGLNTR-LHDMLEFRTYMLNVEFVS
8927997 ESISITFYRQSQTOEYSDYCEWNTGLNLRGTNAESWRYNQFRDRLMVLIDVA
220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. IWSLFKYQLLVSSGANL---YASGSGP-QOTQSTQSDWPFYLSLQVNSNYVLNGFS
8927997 LFPSYDTRMYPIPTSAQLTREVYTDALGTVHPNASFASTTW---YN-----NNAPSFSTIE
270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. GARLSNTFNVIGLDPGSTTTHALLA-----ARVNYSGG--ISSGDIAGSPFNQNCST-
8927997 AAVRN--PHLLDFLEQVTIYSLLSRWSTQYMMNMWGGHKLFRITIGGT-LNTSTQGSTN
320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. -FLPPLLTPTVRSMLDSGREGVAIVTNWQTESP-ETTLGLSGAFTARGNSYFPDYP
8927997 TSINPVLPTFSRDVRYTESLAGLNLFLTQPVNGVPRVDFHMKFVTHPIASDNFYIPGY-
370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. IRNISGVLVVRNEDLRPLHYNEIRNIASPSGTGGARVYVSVNRRKNIHA-VHENG
8927997 ---AGIGTQLODSNELPPTTGPQPNYESYHRL--SHIGLISASHVKALVYVSWTHSA
430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. SMHLAPNDYGTFTISPIHATQVNNQTRTFISEKFGNQGLSLRFEQNNTARTYLRNGN
8927997 DRTNINSD-SITQIPLVKAFNLPFGASVVRGFGTG-GDIL--QRTNTGTGDIRVIN
490 500 510 520 530 540 550

cry2ab2_820. S-----INLYLRVSSIGNSTIRVINGRVYATNVTNTTNDGVNDNGARFSDINIGNVV
8927997 PPFAQRVRLRIRVASTTNLEFHTSINGKAINQGNFATMNR-GEEDLYKAFRTVGTFTFP
560 570 580 590 600 610

cry2ab2_820. ASSNSDVPDLINV-TLNSGTQFDLMNIMLVFTNISPLY
8927997 SFSNAQSTFTIIGAWNFSLNGVEYIDRIEFVEVYEEAYEYDLKKAQDEITAMFTSTNLR
610 620 630 640 650 660 670

8927997 LKTNVTDCHIDQVSNLSLSDSEFYLDKRELFEIVKYAKQLNIERNM
680 690 700 710

cry2ab2_820. pep
NR2A:27413810
27413810 source="GENBANK PROR" crystal endotoxin Cry9Ea [Bacillus
thuringiensis]gi|8928043|sp|Q9ZNL9|CR9EA_BACTA Pesticidal crystal protein
cry9Ea (insecticidal delta-endotoxin CryIXE(a)) (Crystalline entomocidal
protoxin) (130 kDa crystal protein)gi|3986086|dbj|BA034908.1| Cry9 like protein
[Bacillus thuringiensis serovar aizawai]

SCORES Init1: 152 Initn: 183 Opt: 326 z-score: 365.7 E(): 4.5e-12
>>NR2A:27413810
initn: 183 initn: 152 opt: 326 z-score: 365.7 expect(): 4.5e-12
Smith-Waterman score: 326; 22.5% identity in 612 aa overlap
(57-632:76-651)

cry2ab2_820. PFSQKSLDTVKQKWKNNHSLYLDPIVGVASFL-LKKVGLVKGKRLSELRNLI
27413810 LOTDQVTSLLNPNLSINPRDVLQGINIVGRLGLGVFPAGQLV--TFVTFLLNQL
30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. PFGSTNLMODILRETEKFLNORLNTDILARVNAELGLQANVEEFNQNENLN-PNRN
27413810 WPTNDNAWENMAQTEFLIDIKISAQVGNNAADDLTGLHDYEEYLAALAEWLERPNGA
110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. AVPLSITSSVNTMOQLNRLPFQFMQGYQLLLPLFAQAANLHLSFTDVIYNADEWIS
27413810 RANL-VTQRFENHTAFVTRMPSGTSGSGRQVAFATVYAQAANLHLLLRDASITGKENGSL
150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. EWGISAATLRYDYLKNTYDRYSNYCINTYQSNF--KGLNTR-LHDMLEFRTYMLNVEFVS
27413810 RWGLQCGQINLYFNAQOERTRIYTHCHVEIYNGRLEDQETNTSESWHFFRENTLAA
210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. FEYVSIWLSFKYQSLVSSGANLVASGSGPQOSTQSDWPFYLS-----FQVSSG-
27413810 MDLVALFFFYNNVRQ-----YFNGANPOLRTREYTD--PIVYPPFANQGIQVRSNN
260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

cry2ab2_820. VINGFSGARLSNTFPNIVLPGSLTTHALLAARVNYSGGISSG--DIGASFPFNQNCST
320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 216 of 361

```
27413810  PYNIFS--ELENAFIRPHL--FERLNELTISRNYTAPTNTSFLDYSGHTLSQSHANN
          340      350      360      370      380
cry2ab2_820.  FLPLPLTFFVRSMLDGSDREGVATVIMQOT--ESFETTLGLRSGAFTARGNSYFPDYFI
          370      380      390      400      410      420      430      440
27413810  --P---TTVETSYGQITSNTRLFNNTNGARAIIDSRANFNGLYANLYGVSSLINIFFTGVN
          390      400      410      420      430      440
cry2ab2_820.  RNLGVPVVRNEDLR---PLHNEIRNIASP-----SGTPGGARAYMVSVHNRKNN
          430      440      450      460      470
27413810  SEITWAANTCR-QDLTTTEELPLENNF--NLLSHVTFELRNTTQGGPLATLGFVFTYV--
          450      460      470      480      490
cry2ab2_820.  IHAVHENGSMIHLAPNDYTGFTISP--IHATOVNNOTRTFISEKFGNOGDSLRFQNNNTA
          480      490      500      510      520      530
27413810  --WTRDVFDTNITADR--ITQLPFWKASEIGGTTVVGPGFTG--GDILR--RTDGG
          500      510      520      530      540      550
cry2ab2_820.  RYTLRGNNGNS-----YNLYRVSSIGNSTIRVTNGRVYATVNTTNNGVNDNGARF
          540      550      560      570      580      590
27413810  VGTIRANVNAFLTQOYRIRLRVASTTSFVNLFVNNSAAGFTLFPSTMAONGSLTYES--F
          560      570      580      590      600
cry2ab2_820.  SDINIGNVASSNSDVPDLNDVTLN--SGIQFDLMNIMLVPTNISPLY
          600      610      620      630
27413810  NTLVETHTIRFSQSDTLRLNIFPISQGVYVDKLEIVPINPTREAEEDLEDAKAVAS
          610      620      630      640      650      660
27413810  LFTTRDGLQVNVTDYQVDOAANLVSCLSDEQYGHDKKMLLEAVRAAKRLSRERNLLQDP
          670      680      690      700      710      720
cry2ab2_820.pcp
SW:8928043
8928043 description="PESTICIDIAL CRYSTAL PROTEIN CRY9EA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIXE(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version=NA type=PRT
SCORES   Init1: 152   Initn: 183   Opt: 326   z-score: 365.7   E(): 4.5e-12
>>SW:8928043
initn: 183   init1: 152   opt: 326   z-score: 365.7   expect(): 4.5e-12
Smith-Waterman score: 326;   22.5% identity in 612 aa overlap
(57-632:76-651)
cry2ab2_820.  PFSFQHSKSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFL--LKKVGSGLVKRTLSLRNLI
          30      40      50      60      70      80
8928043  LQYDGYGTGSLINPNSINPRDVLQGTGINVGRILGLGPPVAGQLV--TFYIFLNQL
          50      60      70      80      90      100
cry2ab2_820.  FPGSGTNLMQDILRETEKFLNQLNLTDLARVNAELATGLQANVEEFNRQVDNFLN--PNRN
          90      100      110      120      130      140
8928043  WPTNDNAYWEAFMAQIEELIDQKISAOVVNRNALDGLTGLDHYVEEYLALEWEERFNGA
          110      120      130      140      150      160
```

```
cry2ab2_820.  AVPLSITSSVNTMQOLFNLRLPQFQM--QGYQ---LLLLPLFAQAANLHLSFIRDVILNAD
          150      160      170      180      190      200
8928043  RANL--VQRFENLHTAFVTRPMSFGTGPQSQRDAVALLTVTAQAANLHLLKDAEITGA
          170      180      190      200      210      220
cry2ab2_820.  EWGISAATLRTYRDKNVTYDYSNYCINTYQSAF---KGLNTR--LHDMLEFRYTMFLNV
          210      220      230      240      250      260      270      280
8928043  RMWLGQGLNLYFNAQQERTIYTHVCHVETYNRGLEDVRGNTESMLNVHRFRERMTLMA
          230      240      250      260      270      280
cry2ab2_820.  FEYVSINSLFKYQSLLVSSGANLYAGSGPQOTQSTSDMPFLYS-----LFQVNSNY
          260      270      280      290      300      310
8928043  MDLVALFPFVNVVRQ-----YPNGANPQLTRREIYTD--PIVINPFPANOGICRRWGN
          290      300      310      320      330
cry2ab2_820.  VLNFGSGLRSLNTPFNVLGLPGSTTHALLAARVNYSGISSG--DIGASFPNQNFNCST
          320      330      340      350      360
8928043  PYNIFS--ELENAFIRPHL--FERLNRLTISRNYTAPTNTSFLDYSGHTLSQSHANN
          340      350      360      370      380
cry2ab2_820.  FLPLPLTFFVRSMLDGSDREGVATVIMQOT--ESFETTLGLRSGAFTARGNSYFPDYFI
          370      380      390      400      410      420
8928043  --P---TTVETSYGQITSNTRLFNNTNGARAIIDSRANFNGLYANLYGVSSLINIFFTGVN
          390      400      410      420      430      440
cry2ab2_820.  RNLGVPVVRNEDLR---PLHNEIRNIASP-----SGTPGGARAYMVSVHNRKNN
          430      440      450      460      470
8928043  SEITWAANTCR-QDLTTTEELPLENNF--NLLSHVTFELRNTTQGGPLATLGFVFTYV--
          450      460      470      480      490
cry2ab2_820.  IHAVHENGSMIHLAPNDYTGFTISP--IHATOVNNOTRTFISEKFGNOGDSLRFQNNNTA
          480      490      500      510      520      530
8928043  --WTRDVFDTNITADR--ITQLPFWKASEIGGTTVVGPGFTG--GDILR--RTDGG
          500      510      520      530      540      550
cry2ab2_820.  RYTLRGNNGNS-----YNLYRVSSIGNSTIRVTNGRVYATVNTTNNGVNDNGARF
          540      550      560      570      580      590
8928043  VGTIRANVNAFLTQOYRIRLRVASTTSFVNLFVNNSAAGFTLFPSTMAONGSLTYES--F
          560      570      580      590      600
cry2ab2_820.  SDINIGNVASSNSDVPDLNDVTLN--SGIQFDLMNIMLVPTNISPLY
          600      610      620      630
8928043  NTLVETHTIRFSQSDTLRLNIFPISQGVYVDKLEIVPINPTREAEEDLEDAKAVAS
          610      620      630      640      650      660
8928043  LFTTRDGLQVNVTDYQVDOAANLVSCLSDEQYGHDKKMLLEAVRAAKRLSRERNLLQDP
          670      680      690      700      710      720
cry2ab2_820.pcp
NRAA:46409859
46409859 source="GENBANK_PROT" cry1B type crystal protein [Bacillus
thuringiensis serovar kuistaki]
```


Study No. 06-01-62-01
MSL No. 20307
Page 217 of 361

[illegible]

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 218 of 361

```
8927979      TSINPVLQTSRDVYTESFAGINILITTPVGVFWARFNRWPLNSLRGSLTYIGY-
380          390      400      410      420      430      440      450      460      470      480      490      500
cry2ab2_820.  IRNLSGVPLVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNIIHA-VHENG
430          440      450      460      470      480      490      500      510      520      530      540      550
8927979      ---TGVTQLFDSFTELPPETTERPNVESYSHRLSNIR--LISGNTLRAPVYSWTHRSA
440          450      460      470      480      490      500      510      520      530      540      550
cry2ab2_820.  SMILHAPNDVGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNTARTYTLRGNG
500          510      520      530      540      550      560      570      580      590      600      610      620
8927979      DRNTISSD-SITQIPLVKSFLNSGTSVSGPGFTG-GDIIRTNVNGSVLSMGLNFNT
500          510      520      530      540      550      560      570      580      590      600      610      620
cry2ab2_820.  SYNLV-LRVSSIGNST--IRVTINGRV-YTATNVNTTNNQGVNDGARFSDINIGNVVA
550          560      570      580      590      600      610      620      630      640      650      660      670
8927979      SLQRYRVRYVAASQIWLVRVTVGGSTFDQGFPTSWSANESLTSQSFRFAEPVG--IS
560          570      580      590      600      610      620      630      640      650      660      670      680
cry2ab2_820.pcp
NRAA:8927979      EGNIDPFVSAIVQGINIAGRILGVLPVFPAGQIASPY-----SFLVGE-----L
50          510      520      530      540      550      560      570      580      590      600      610      620
cry2ab2_820.  PPSGSLNMDILRETEKFLQNRINTDTLARVNAELTGLQANVEEFNRQVDNFIENRNA
90          100      110      120      130      140      150      160      170      180      190      200      210
8927979      WPRGR-DPWEIFLHEVQELIQOVTENTRTDALTARLQGLGNSFRAYQOSLMDLENRDA
90          100      110      120      130      140      150      160      170      180      190      200      210
cry2ab2_820.  VPLSITSVNTMOQL-FLNRLPQFOMQGYQLLLPLFAQAANLHLSFIRDVILNADWGI
150          160      170      180      190      200      210      220      230      240      250      260      270
8927979      RTRSVLYTQVIALELDFLNAMFLFAIRNQEVPLIMVYAQAANLHLLLRDASLFGSEFGL
150          160      170      180      190      200      210      220      230      240      250      260      270
cry2ab2_820.  SAATIRYRDLKMYTRDYSYNCINTQSAFKGL-NTRLHDML---EPTYMLFNVEYV
210          220      230      240      250      260      270      280      290      300      310      320      330
```

```
8927979      TSIEIQRYYERQVEKREYSDICARWYNGLNLRGNAESWLRYNQFRRDITJGVLDLV
210          220      230      240      250      260      270      280      290      300      310      320      330
cry2ab2_820.  SIWSLFKQSLVSSGANL----YASGSGPQQTOS-FTSQDWPFLYSLFQVNSVNLNGF
270          280      290      300      310      320      330      340      350      360      370      380      390
8927979      ALFPPSDYRVRVPMNTSQAQLREIYTDPIGRTNAPSGFASTNW-----FN-NNAPSFSAI
270          280      290      300      310      320      330      340      350      360      370      380      390
cry2ab2_820.  SGARLSNTFPNIVLPGSTTHALLA----ARVNYSGG-ISSGDI-CASPFNQNFNCS
320          330      340      350      360      370      380      390      400      410      420      430      440
8927979      EAAVIRP--PHLLDPPEQLTIFSVLSRMSNTQYMYWVGHRLSRTIRGSLSTSTHGNTN
330          340      350      360      370      380      390      400      410      420      430      440      450
cry2ab2_820.  TFLPELLTFFVRSMLDGSDPREGVAIVTNWQTESFE-TTIGLSSGAFTARGNSVFPDYF
370          380      390      400      410      420      430      440      450      460      470      480      490
8927979      TSINPVLQTSRDVYTESFAGINILITTPVGVFWARFNRWPLNSLRGSLTYIGY-
380          390      400      410      420      430      440      450      460      470      480      490      500
cry2ab2_820.  IRNLSGVPLVRNEDLRPLHYNEIRNIASPGTGGARAYMVSVHNRKNIIHA-VHENG
430          440      450      460      470      480      490      500      510      520      530      540      550
8927979      ---TGVTQLFDSFTELPPETTERPNVESYSHRLSNIR--LISGNTLRAPVYSWTHRSA
440          450      460      470      480      490      500      510      520      530      540      550      560
cry2ab2_820.  SMILHAPNDVGTFTISPIHATQVNNQTRTFISEKFGNQGDSLRFEQNNTARTYTLRGNG
490          500      510      520      530      540      550      560      570      580      590      600      610
8927979      DRNTISSD-SITQIPLVKSFLNSGTSVSGPGFTG-GDIIRTNVNGSVLSMGLNFNT
500          510      520      530      540      550      560      570      580      590      600      610      620
cry2ab2_820.  SYNLV-LRVSSIGNST--IRVTINGRV-YTATNVNTTNNQGVNDGARFSDINIGNVVA
550          560      570      580      590      600      610      620      630      640      650      660      670
8927979      SLQRYRVRYVAASQIWLVRVTVGGSTFDQGFPTSWSANESLTSQSFRFAEPVG--IS
560          570      580      590      600      610      620      630      640      650      660      670      680
cry2ab2_820.pcp
NRAA:9087135      SSSNDVPLDINVLNSGTQ-FDLNMLVPTNISPLY
610          620      630      640      650      660      670      680      690      700      710      720      730
8927979      ASGSQTA-GISISNAGRQTFHFDEKIEFIPITATFEAEYDLERAQEAVALFTNPRRL
610          620      630      640      650      660      670      680      690      700      710      720      730
cry2ab2_820.pcp
NRAA:9087135      SSSNDVPLDINVLNSGTQ-FDLNMLVPTNISPLY
610          620      630      640      650      660      670      680      690      700      710      720      730
9087135 source="GENBANK PROT" Pesticidal crystal protein cry7Ab (Insecticidal
delta-endotoxin CryVIIA(b)) (Crystalline entomocidal protoxin) (130 kDa crystal
protein)|g|436841|gb|AAA21121.1| CryIII delta-endotoxin
protein|g|436841|gb|AAA21121.1| CryIII delta-endotoxin
SCORES      Init1: 231      Initn: 260      Opt: 319      Z-score: 357.8 E(): 1.2e-11
-->NRAA:9087135
Initn: 260 Init1: 231 opt: 319 Z-score: 357.8 expect(): 1.2e-11
Smith-Waterman score: 319; 26.0% identity in 215 aa overlap
(57-266:65-277)
cry2ab2_820.  PFSFQHKSLDTQKQEWTEWKNHNSLYLDPVIGTVASFLKLVKGVSLGKRILSELNLI
30          40      50      60      70      80      90      100      110      120      130      140      150
```


9087135 MNYQDFISITERQEPALASGNTAINTVSVTGATLSALGVGASFTINFYI-KITGLLW
40 50 60 70 80 90

cry2ab2_820. PFGSNLMQDLRETEKFLNQINLNTTLARVNAELTGLQANVEENRQVDNFLN-PNENA
90 100 110 120 130 140

9087135 PHDK-NIWDEFMEVEETLIEQIEQYARNKALELGLGNLTIYQOALEDWLNPDPA
100 110 120 130 140 150

cry2ab2_820. VPLSITSSVNTMQDLNRLNLPQFMQMGYQLLLPLFAQAANLHLSFIRDVILNADENGIS
150 160 170 180 190 200

9087135 TITRVIDRFRILDALFESYMPFRVAGVEIPLLTVAQAANLHLLALRDSLYGDKWEFT
160 170 180 190 200 210

cry2ab2_820. AAILRTYRDYIKNYTRDYSNYCINTYQSAFKLNRLHDMV--EFTYMFNLNVEFYS
210 220 230 240 250 260

9087135 QNNIEENYRQKKHISEYNSHCWKYNSGLSRLNGSYEQWYNINFRFRMILMVLDAIA
220 230 240 250 260 270

cry2ab2_820. IWSLFYQSLVSSGANLYASGSGPQQTQSFDWPFYLSLFOVNSVNLNGFSARL
270 280 290 300 310 320

9087135 VFPIYDPRMYSMETISQTLTREVTDPISLSISNPGIGPSFSQMENTAIRTPHLVDYDEL
280 290 300 310 320 330

cry2ab2_820.pgp
SW:9087135

9087135 description="PESTICIDIAL CRYSTAL PROTEIN CRYTAB (INSECTICIDAL
DELTA-ENDOTOXIN IN CRYVIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN) " library=NA species="Bacillus thuringiensis serovar kumamotoensis"
source="swissprot_prot" version=NA type=PRT

SCORES Initl: 231 Initn: 260 Opt: 319 z-score: 357.8 E(): 1.2e-11
>>SW:9087135
Initn: 260 Initl: 231 Opt: 319 z-score: 357.8 expect(): 1.2e-11
Smith-Waterman score: 319; 26.0% identity in 215 aa overlap
(57-266:65-277)

cry2ab2_820. PFSFOKSLDTVQKWEKWKNNHSLYLDPIVGTVAFLKKVGLGKRLSELRLNLP
30 40 50 60 70 80

9087135 MNYQDFISITERQEPALASGNTAINTVSVTGATLSALGVGASFTINFYI-KITGLLW
40 50 60 70 80 90

cry2ab2_820. PFGSNLMQDLRETEKFLNQINLNTTLARVNAELTGLQANVEENRQVDNFLN-PNENA
90 100 110 120 130 140

9087135 PHDK-NIWDEFMEVEETLIEQIEQYARNKALELGLGNLTIYQOALEDWLNPDPA
100 110 120 130 140 150

cry2ab2_820. VPLSITSSVNTMQDLNRLNLPQFMQMGYQLLLPLFAQAANLHLSFIRDVILNADENGIS
150 160 170 180 190 200

9087135 TITRVIDRFRILDALFESYMPFRVAGVEIPLLTVAQAANLHLLALRDSLYGDKWEFT
160 170 180 190 200 210

cry2ab2_820. AAILRTYRDYIKNYTRDYSNYCINTYQSAFKLNRLHDMV--EFTYMFNLNVEFYS
210 220 230 240 250 260

9087135 QNNIEENYRQKKHISEYNSHCWKYNSGLSRLNGSYEQWYNINFRFRMILMVLDAIA
220 230 240 250 260 270

cry2ab2_820. IWSLFYQSLVSSGANLYASGSGPQQTQSFDWPFYLSLFOVNSVNLNGFSARL
270 280 290 300 310 320

9087135 VFPIYDPRMYSMETISQTLTREVTDPISLSISNPGIGPSFSQMENTAIRTPHLVDYDEL
280 290 300 310 320 330

cry2ab2_820.pgp
NSAA:54112021

54112021 source="GENBANK_prot" Cry9Bb delta-endotoxin [Bacillus thuringiensis
serovar japonensis]

SCORES Initl: 145 Initn: 209 Opt: 319 z-score: 357.6 E(): 1.3e-11
>>NSAA:54112021
Initn: 209 Initl: 145 Opt: 319 z-score: 357.6 expect(): 1.3e-11
Smith-Waterman score: 330; 22.1% identity in 611 aa overlap
(61-632:73-664)

cry2ab2_820. QHKSLOTVQKWEKWKNNHSLYLDPIVGTVAFLKKVGLGKRLSELRLNLP
40 50 60 70 80

54112021 KEYLQMYGGDYADAFINFGNVRITGLQTDIVALLVGTGLGAVGGILTLGLTFLGFLWP
50 60 70 80 90 100

cry2ab2_820. SSGTNLMQDLRETEKFLNQINLNTTLARVNAELTGLQANVEENRQVDNFLN-PNENA
90 100 110 120 130 140

54112021 SNOQAVNFAEQMELIEQISQVVRALDNLIGIQINQYLLAFEFEEAENSVRS
110 120 130 140 150 160

cry2ab2_820.pgp
SW:9087135

9087135 description="PESTICIDIAL CRYSTAL PROTEIN CRYTAB (INSECTICIDAL
DELTA-ENDOTOXIN IN CRYVIA(B)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN) " library=NA species="Bacillus thuringiensis serovar kumamotoensis"
source="swissprot_prot" version=NA type=PRT

SCORES Initl: 231 Initn: 260 Opt: 319 z-score: 357.8 E(): 1.2e-11
>>SW:9087135
Initn: 260 Initl: 231 Opt: 319 z-score: 357.8 expect(): 1.2e-11
Smith-Waterman score: 319; 26.0% identity in 215 aa overlap
(57-266:65-277)

cry2ab2_820. PFSFOKSLDTVQKWEKWKNNHSLYLDPIVGTVAFLKKVGLGKRLSELRLNLP
30 40 50 60 70 80

9087135 MNYQDFISITERQEPALASGNTAINTVSVTGATLSALGVGASFTINFYI-KITGLLW
40 50 60 70 80 90

cry2ab2_820. PFGSNLMQDLRETEKFLNQINLNTTLARVNAELTGLQANVEENRQVDNFLN-PNENA
90 100 110 120 130 140

9087135 PHDK-NIWDEFMEVEETLIEQIEQYARNKALELGLGNLTIYQOALEDWLNPDPA
100 110 120 130 140 150

cry2ab2_820. VPLSITSSVNTMQDLNRLNLPQFMQMGYQLLLPLFAQAANLHLSFIRDVILNADENGIS
150 160 170 180 190 200

9087135 TITRVIDRFRILDALFESYMPFRVAGVEIPLLTVAQAANLHLLALRDSLYGDKWEFT
160 170 180 190 200 210

cry2ab2_820. AAILRTYRDYIKNYTRDYSNYCINTYQSAFKLNRLHDMV--EFTYMFNLNVEFYS
210 220 230 240 250 260

54112021 FTRNYGITTFPIINSYNFANGSDVQINTRNSLTSLAFENALFGITRAQFGPGGYSVTQR
370 380 390 400 410 420 430 440 450


```
CRY2AB2_820. YFI--RNISG---VPLVRNEDLRRLHYNEIRNTASPGTGGARAYWVSHN-RKNNI
      430      440      450      460      470
54112021 TLLCEQVNSTDELPDPPIRS-YSHRLSHITSYLH-----RVFTIDGNNGYSL
      460      470      480      490      500
CRY2AB2_820. HAVHENGSMIHLAPNDVTGTFISPIHATOVNNOQTRTFISEKFG-NQGDLSRFEQNNITAR
      480      490      500      510      520
54112021 PTVWTHRDVDLT-NTITADRIHLPLIKSNQSRGLPVKPGFTGGDLRSSDDAIVS
      510      520      530      540      550
CRY2AB2_820. YTLRGNG----NSYNLXLRVSSIGNSTIR-VTINGRVYATATNVNTITNDGVNDNGARFS
      540      550      560      570      580
54112021 IIGVSAGALPTQQRIRVRVASVDVITIRVHRNTHSLGIGTILSRMTMSGEESRYESYR
      570      580      590      600      610
CRY2AB2_820. DIN-IGNVASSNSDVPLDINVTLSNGTQFDLMNIMLVPTNISPLY
      600      610      620      630
54112021 TVDVTNFRSNSSEQIRIVTEGLRANGQLYDLSLEFIPNPTREAEDELEAKKAVASL
      630      640      650      660      670
54112021 FTRTRDGLQANVTDYQVDRAANLVLCISDEQVADHKMMLLEAVRAAKRLSRERNLLQDPD
      690      700      710      720      730
CRY2AB2_820.pep
SW:8928039
8928039 description="PESTICIDIAL CRYSTAL PROTEIN CRY26AA (INSECTICIDAL
DELTA-ENDOTOXIN CRYXXVIA(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA CRYSTAL
PROTEIN)." library=NA species="Bacillus thuringiensis serovar finitimus"
source="swissprot_prot" version=NA type=PRT
SCORES      Initl: 156      Initn: 156      Opt: 317      Z-score: 355.4 E(): 1.7e-11
>>SW:8928039
      Initn: 156      Initl: 156      Opt: 317      Z-score: 355.4 expect(): 1.7e-11
Smith-Waterman score: 317;      24.5% identity in 216 aa overlap
(57-266:74-287)
CRY2AB2_820. PFSFQHKSLDTQKEWTEKKNHSLYLDPIVGTVASFL-LKKVGLVGRKILSELNLI
      30      40      50      60      70      80
8928039      LOSYGFENMDNFGSESEPFIDASGAINAAGVTGVLGFLVPFGALT--TFYQKLFGL
      50      60      70      80      90      100
CRY2AB2_820. PFGSTNLMDQILRETEKFLNRLNTDLARVNAELTGLQANVEEFNRQVDNFLNPNRN-
      90      100      110      120      130      140
8928039      FPNNTKQWEFMKQVEALIDEKISDAVRNKAISELQGLVNNITLYTEALEEWLENKENP
      110      120      130      140      150      160
CRY2AB2_820. AVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQANLHLSFTRDVLNADWGI
      150      160      170      180      190      200
8928039      AVRDLVLRWRLDGLDFEQMPFSAVKGFVLLLVYVYTAQANLHLSLRDAYIYGAEWGL
      170      180      190      200      210      220
CRY2AB2_820. SAATLRTYRDYLNKNTYRDYSNYCINTYQSAFKGL-NTRLHDWLE---FRTYMFNLNVEFY
      210      220      230      240      250      260
8928039      TPTNDQNHTELLRHAETIDHCVMWYNYIGLKQLENSDAKSWFQYNNRFRREMTLSLVDVI
      230      240      250      260      270      280
CRY2AB2_820. SIWSLFYQSLVSSGANLYASGSGPQQTQFTSQDWPFLYSLFQVNSNYVINGFSGARL
      270      280      290      300      310      320
8928039      ALFPAYDKVMYPIPTNFQLTREVYTDVIGKIGRNDSDHWYSANAFSNNLESTLIRTPHV
      290      300      310      320      330      340
CRY2AB2_820.pep
NRAA:4583416
4583416 source="GENBANK_PROT" CRY26Aa1 protein [Bacillus thuringiensis serovar
finitimus][gi|8928039|sp|Q9X597|C26AA_BACTF Pesticidial crystal protein cry26Aa
(Insecticidal delta-endotoxin CryXXVIA(a)) (Crystalline entomocidal protoxin)
(131 kDa crystal protein)]
SCORES      Initl: 156      Initn: 156      Opt: 317      Z-score: 355.4 E(): 1.7e-11
>>NRAA:4583416
      Initn: 156      Initl: 156      Opt: 317      Z-score: 355.4 expect(): 1.7e-11
Smith-Waterman score: 317;      24.5% identity in 216 aa overlap
(57-266:74-287)
CRY2AB2_820. PFSFQHKSLDTQKEWTEKKNHSLYLDPIVGTVASFL-LKKVGLVGRKILSELNLI
      30      40      50      60      70      80
4583416      LOSYGFENMDNFGSESEPFIDASGAINAAGVTGVLGFLVPFGALT--TFYQKLFGL
      50      60      70      80      90      100
CRY2AB2_820. PFGSTNLMDQILRETEKFLNRLNTDLARVNAELTGLQANVEEFNRQVDNFLNPNRN-
      90      100      110      120      130      140
4583416      FPNNTKQWEFMKQVEALIDEKISDAVRNKAISELQGLVNNITLYTEALEEWLENKENP
      110      120      130      140      150      160
CRY2AB2_820. AVPLSITSSVNTMQQLFLNRLPQFMQGYQLLLPLFAQANLHLSFTRDVLNADWGI
      150      160      170      180      190      200
4583416      AVRDLVLRWRLDGLDFEQMPFSAVKGFVLLLVYVYTAQANLHLSLRDAYIYGAEWGL
      170      180      190      200      210      220
CRY2AB2_820. SAATLRTYRDYLNKNTYRDYSNYCINTYQSAFKGL-NTRLHDWLE---FRTYMFNLNVEFY
      210      220      230      240      250      260
4583416      TPTNDQNHTELLRHAETIDHCVMWYNYIGLKQLENSDAKSWFQYNNRFRREMTLSLVDVI
      230      240      250      260      270      280
CRY2AB2_820. SIWSLFYQSLVSSGANLYASGSGPQQTQFTSQDWPFLYSLFQVNSNYVINGFSGARL
      270      280      290      300      310      320
4583416      ALFPAYDKVMYPIPTNFQLTREVYTDVIGKIGRNDSDHWYSANAFSNNLESTLIRTPHV
      290      300      310      320      330      340
CRY2AB2_820.pep
NRAA:2815886
2815886 source="GENBANK_PROT" delta-endotoxin [Bacillus thuringiensis]
SCORES      Initl: 156      Initn: 257      Opt: 313      Z-score: 355.1 E(): 1.7e-11
```



```

>>NAME 2815886
init: 257 init1: 356 opt: 313 Z-score: 355.1 expect(): 1.7e-11
Smith-Waterman score: 917; 92.1% identity in 580 aa overlap
(57-592:64-594)

cry2ab2_820. PFSQNKSDTYQKFTATKANKNSHSLADPMTGTVASFLKGVSLGKRILSENLRLIF
2815886 LOTVGGDYTDRLINLNSVSKDYQUGINIVBELSLFFGFPSSQW-VTVYTYLLNSLW
cry2ab2_820. PSGSTNLMQDILRETEKELNGLNLDTLAFDAEELGLOANVSEFFNOVDNFN-PRRHA
2815886 PDDNSVMDAFMERVEELIDOKISENKGALDDDDGJGVANLYVEMADEMLNRPNGAR
cry2ab2_820. VPLSITSVNTMOQLNRLFOFOM---GGYQLLDLPERKQANHLSEITVDVNLSE
2815886 ASL-VSQRFNILDLSLTFMFSPSGSGSONATILLIPEVYAAANHLKLLKDDKQAR
cry2ab2_820. WCISAAILRYDYLKNYTRDYSNYCINTYQSFAKGL-NTRLHDMLEFRTMELNLEFV
2815886 WGLNQTOIDQFHSROOSLTQTYTHCHVTAYNDGLAELGKTGTAESWFKYINQYRRETFTR
cry2ab2_820. SIWSLFKYQSLVSSGANLYASGSGPOOTQ---SFTSDQWPE---FLYSLFQ
2815886 DLVALFPYVNL-----ROYPDGNTROLTEVYTDPIADPLEQPTTLCLCRSWYNINPAFR
cry2ab2_820. VNSNVLNFGSGARLSNTFPNIVGLP---GSTTHALLAARVNY-----SGGI
2815886 NHLNFSVLNSLRPHLPERLSNLQLVLVNYQTNGSAWRGKRVHYHLHSSITQEKSYGL
cry2ab2_820. SSGDIGASPNQFN-----CSTFLPPLLTFFVRSMLDSSDREG-VATVNNWQTESF
2815886 LSDPVGANINVQNDIYQIISQVNSAPVGSY-SVMDTFYLSQQVSGISGY-----
cry2ab2_820. ETTGLRSAGTARGNSYFPDYFIRNISGPLVAVNEDLRPLHYNEINTASPSGTPG
2815886 -TQQGITPAVCLQORNSIDELPSL---NPEGD--IIRNYSKRLS-HITQIRFQATQSGSFS
cry2ab2_820. GARAYVSVNHRKNTHAVHENGSMIHLANDYGTFTSPIAHQVNNQTRTFISEKGFN
2815886 TVSANLFTCVWTHRDVDL--DNT-----ITANQITOLPL--VKAVELSSGATVVKGGPGET
cry2ab2_820. QGDSLRFPQNNVTARYTLRGNNSYNLVAVSSIGNSTIRVTINGRYVYVNTNITNN
2815886 -GDVIR--RTVIG-----GFCA-----IRVSYGLTQIRVIRFVASTIDDFDFVTRG

```

[illegible]

Study No. 06-01-62-01
MSL No. 20307
Page 222 of 361

[illegible]

8469157 LSPVYVANTVNDIVYIIISQVNFASPVGSSY-SVWDTNFFYLSSGVGSGY-----
400 410 420 430 440 450

cry2ab2_820. ETLGLRSGAFARNGSNYFPLVNRNEDLRPLHNEIRNIASPSGPG
410 420 430 440 450 460

8469157 -TQSTPNCLOQASDEKPSL---WREGS--IIRNYSHELS-HITQYRFQATGSGFS
410 420 430 440 450 460

cry2ab2_820. GARAYVSVHNEKNIHAHENGSMTRNADYTGFNKSPHATQVNNQTRFISEKEGN
470 480 490 500 510 520

8469157 TVSANLPCTCVWTHRDVLD--DNT---ITANQTLPL--VNAEYSSGATVVGPGFTG
510 520 530 540 550

cry2ab2_820. QGSLRFEQNNTIARYTLRNGNSYNLYLRKSSNSITPRTINGRVYATNTNTTND
530 540 550 560 570 580

8469157 -GDVIR--RINTG-----GFGA-----IRSVTQNTQTRIRFRVSTIDPFFVREG
560 570 580 590 600

cry2ab2_820. GVDNGARTSDINIGNVASSNSDVLIDINVLNISTQFDLMNIMPVNIISPL
590 600 610 620 630 640 650 660

8469157 GTTINFRTRTMWREGSRYESYRTVEFTTPTFTQODIIRTSIOGLSSNGEYLDRI
610 620 630 640 650 660

cry2ab2_820.pap
NRAA:62001772

62001772 source="GENBANK_PROT" CryII toxin [Bacillus thuringiensis]

SCORES Initl: 205 Initn: 241 Opt: 308 Z-score: 350.1 E(): 3.3e-11
>NRAA:62001772
Initn: 241 Initl: 205 Opt: 308 Z-score: 350.1 expect(): 3.3e-11
Smith-Waterman score: 323; 21.7% identity in 545 aa overlap
(57-574:70-586)

cry2ab2_820. PFSQHKSLDTQKQEWTEWKKNNHSLYLDPIVGTVASFLKKKVLGVKRIILSELNLI
30 40 50 60 70 80

62001772 EDCLKISEYENVEPFSASTIQTGISTAGKILGTGLGVPPAGVASLYS-FILGEL----W
40 50 60 70 80 90

cry2ab2_820. PSGSTINMQDILRETEKFLNQLRNTDLARVNAELTGLQANVEEFNRQVDFLNPRNAV
90 100 110 120 130 140

62001772 PKGK-NQWEIFMEHVEEIIQKISTYARNKALTDLKGDLAVVHESLESWSVGNKNTNR
100 110 120 130 140 150

cry2ab2_820. PLST-SSVNTMQOLFNLPLFOFOMQCYQLLLPLPAQANLHLSIFRDVILNADEMGIS
150 160 170 180 190 200

62001772 ARSVKSYIALELMFVQKLPFSFVSGEEVPLPIYAQANLHLLURDASIFGKEWGLS
160 170 180 190 200 210

cry2ab2_820. AATRTYRDYLNKNTYDSNYCINTYQSAFKGL-NTRLHDML---EFTYMLNVEFYVS
210 220 230 240 250 260

62001772 SSEISTYNRQVERAGDYSDHCVKWYSTGLNNLRGNAESWVRVNOERKQNTLMLVLDLVA
220 230 240 250 260 270

cry2ab2_820. IWSLFKQSLVSSGANL-----YASGSGP-QQIQSFSTQDWFFLYSLFQVNSYVLNGFS
270 280 290 300 310

62001772 LFPSYDLVYPIKITTSQTLREYVDAIGTGHVHPNASTTW---YN---NNAPSFSTIE
280 290 300 310 320

cry2ab2_820. GARLNTFPMIVGLPGSTTTTHALLA-----ARVNYSGG-ISSGDIGASFPNQFNCS--
320 330 340 350 360

62001772 SAVVRN--PHLLDFEQQVTVISLSRWKSNQYMNWGGHRLFEFTIGCM-LNTSTOGSIN
330 340 350 360 370 380

cry2ab2_820. TFLPPLTTPFVRWLDGSDREGVAIVTNMQTESF-ETTLGLRSGAFTARGNSNYFPDYF
370 380 390 400 410 420

62001772 TSINPVLTPFTSRDVRVYRTESLAGNLFLTQPVNGVRVDFHMKVTHPIASDNFYFPGY-
390 400 410 420 430 440

cry2ab2_820. IRNISGVPLVRNEDLRPLHNEIRNIASPSGTFGAGAYVSVHNEKNIHA-VHENG
430 440 450 460 470 480

62001772 ---AGICTQDQSENELPPTTQPTQNTYESYHRL--SHIGLISASHVKALVYSWTHRSA
450 460 470 480 490

cry2ab2_820. SMIH-LAPNDYTGFTISPITHATQVANNQRTFISEKFGNCGDSLRFEQNNTIARYTLRNG
490 500 510 520 530 540

62001772 DRNTNIENSITQPL--VKANLSSGAAVVRGPGFTG-GDILR--RINTGTGDIRVNI
500 510 520 530 540 550

cry2ab2_820. NS-----NLVLRVSSIGNSTIRVTINGRVYATNTNTNDGVNDNGARFSDINIGNV
550 560 570 580 590

62001772 NPPFAQRYNRLRYASTTIDIQHTSINGKAINQGN
560 570 580

cry2ab2_820. VASSNSKPLDINVLNNSQFALNMIMLVPTNISPLY
600 610 620 630

cry2ab2_820.pap
NRAA:62288329

62288329 source="GENBANK_PROT" cry2ab2 protein [Bacillus thuringiensis]

SCORES Initl: 159 Initn: 159 Opt: 304 Z-score: 340.6 E(): 1.1e-10
>NRAA:62288329
Initn: 159 Initl: 159 Opt: 304 Z-score: 340.6 expect(): 1.1e-10
Smith-Waterman score: 312; 25.6% identity in 536 aa overlap
(57-566:76-563)

cry2ab2_820. PFSQHKSLDTQKQEWTEWKKNNHSLYLDPIVGTVASFLKKKVLGVKRIILSELNLI
30 40 50 60 70 80

62288329 LQTYGDYTGSLINPLNSINTRDVLQITIGTVGVLFGLGVPPAGVLY--TFYFELNLI
50 60 70 80 90 100

cry2ab2_820. FFGSGTINMQDILRETEKFLNQLRNTDLARVNAELTGLQANVEEFNRQVDFLNPRNAV
90 100 110 120 130 140

62288329 WPTNNAYWEAFMAQVVELIDQRIISDOVVNRNALDGLGHDYNYEYLAALAEWLDPRNGA
110 120 130 140 150 160

Study No. 06-01-62-01
MSL No. 20307
Page 224 of 361

[illegible]

Study No. 06-01-62-01
MSL No. 20307
Page 225 of 361

```
cry2ab2_820. STTHALLARVNYSGGISGDIAGSPFNFCNSTFLPPLLTFFVRSLWDSGDREGVA
      |||::||| | |||||
MYNHPLIYGFQV--GYSSSNINKITTIINLGSYDKXIYSINTESRNLVOGSTTFDKINF
    370   380     390       400         410          420

cry2ab2_820.pep
NRAA:8928030

8928030 source:"GENEBANK PROT" Pesticidal crystal protein cry27Aa (Insecticidal
delta-endotoxin CryXXVII(a)) (Crystalline entomocidal protoxin) (94 kDa crystal
protein)[gi|3689049|dbj|BAA82796.1] 94kDa mosquitocidal toxin [Bacillus
thuringiensis]

SCORES Initl: 184 Inltm: 184 Opt: 295 z-score: 332.8 E(): 3e-10
>>NRAA:8928030
Initl: 184 Inltl: 184 opt: 295 Z-score: 332.8 expect(): 3e-10
Smith-Waterman score: 295; 23.% identity in 353 aa overlap
(15-355:49-386)
```

```

civ2ab2_020.      10      20      30      40
MQAMONSVINSGRTTICDAYN-VAADHPFSQHKSLDTQKKEWT
: : : : :
NCHMSNGVPRHPLANDPQMYLNHAYKDWLSMCKNPNVGLIPESFEWTLNGTVAALIT
20      30      40      50      60      70

```

50 60 70 80 90 100
 CY2AB2-20. EWKNNHSLYLDPIVGTVASFLKKVGSVGRKRIJSELRNIPFSGSTNIMQDLRETEK
 50 60 70 80 90 100
 NSVNIAGILVTPV-SVTAGIITVLGA-GAALLAGITPLIWEATDNTFNKTIIDATEV

77
C#42a3_820.. FLNGLMIDTDFARNAELTGLOANVEFNRQDNFL-IPNSRNAVPISITSSVNTWQQFLF
::: : |::: : |||: : |::: : |::: :
LNKLSLRKTKANKIDSLOOLYYQNLAENKKKPNDASARNVTSTRGQIVNAEFV

8928030

[illegible][illegible]

~~cry2ab2_820. ---GANIYASGGPOQTOFTSQDWPPELYSLFQVNSNTWNGPFGSGLSNSTFNFTVSJLP
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
ELIRTYITDVGNVRNEPKSIHN--POLGFRRLEOKMLHYE-YQSOPFLSGCN-PRR
320 330 340 350 360~~

cry2ab2_820. STTHALLAARNYSGYSGSDIGASPNFNCSTIFPLITPFVSRMLDGSBEGVAA
 340 350 360 370 380 390
 : : : : :
 MYNHPLIYGFVQ--GYSSNNIKITTLNGDYKIYSINTESRNLVQGSTTFDYNF
 370 380 390 400 410

Study No. 06-01-62-01
MSL No. 20307
Page 226 of 361

	40	50	60	70	80	90
(a) $\frac{1}{n} \sum_{j=1}^n x_j$	1.00	1.00	1.00	1.00	1.00	1.00
(b) $\frac{1}{n} \sum_{j=1}^n y_j$	1.00	1.00	1.00	1.00	1.00	1.00
(c) $\frac{1}{n} \sum_{j=1}^n z_j$	1.00	1.00	1.00	1.00	1.00	1.00
(d) $\frac{1}{n} \sum_{j=1}^n w_j$	1.00	1.00	1.00	1.00	1.00	1.00
(e) $\frac{1}{n} \sum_{j=1}^n v_j$	1.00	1.00	1.00	1.00	1.00	1.00
(f) $\frac{1}{n} \sum_{j=1}^n u_j$	1.00	1.00	1.00	1.00	1.00	1.00
(g) $\frac{1}{n} \sum_{j=1}^n t_j$	1.00	1.00	1.00	1.00	1.00	1.00
(h) $\frac{1}{n} \sum_{j=1}^n s_j$	1.00	1.00	1.00	1.00	1.00	1.00
(i) $\frac{1}{n} \sum_{j=1}^n r_j$	1.00	1.00	1.00	1.00	1.00	1.00
(j) $\frac{1}{n} \sum_{j=1}^n q_j$	1.00	1.00	1.00	1.00	1.00	1.00
(k) $\frac{1}{n} \sum_{j=1}^n p_j$	1.00	1.00	1.00	1.00	1.00	1.00
(l) $\frac{1}{n} \sum_{j=1}^n o_j$	1.00	1.00	1.00	1.00	1.00	1.00
(m) $\frac{1}{n} \sum_{j=1}^n n_j$	1.00	1.00	1.00	1.00	1.00	1.00
(n) $\frac{1}{n} \sum_{j=1}^n m_j$	1.00	1.00	1.00	1.00	1.00	1.00
(o) $\frac{1}{n} \sum_{j=1}^n l_j$	1.00	1.00	1.00	1.00	1.00	1.00
(p) $\frac{1}{n} \sum_{j=1}^n k_j$	1.00	1.00	1.00	1.00	1.00	1.00
(q) $\frac{1}{n} \sum_{j=1}^n j_j$	1.00	1.00	1.00	1.00	1.00	1.00
(r) $\frac{1}{n} \sum_{j=1}^n i_j$	1.00	1.00	1.00	1.00	1.00	1.00
(s) $\frac{1}{n} \sum_{j=1}^n h_j$	1.00	1.00	1.00	1.00	1.00	1.00
(t) $\frac{1}{n} \sum_{j=1}^n g_j$	1.00	1.00	1.00	1.00	1.00	1.00
(u) $\frac{1}{n} \sum_{j=1}^n f_j$	1.00	1.00	1.00	1.00	1.00	1.00
(v) $\frac{1}{n} \sum_{j=1}^n e_j$	1.00	1.00	1.00	1.00	1.00	1.00
(w) $\frac{1}{n} \sum_{j=1}^n d_j$	1.00	1.00	1.00	1.00	1.00	1.00
(x) $\frac{1}{n} \sum_{j=1}^n c_j$	1.00	1.00	1.00	1.00	1.00	1.00
(y) $\frac{1}{n} \sum_{j=1}^n b_j$	1.00	1.00	1.00	1.00	1.00	1.00
(z) $\frac{1}{n} \sum_{j=1}^n a_j$	1.00	1.00	1.00	1.00	1.00	1.00

[illegible][illegible]

```

cy2ab2_820.  AAUURVRYDLKKNYDRSDYSCYINCYOSAFKUNLTHLHML-----EFTYMFUNLVEYYS
              : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
8469158      QNNIEYNRQKKRISEYSDHCTKWYNSGLSRINGSTYEQWINTNFRFRMILMALDLVA
              220   230   240   250   260   270

```

cry2ab2_820. IWSLFKYSQVLLSSGANLVSAGSGPQQTQFTSQDMPFFYLSLFLQNVNVLNGFSGARLUS
 ::
 8469158 VPFPHDPRRYSMETSLQTLREVTYDPSVLSINSPDIPGFSQSMENAIRPHLVLDYLDDEL
 280 290 300 310 320 330

cry2ab2_920.pep
NRAA:22122188
22122188 source="GENBANK_PROT" cry8 [Bacillus thuringiensis serovar gallerie

```

SCORES      Init1: 163      Initn: 195      Opt: 297      z-score: 332.7 E(): 3.1e-10
>>NRPA: 22122188
      initn: 195      init1: 163      Opt: 297      z-score: 332.7      expect(): 3.1e-10
      Smith-Waterman score: 326;      23.0% identity in 617 aa overlap
      (56-634; 86-668)

```

cy2ab2_820. DPFSFQHKSLDTVQKEWTWKQNNHSLYLDPVGTVASFLKKGYSVUGKRIILSELRNLI
22122188 LFGNPETFISSTVQTGIGVQGVILGVPFPAQGIASFPYVQL-
60 70 80 90 100

```

cry2ab2_820. FPGSTNLMODILRETEKELFORNLTTTLARVN-ASLTQLQANVEEENROVDNFLPNRNN
|||||: : : : : ||||: : : : : ||||: : : : : ||||: : : : : ||||: : : : : ||||: : : : :
WPSSTVSVMEMIKVEDIYDOKIT-TSVSRKTALAGLQSLGDLGVTKSLKNWLK-NRN
110      120      130      140      150      160      170      180      190      200

```

```

22122188      DTRASVVVTOYI-ALELDFNAKIPSAISQGEVPLLSVYQAANLHLLLRDASIFGAE
170          180      190      200      210
          220      230      240      250
WGISAATLRTVBDVILKNVETSYNSVNCVTSVASP---KGLNT---HMDLREPTVMFL
rrv2ab2 820

```

22122188
WGTFGEISFYDQVTRTAQYSDYCVKWNTGLDKCTNAASLKVH--OFRRMELT
220 220 230 240 250 260 270 280 290 300

cry2ab2_820.pep
NPAA:22122188

22122188 source="GENBANK PROT" crv8 [Bacillus thuringiensis serovar galleriae]

```

SCORES      Init1: 163      Initn: 195      Opt: 297      z-score: 332.7 E(): 3.1e-10
>>NRPA: 22122188
      initn: 195      init1: 163      Opt: 297      z-score: 332.7      expect(): 3.1e-10
      Smith-Waterman score: 326;      23.0% identity in 617 aa overlap
      (56-634; 86-668)

```

cy2ab2_820. DPF^SFQ^HK^SLD^TVQ^KEW^TE^WK^NQ^NH^SY^LY^LQ^IP^VT^VAS^LK^VY^SLG^RK^IL^SERN^LI
22122188 L^FQ^NP^ET^IF^SS^ST^VQ^IG^IV^QV^LG^VY^SF^IQ^L-----
60 70 80 90 100

```

cy2ab2_820.  FPGSTNLMODIRETEKFLNRLNTTLARVN-ASLTQLANVEEFNRQVDNFLPNRNN
|||||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : : |||: : : : :
WFSSTVSVMIMKQVEDLIDOKI-TSIVAKTALAGLOGLDGLGVTKQSKJWLKE-NRN
110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300

```

```
cry2ab2_820. ---AVPLSITSTVNTWQQQLFNRLPQFMQGYQLLLPFLUFAQAANHLSTROVINADAE
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
DTRASVVVTQYI-ALEDFVAKIPSAIGSEVPVLSVYVAQAANHLHLLLRDARSIFGAIE
```

```

cry2ab2_020. WCISAAUUYRYDLYKNYTRDYNSVNCINTQSAF---KGNL-----RLHDLMEFRYMEL    210      220      230      240      250
|||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||:::||
WGFTGEISTFYDRQVTRAQAQSDYCVKWNTGLDKLKGTNAASLVKH---GFRREMTL    260      270

```

260	270	280	290	300
-----	-----	-----	-----	-----

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 227 of 361

cry2ab2_820. NVFEXVSIWLSKYQSLVSSGANL-YASGSGP-----QQTQFTSQDWPFL--YSLFQVFN
22122188 LVLQAVLQVNYDTRTRPRTAQLTREVYDPIVFNRETSIGGFCRRWSLNSDISFSEVE
cry2ab2_820. SNVYNGSGRISAT--FENVIGFSTTHALLAARVNYSGGSGDGIASPFQNFN
22122188 SAVIRSHLPRLISSEIEFTYTRAPLNNTEY--LQVWGHKIKYNTN-ASSALEENYG
cry2ab2_820. CSTF---LPLLTFFVRSMDSQDREG--LQVWGHKIKYNTN-ASSALEENYG
22122188 TITSNKIKYDNLANKDIFQVRSGLRSMANVYQVGFYFASP-TLLDNITGSSVGGFTY
cry2ab2_820. YFPDYFIR---NISGVPLVW-RNEDLRRLPHYNE--NTASPSGTPGGARAYMVSVHNEK
22122188 SKPHTTMQVCTQNTVIDEIPPENEPLSKG-YSHRLSHITS-SF-SKNA--S-SGARY
cry2ab2_820. NNHIA---VHNGSMHLPNDYGTFTTSPHATQVNNQTRTFISEKFGNCGDSFEQN
22122188 GNLPPVFAWTHRSADVNTVYSQKIT-QIPVVKHATLSVSGTVIKGPGFTG-GNILLRTSS
cry2ab2_820. NTATRYTLRGNG--NSYNLYLRVSSIGNSTIRVING-RVYATVNTVNTTNDGVNDNG
22122188 GLPATSYSVKSPLSQRYARIRYASTTNLFLVTSIGTFIYSI-NVNTKWK-GDGLTF
cry2ab2_820. ARFSDINTGNVASSNSDVPLOINV-TLNSGTQFDLMNIMLVPTNISPLY
22122188 NTFDLATIGTATFNSYSDSLTVGADSFAGSGEVYVVKFELIPVNAPEAEEDLDVAKKA
22122188 VKNLVECLSDELYENEKELMDQAVKEKLVQARNLLODTGFNRINGENGWGTSGTGLEVA
cry2ab2_820.pep
NRAA:45593719
45593719 source="GENBANK PROT" insecticidal protein Cry9Ec (Bacillus
thuringiensis serovar galleriae)
SCORES Init1: 148 Initn: 148 Opt: 294 z-score: 329.3 E(): 4.8e-10
>>NRAA:45593719
initn: 148 init1: 148 opt: 294 z-score: 329.3 expect(): 4.8e-10
Smith-Waterman score: 305; 23.7% identity in 617 aa overlap
(57-632:76-655)
cry2ab2_820. PRSFQHSKLDIVQEWENTEMKNNHSLYLDPIVGTVASFL-LKKVGLACKRLTSELNLI
45593719 LQTYGDYTGSLINPNLSINTNRDVLQGTGINIVGLVGLGVPAGQLV--TFYIFLNLQ
cry2ab2_820. NVFEXVSIWLSKYQSLVSSGANL-YASGSGP-----QQTQFTSQDWPFL--YSLFQVFN
22122188 LVLQAVLQVNYDTRTRPRTAQLTREVYDPIVFNRETSIGGFCRRWSLNSDISFSEVE
cry2ab2_820. SNVYNGSGRISAT--FENVIGFSTTHALLAARVNYSGGSGDGIASPFQNFN
22122188 SAVIRSHLPRLISSEIEFTYTRAPLNNTEY--LQVWGHKIKYNTN-ASSALEENYG
cry2ab2_820. CSTF---LPLLTFFVRSMDSQDREG--LQVWGHKIKYNTN-ASSALEENYG
22122188 TITSNKIKYDNLANKDIFQVRSGLRSMANVYQVGFYFASP-TLLDNITGSSVGGFTY
cry2ab2_820. YFPDYFIR---NISGVPLVW-RNEDLRRLPHYNE--NTASPSGTPGGARAYMVSVHNEK
22122188 SKPHTTMQVCTQNTVIDEIPPENEPLSKG-YSHRLSHITS-SF-SKNA--S-SGARY
cry2ab2_820. NNHIA---VHNGSMHLPNDYGTFTTSPHATQVNNQTRTFISEKFGNCGDSFEQN
22122188 GNLPPVFAWTHRSADVNTVYSQKIT-QIPVVKHATLSVSGTVIKGPGFTG-GNILLRTSS
cry2ab2_820. NTATRYTLRGNG--NSYNLYLRVSSIGNSTIRVING-RVYATVNTVNTTNDGVNDNG
22122188 GLPATSYSVKSPLSQRYARIRYASTTNLFLVTSIGTFIYSI-NVNTKWK-GDGLTF
cry2ab2_820. ARFSDINTGNVASSNSDVPLOINV-TLNSGTQFDLMNIMLVPTNISPLY
22122188 NTFDLATIGTATFNSYSDSLTVGADSFAGSGEVYVVKFELIPVNAPEAEEDLDVAKKA
22122188 VKNLVECLSDELYENEKELMDQAVKEKLVQARNLLODTGFNRINGENGWGTSGTGLEVA
cry2ab2_820.pep
NRAA:45593719
45593719 source="GENBANK PROT" insecticidal protein Cry9Ec (Bacillus
thuringiensis serovar galleriae)
SCORES Init1: 148 Initn: 148 Opt: 294 z-score: 329.3 E(): 4.8e-10
>>NRAA:45593719
initn: 148 init1: 148 opt: 294 z-score: 329.3 expect(): 4.8e-10
Smith-Waterman score: 305; 23.7% identity in 617 aa overlap
(57-632:76-655)
cry2ab2_820. PRSFQHSKLDIVQEWENTEMKNNHSLYLDPIVGTVASFL-LKKVGLACKRLTSELNLI
45593719 LQTYGDYTGSLINPNLSINTNRDVLQGTGINIVGLVGLGVPAGQLV--TFYIFLNLQ

cry2ab2_820. FPGSGTNLMQDILARETEKFLNQINLTDITLARVNAELTGLQANVEEFNRQVDNFLN-PNRR
45593719 WPTNNVNAWEAPMAQIEELIDQISQOVVNALDALTGIHDYNYEYLALEEWLERPNGA
cry2ab2_820. AVLSITSSVTMQQLFLNLPQF-QMGOYQ---LILLPLFAQAAHLHSFIRDVLNAD
45593719 RANLAFQRFEN-LHQLFQVQMPSPGSGPQSGSERDAVALLTVYQAQANLHLLLLKDAEIIYGA
cry2ab2_820. EWGISAATLRTYRDLYLNTRDYXNYCINTYOSAF---KGINTR-LHDMLEPRTYVFLNV
45593719 RWLNGOQINLFNAQQDRTQIYNHCVAIYNGLENLNGINTESWYNYHQFRREMTLMA
cry2ab2_820. FEYVSIWLSFKYQSLVSSGANLYASGSGPQQTQFTSQ---DMPFLXSLFQVNSYVL
45593719 MDLVA---LFPYVNL-----RQVPGANPQLTREIYTDVVPVFPANQGLCRRWRNPFY
cry2ab2_820. NGFSGARLNTFPNIVGLFGSTTHALLAARVNYSGGSGDGIASPFQNFNCSTFLPP
45593719 MTFS--ELENITFIRPHFLDLNLSLINSHRFPISSNPMYDWMYAGHTLRRSYMNSAVQED
cry2ab2_820. LLTPVRSMLDSSGDSRGVATVNTWQTESFETTLGLRSCAFTARG--NSNPPD-YFIRN
45593719 -----SPTSPSTRVINTGVNGTNRISTAVDFRSGLLGVYGVHRASFVPGGLFNGT
cry2ab2_820. ISGVPLVWEN-EDLRRLPHYNE--NTASPSGTPGGARAYMVSVHNRKNNIHAVHNGSM-
45593719 ISPNAROCNLMHDKQSPLEEE---NNGSPSHRLSHVTLFSLTLDQAGSIRNSGAVP
cry2ab2_820. -----HLAPNDYFTTIS--PAPATQVNNTRTFISEKFGNCGDLSRPEQNNTA
45593719 LYVWARQDIDLN-NTITANRITPLVWSSSTPAGTIVVNGPFTG-GDILRRTSAGTLG
cry2ab2_820. RYTLRNGNS-----YNLYLRVSSIGNSTIRVINGVATA-NVNTTNDGVNDNG-AR
45593719 --TIRVNSPLTORVRYFRYASTTDFNFFVING--TTVNNTRTFITNSQESR
cry2ab2_820. FSDINIGNVASSN-----SDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
45593719 YESVYTRFSTFNFNLOQDT-LRLTVQSFSSQGVYVVDREIIPVNPFPNAPAEEDLDVAKKA
45593719 KAVANLFTHRDGLQVNTDYQVDOQAANLVSCLSDEQYSHDKMLLLEAVEAARLSREN
cry2ab2_820. FSDINIGNVASSN-----SDVPLDINV-TLNSGTQFDLMNIMLVPTNISPLY
45593719 YESVYTRFSTFNFNLOQDT-LRLTVQSFSSQGVYVVDREIIPVNPFPNAPAEEDLDVAKKA
45593719 KAVANLFTHRDGLQVNTDYQVDOQAANLVSCLSDEQYSHDKMLLLEAVEAARLSREN

Study No. 06-01-62-01
MSL No. 20307
Page 228 of 361

```

100      110      120      130      140      150
cry2ab2_820.  RETEKFLNORLNTDTLARVNAELTGLQANVVEFNQRQVDNFL-NPNRNAVPLSITSVNTM
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
117529  AQEQLISRIEIEFARNOALSRLEGLSNLYKVVYVRAFSDEWKDPTNPALREEMRIQFNDM
      80      90      100      110      120      130
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
160      170      180      190      200      210
cry2ab2_820.  QQFLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVILNADEWGISAAATLRTYDYLK
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
117529  NSALITAIPLFRVQNYEVALSVYQAOANLHLSIRDVSVFGERMGYDTATINNRYSDLT
      140      150      160      170      180      190
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
200      210      220      230      240      250
117529  SLIHVTNHCVDITYNOGLRLEGRLSDWIIVNFRERQLTISVLDIVAFFNVDIRT---
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
280      290      300      310      320      330
cry2ab2_820.  SSGANLYASGSGPQGTQSTFSQWPLYSFLQVNSNTVNLVNGSFGARLSNTF-PNIVGLPG
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
117529  -----YPTQTATQLTRE-VYLDLPFPINENISPAASYPT-FSAAESAIIIRSPHLVDFLN
      260      270      280      290      300
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
340      350      360      370      380      390
cry2ab2_820.  STTHALLAARVNVSGYSSIGSSDGAPFNQFNCSFLPELLTPFVRSWLDGSGDREGVA
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
117529  SFTIYDLSLARVYWGSHLVNSFRGTITNLRISFLPYGREGNTERPVTITASPSVLPFRT
      310      320      330      340      350      360
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
400      410      420      430      440      450
cry2ab2_820. pep
NRAA:40280
40280 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|117529|sp|P19415|CryIIa BACTA Pesticidal crystal protein cryIIa
(Insecticidal delta-endotoxin CryIID(a))-(Crystalline entomocidal protoxin) (132
kDa crystal protein)

SCORES   Initi: 159   Initn: 183   Opt: 286   z-score: 320.1 E(): 1.6e-09
>>NRAA:40280
Initn: 183   Initl: 159   opt: 286 z-score: 320.1 expect(): 1.6e-09
Smith-Waterman score: 286;   26.1% identity in 287 aa overlap
(70-349;54-321)

400      50      60      70      80      90
cry2ab2_820.  KENTWKKNNHSLYLDIPVGTVASFLKKVQSLGYKRLSELNLIFFSGSTNIMODI-L
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
40280  GEERLETGNTVADISLGLINFLYNSVFPGGGFIVG--LLELWIGFISG-----QWDIFL
      30      40      50      60      70
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
100      110      120      130      140      150
cry2ab2_820.  RETEKFLNORLNTDTLARVNAELTGLQANVVEFNQRQVDNFL-NPNRNAVPLSITSVNTM
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
40280  AQEQLISRIEIEFARNOALSRLEGLSNLYKVVYVRAFSDEWKDPTNPALREEMRIQFNDM
      80      90      100      110      120      130
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
160      170      180      190      200      210
cry2ab2_820.  QQFLNRLPQFMQGYQLLLPLFAQANLHLSFIRDVILNADEWGISAAATLRTYDYLK
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
40280  NSALITAIPLFRVQNYEVALSVYQAOANLHLSIRDVSVFGERMGYDTATINNRYSDLT
      140      150      160      170      180      190
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```



```

290      300      310      320      330      340
cry2ab2_820.  SGQQQQTQFTSQDPFFYLSLQFVNSNVYLVNGSGARLSNTFFPNIWGLPGSTTTHALLA
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
TDIFTLNALQEQYGFTESSIIENSRKPLHPDYLGRGFETRIRLP--GYSCKGSFYVWSG
320      330      340      350      360      370
cry2ab2_820.  350      360      370      380      390      400
ARVNSGGIGSSGDIGASGFQNFQNCSTFLPELPLFFVRSWLDGSDREGVAIVNNQTES
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
:      :      :      :      :      :      :      :      :      :      :
NYVETRPSIGSNDITISPFYFGDKSTPEPTQKLSFDGQKVRTIANTDIAAFPDGKXIFGVV
380      390      400      410      420      430
cry2ab2_820.pep
SW:117324
1117324 description="PESTICIDIAL CRYSTAL PROTEIN CRY3BA (INSECTICIDAL
DELTA-ENDOTOXIN CRYIIIB(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (75 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar tolworthi"
source="swissprot" version="NA type="PRT

```

```

SCORES      Init1: 97      Intn: 97      Opt: 282      z-score: 319.7  E(!): 1.6e-09
>>>S1117324
>>>Init1: 97      Intn: 97      Opt: 282      z-score: 319.7  expect(!): 1.6e-09
>>>Smith-Waterman score: 283;      22.9% identity in 349 aa overlap
(40-360,334-389)

```

```

cry2ab2-q20: LLKVGSI70SKRI80LSER-----NLI90PSGS100TM110MOD120IL130RE140TE150KL160QR170LT180DL190
117324 UG200RI210G220-V230VG240PP250AA260LL270TS280F290SP300EA310IP320SD330-D340E350W360K370AF380MA390Q400VE410LD420IK430EE440Y450AK460SA470KA480

```

[illegible]

```

cry2ab2_820.  QGYGLLELPLFAQAANLHLSFRVNLNASEWGISATLHNVRYLNSYDLYNSVNCINT
               : : : : : | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :
SKFVELFLPTYAQAANTHLLLLKDAQVFGWGYGSEDIHFFYRQLKTCQSTDMCNVW
117324         200      210      220      230      240      250

```

```

cry2ab2_820.  YQSAFKGNTLRHDLML---BFTYMFANFYEXVSIWLEFKQSLNVSSMGLTGG---
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
YNVGINSLSRGSTYDAWVKFKFRREMTLTIVDLIVLFPFYDVR--LASKKQKTELVDHIE
117324          240      250      260      270      280      290      300

```

[illegible]

cry2ab2_820. ARVNVGGSSGSDIGAGFPNQFNCSFELPPLLPFRSMWLDGSGREGVAIVTWQTES
117324 NYVERPSIGSNDITTSFPYGDKSIEPIQKLSFDGQVKYRTIANTIDIAAPPDGKIYFGVT
crys2ab2_820.pap
NRAA:15721993
15721993 source="GENBANK_PROT" crystal protein [Bacillus thuringiensis serovar
yunnanensis]
SCORES Initl: 159 Initn: 226 Opt: 286 z-score: 319.7 E(): 1.6e-09
>NRAA:15721993
initn: 226 initl: 159 opt: 286 z-score: 319.7 expect(): 1.6e-09
Smith-Waterman score: 288; 24.2% identity in 252 aa overlap
(40-266:39-287)
crys2ab2_820. ARVNAELTGLQANVEEFNRQV-DNFLNPNRAVPLSITSSVNTWQQLNRLNPQFOMGY
15721993 ANAELEGVHNAILYQDAVCDWKODPTNAQLKEQLRIQYIATNTVIESRPFVGRG
crys2ab2_820. QLLLELPLFAQANLHLSFIRDVILNADWEGISAATLRTYRDYLNKNTYRDSNYCINTYQS
15721993 EVPLLSYVQAANLHLHLKDGQVQGEWGMSATVDFYSYLKSDIEITYTYNCIDWYN-
crys2ab2_820. AFKGLNTRLHD-----MLSEFTYMLNVEFYVSTWSLFXQSLLVSSGANLYASGS
15721993 --KGLSDSIESEPTWNGWNTFNFRDMLMWLDLVSIMPTYDFRYPRLPTKSQLTREL
crys2ab2_820. GPOQTGSETSDWPFYLSLFQVNSVNLGFGSGARLSNTFNIVGLPGSTHTHALLAARV
15721993 TOAIGSYKSVFPLPPSPFRWLRETEFFLRDSQDAEQFAGQOGVQYLTDTTLIRPPV
crys2ab2_820.pap
NRAA:15721993
15721993 source="GENBANK_PROT" cancer cell-killing Cry protein parasporin-3
[Bacillus thuringiensis]gi|51090228|dbj|BAD35157.1| cancer cell-killing Cry
protein parasporin-3 [Bacillus thuringiensis]

SCORES Initl: 110 Initn: 139 Opt: 283 z-score: 319.2 E(): 1.7e-09
>NRAA:51090232
initn: 139 initl: 110 opt: 283 z-score: 319.2 expect(): 1.7e-09
Smith-Waterman score: 291; 27.2% identity in 268 aa overlap
(8-251:12-268)
crys2ab2_820. MQAMDNSVLNSGRITICDAVNAADHPFQFQHSKSLDTVQKEWTEWKNHSLYL--
51090232 MNQCNNGVEVLNSGKGYCOPRYPPFAQAGS-ELQNMG--YKEMNMCTSGDPTVLGE
crys2ab2_820. -----DPIVGT--VASFLK---KVGSLVGRKILSELRLNLIFFPSGSLNMQDILRET
51090232 GYSADVRDAVITSINTASYLLSVPPPPAGVAAG--ILGALLGLLWPTNTQAVWEAFMTIV
crys2ab2_820. EKFLNQRLNTDLIARVNAELTGLQANVEEFNRQV-DNFLNPNRAVPLSITSSVNT
51090232 EALINQKLDYARSAKISSELNGLKNVLELYQDAADWNNENPGDLNKNRV-LTEFRNVNG
crys2ab2_820. WQQLFLNRLPQFOMGYQQLLLPLFAQANLHLSFIRDVILNADWEGIS----AATIRTY
51090232 H---FENSMPSFAVRNFEVNLVYVYAAANLHLLLRDAVKEFGEGWMSDTPGAERDDMY
crys2ab2_820. RYLNKNTYRDSNYCINTYQSAAFGLNTRLHDMLEFTYMLNVEFYVSTWSLFXQSL
51090232 R-RLRSRTIYTDHCVTNTYNOGLQAKSLQANVSDYSRYPTQYNQSGSGESYREAKEYR
crys2ab2_820. VSSGANLYASGSGFOQTGSETSDWPFYLSLFQVNSVNLGFGSGARLSNTFNIVGLPG
51090232 GTENWNLNFAFRDMLTILVDIIAQFPTYDPGLYSRPVKSELTREVTYDITRGTWRSAN
crys2ab2_820.pap
NRAA:51090236
51090236 source="GENBANK_PROT" cancer cell-killing Cry protein [Bacillus
thuringiensis]
SCORES Initl: 110 Initn: 139 Opt: 283 z-score: 319.2 E(): 1.7e-09
>NRAA:51090236
initn: 139 initl: 110 opt: 283 z-score: 319.2 expect(): 1.7e-09
Smith-Waterman score: 306; 22.3% identity in 703 aa overlap
(8-635:12-684)
crys2ab2_820. MQAMDNSVLNSGRITICDAVNAADHPFQFQHSKSLDTVQKEWTEWKNHSLYL--
51090236 MNQCNNGVEVLNSGKGYCOPRYPPFAQAGS-ELQNMG--YKEMNMCTSGDPTVLGE

51090236 YQIVTALNNSSVVTSEFCMGIGLTRCGVNLWNNGNLTQKRFVINGDQNAFKPTSP
700 710 720 730 740 750

crv2ab2_820.pgp
SW:8469154

8469154 description="PESTICIDIAL CRYSTAL PROTEIN CRY1GB (INSECTICIDAL DELTA-ENDOTOXIN CRY1GB) (CRYSTALLIN ENTOXICIDAL PROTOXIN) (I33 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar wuhanensis" source="swissprot_prot" version="NA type="PRT

SCORES Init1: 191 Initn: 191 Opt: 285 Z-score: 318.9 E(): 1.0e-09
>>SW:8469154
initn: 191 init1: 191 opt: 285 Z-score: 318.9 expect(): 1.0e-09
Smith-Waterman score: 301; 22.4% identity in 577 aa overlap
(81-634:58-598)

crv2ab2_820. SLYLDPVIVGASFLVSLKKVSGLVGKRILSELRLNLPFSGSNLMQDLRETKFLNQRLN
60 70 80 90 100 110
8469154 FSSEQVAEHLKTRILLLENPLGGSAFGLDINGIFNEDQSAFLRQVEELINQRLT
30 40 50 60 70 80
crv2ab2_820. TDTLARNVAELTGLQANVEEFNRQVDNFLN-PNRNAVPLSITSSVNTMQQLFLNRLPQFQ
120 130 140 150 160
8469154 EFAPGQAIQRLVGVGRSDEYITALKEWENDPNPASKERVTRFRITTDALLTGVLMA
90 100 110 120 130 140
crv2ab2_820. MOGVOLLRLAFARANDHLSTIRVILNADWGIISAATIRTYRDYLNKNTRYSNYNCIN
170 180 190 200 210 220
8469154 IPGSLAIVYVQASNDLHALLRDVAFVGGRMGLTQTNIDPLVSLRKNISRDYTNHCVR
150 160 170 180 190 200
crv2ab2_820. TVQSFKNRNLRLHLPRTYMFNPEVYVWSLFWKQSLVSSGANL---VYASGS-
230 240 250 260 270 280
8469154 FYNIGLNDVINEFYRQVQETISVLDLHLLPNDYDRTYPIPTKSQATRELYTDPII
210 220 230 240 250 260
crv2ab2_820. GPQQTOSFTSDM---PFLASIPQNSNWLWSPFGSARLSTPNIVIGLP-GSTTHAL
290 300 310 320 330
8469154 SGAQAGYTLQDVLREPHLMDEL-NRLIYVTEAGIR-----WAGNVESSRTGMM
270 280 290 300 310
crv2ab2_820. LLAARNVSGGISGDIAGSPFNQFCSTFPLPPLPFPKSMWLS--SDREGVNTNM
340 350 360 370 380 390
8469154 TNIRPFLYGTAA-----AEP-TRFITPSTF--PGLNLFYRTLSAIFRPSG--LIRIY
320 330 340 350 360 370
crv2ab2_820. QTESFETTLGL---RSCA---FTARGNSYFPDYFIRNISGVPLIVNEDDREPLNNEH
400 410 420 430 440 450
8469154 RT-SLVGEGVFQPNNGEQLYRVGTLGSLDQLPLEGSS--LTEYSHRLCHVRFPSQSR
360 370 380 390 400 410 420 430
crv2ab2_820. 460 470 480 490 500

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 232 of 361

```
cry2ab2_820. NIASPSCTPGGARAYMVS-VHNRKNNIHAVHENG-SMIHL--APNDYTGFTISPIHATQV
8469154 N-AEPLDY---ARVPFMSWTHRSATPTNIDPDVITQIPLVKAFNLHSGAIVVRGPGFTG
430 440 450 460 470 480 490

cry2ab2_820. NNQTRTFISEKFGNQGSLRFEQNNTIARYTLRGNNSVNLVLRVSSIGNSTIRVTNGR
8469154 GDILRRRNA---GNFGD-MRV---NITAPLSQR-----YRVIRVASTANLQPHTSINGR
490 500 510 520 530 540 550

cry2ab2_820. VYTATNVNTTNDGNDGNGARFSDINIGNVASSNSDVELDINV-TLNSGTQFDLMNIM
8469154 AINQANFPATMNS-GENLOSQSFVRVAGFTTPTTFSDALSTFTIGAFSSNNVEVYIDGIE
540 550 560 570 580 590

cry2ab2_820. LVPTNISPLY
8469154 FVPAEVTATESDQDRAQKAVNALFTSSNQIGLKTVDVNYHIDQVSNLVECLSDFECLDE
600 610 620 630 640 650

cry2ab2_820.pcp
NRAA:8469154

8469154 source="GENBANK PROT" Pesticidal crystal protein cry1Gb (Insecticidal
delta-endotoxin CryI(gb)) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)gi|4097876|gb|AAD10291.1| insecticidal crystal protein CryH2 (Bacillus
thuringiensis serovar wuhanensis)

SCORES Initl: 191 Initn: 191 Opt: 285 z-score: 318.9 E(): 1.8e-09
>>NRAA:8469154
initn: 191 initl: 191 opt: 285 z-score: 318.9 expect(): 1.8e-09
Smith-Waterman score: 301; 22.4% identity in 577 aa overlap
(81-634:58-598)

cry2ab2_820. SLYLDPIVGTVASFLLKKVGLVKRILSELNLIFFPGSGTNLMQDILRETEKFLNQRIN
8469154 FSSEQVAEHLKTRILLENLFLPGGSPAFGLFDLWIGFIDQWQSAFLRQVEELINQRIIT
30 40 50 60 70 80 90 100 110

cry2ab2_820. TDTLARVNAELTGLQANVEENRQVDNFLN-PNRNAVPLSLITSSVNTMOQLFLNRLPQFQ
8469154 EFARGQAIQRLVGFGRSYDEVILALKEWENDPNASKERVTRFRITDDALLTGVLPLMA
90 100 110 120 130 140 150 160

cry2ab2_820. MQGYQLLLPLFAQANLHLSDIRVDILNADWGISAAATLRTYRDYLNKYTRDYSNYCIN
8469154 IPGFELATLSVVAQSANLHLALLRDAVFFGERWGLTQTNINDLYSLKNSIRDTYHNCVR
150 160 170 180 190 200 210 220

cry2ab2_820. TYGSAFKGNTLRLHMLERFTYMPFNVEYVSTWSLFYQSLVSSGANI---YASSG-
8469154 FYNIGLGNLVNIRPEYFRQELRTISVLQDLVALFPNIDRTYPIPTKRSQTRITYDPII
210 220 230 240 250 260 270 280 290 300 310 320 330
```

```
cry2ab2_820. GPQQTQSTSDM---PFLYSLFQVNSVNLNG-FSCARLSNTFFNIVCLP-GSTTTHAL
8469154 SQAQAGTILQDLVRLEHLMDFI--NRLIITYGEYRGIR-----HWACHEVESRRTGMM
270 280 290 300 310

cry2ab2_820. LAARVNVSGISSGDIAGSFQNFQNCSTFLPPLITPFVRSWLDG--SDREGVATVNW
8469154 TNIRFPLVGTAT---AEP-TRFITPSTF--PGLNLFYRT-LSAPIRDEPGANILIRY
320 330 340 350 360 370 380 390

cry2ab2_820. QTESFETTLGL---RSCG--FTARGNSYFPDYFIRNISGVPLVVRNEDLRPLHYNEIR
8469154 RT-SLVEGVGFIQPNNGEQLYRVGTGLDQLPLEGESS--LTEYSHRLCHVRFAQSLR
380 390 400 410 420 430 440 450

cry2ab2_820. NIASPSCTPGGARAYMVS-VHNRKNNIHAVHENG-SMIHL--APNDYTGFTISPIHATQV
8469154 N-AEPLDY---ARVPFMSWTHRSATPTNIDPDVITQIPLVKAFNLHSGAIVVRGPGFTG
430 440 450 460 470 480 490

cry2ab2_820. NNQTRTFISEKFGNQGSLRFEQNNTIARYTLRGNNSVNLVLRVSSIGNSTIRVTNGR
8469154 GDILRRRNA---GNFGD-MRV---NITAPLSQR-----YRVIRVASTANLQPHTSINGR
490 500 510 520 530 540 550

cry2ab2_820. VYTATNVNTTNDGNDGNGARFSDINIGNVASSNSDVELDINV-TLNSGTQFDLMNIM
8469154 AINQANFPATMNS-GENLOSQSFVRVAGFTTPTTFSDALSTFTIGAFSSNNVEVYIDGIE
540 550 560 570 580 590

cry2ab2_820. LVPTNISPLY
8469154 FVPAEVTATESDQDRAQKAVNALFTSSNQIGLKTVDVNYHIDQVSNLVECLSDFECLDE
600 610 620 630 640 650

cry2ab2_820.pcp
NRAA:27447986

27447986 source="GENBANK PROT" delta-endotoxin CryI (Bacillus thuringiensis)

SCORES Initl: 191 Initn: 191 Opt: 285 z-score: 318.9 E(): 1.8e-09
>>NRAA:27447986
initn: 191 initl: 191 opt: 285 z-score: 318.9 expect(): 1.8e-09
Smith-Waterman score: 300; 22.4% identity in 577 aa overlap
(81-634:58-598)

cry2ab2_820. SLYLDPIVGTVASFLLKKVGLVKRILSELNLIFFPGSGTNLMQDILRETEKFLNQRIN
27447986 FSSEQVAEHLKTRILLENLFLPGGSPAFGLFDLWIGFIDQWQSAFLRQVEELINQRIIT
30 40 50 60 70 80 90 100 110

cry2ab2_820. TDTLARVNAELTGLQANVEENRQVDNFLN-PNRNAVPLSLITSSVNTMOQLFLNRLPQFQ
27447986 EFARGQAIQRLVGFGRSYDEVILALKEWENDPNASKERVTRFRITDDALLTGVLPLMA
120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330
```


©01 Properties of Monsanto Company

cry2ab2_820. MOGYQLLLPFAQAANLSIRDVILNADEWGISAAITRTYRDYLNKYRDSNYCIN
170 180 190 200 210 220
27447986 LSGFELATLSVAGASNLHLALLANVAFGERWGLTQTNINDYSELKNSRDTYNHCVR
150 160 170 180 190 200
230 240 250 260 270 280
cry2ab2_820. TYOSAFKGLNTNRHMLFRTNLFNFEYVSIMELFVQSLVSSGANL----YASGS-
170 180 190 200 210 220
27447986 FYNIGLGNLVRDEYVRFQRELTISLDDVAFPPNVDNFTYALPTKSLQREIYTDPII
210 220 230 240 250 260
290 300 310 320 330 340
cry2ab2_820. GPQIQSTFSQDW---PFLYSLFQVNSNIVNG-FSGRURNTFFNIVSP-EGTTHAL
270 280 290 300 310 320
27447986 SPGAQAGYTLQDVLRLEPHLMDFL--NRLIITYSEYGRK-----HMAQHEVESRFTQWM
270 280 290 300 310 320
340 350 360 370 380 390
cry2ab2_820. LAARVNYSGGISGSDIGASPFQNFQNCSTFLPPLTFPVRSMDSQ--SDRGSVATNW
320 330 340 350 360 370
27447986 TWIRFLYGTAT---AEP-TEFTPSIF--PGNLFYAT-LSAFINDEGANIIR
320 330 340 350 360 370
400 410 420 430 440 450
cry2ab2_820. QTESFETTLGL---RSGA--FTARGSNYPDPYFIRMISGVPLVVRNEDLRPLHYNR
380 390 400 410 420 430
27447986 RT-SLVEGVGFIQPNNGEQLYRVRGTLDSLDQPLEGESS--LTEXSHRLCHVFAQSLR
380 390 400 410 420 430
460 470 480 490 500
cry2ab2_820. NTASGTFPGCARAYVUS-VHNEKNIHNVHENG-SMIHL--APNDYTGFTISPIHATQV
440 450 460 470 480 490
27447986 N-AEPLDY---ARVPMSWTHRSAPTNIIDPDVITQILPLVRAFNLHSGATVVRGPGFTG
430 440 450 460 470 480
510 520 530 540 550 560
cry2ab2_820. NQOTRIFISEKFGNQSLSRFEQNNITARYTLRGNNSYNLVLRVSSIGNSTIRVTNGR
490 500 510 520 530 540
27447986 GDLIRRTNA---GNFGD-MRV---NITAPLSOR-----YKVRIRVASTANLQFHTSINGR
490 500 510 520 530 540
570 580 590 600 610 620
cry2ab2_820. VTATNVNTIINDGUNDGARPSQINGNVVASSNDVPLDINV-TLNSGTQDPLNMIM
550 560 570 580 590 600
27447986 ATNQANFATWNS-GENLOSRSFRVAGFTTPTFSDALSTFTTIGAFSFSNNVEYIDRIE
540 550 560 570 580 590
630
cry2ab2_820. LVPTNINISPLY
630
27447986 FVPAEVTATESDODRAQAVNALFTSSNQIGLYDVTYVHIDQVSNLVECLSDPECLDE
600 610 620 630 640 650
cry2ab2_820.psp
NRAA:8928012
8928012 source="GENBANK PROT" Pesticidal crystal protein cry24Ba (Insecticidal
delta-endotoxin CryXXIVA(a)) (Crystalline entomocidal protoxin) (Crystal protein)
(Insecticidal protein Jcg72)gi|366833|gb|AAC61891.1| insecticidal protein Jcg72
[Bacillus thuringiensis serovar jegathesan]

SCORES Init1: 93 Initn: 125 Opt: 281 z-score: 318.4 E(): 1.9e-09
>NRAA:8928012
Initn: 125 Init1: 93 Opt: 281 z-score: 318.4 expect(): 1.9e-09
Smith-Waterman score: 284; 20.2% identity in 668 aa overlap
(18-634:18-651)

cry2ab2_820. MQAMDNSVLNSGRITCIDAYNVAADPFQFQKSLDTVQKE--WTEWKNKNSHSLVDP--
10 20 30 40 50
8928012 MNQYQNKVEIILESSQNMMNPNRYPPA---DDPNVAKMGNYKDWVNECEGSNISPS
10 20 30 40 50

cry2ab2_820. ---IVGTVASFLKXKVLGKRLSELRLNLIFFPSG---TNLMQDILRETEKFNQRLN
60 70 80 90 100 110
8928012 AAATSKIVSVILKTAKAVASSLADSIKSSGLGSKITENNVSQVSMQVQHOIINRIQ
60 70 80 90 100 110

cry2ab2_820. TDTLARVNRELTCLQANVEEFNRQVDNFI---NPENAV---PLSITSSVNTMQOLFANL
120 130 140 150 160
8928012 ETILDGESSLNGL---VAIYRNDYLGALAEANNNKSNINQTNVAEAFKIVEREFTKL
120 130 140 150 160 170

cry2ab2_820. PQ-FOMQGYQLLLPFAQAANLSIRDVILNADEWGISAAITRTYRDYLNKYRDS
170 180 190 200 210 220
8928012 KSIYVTSSSQITLLPTTQAAANLHLSMLRDAVNYOEGNQLQSHI--NYSKELDDALEDYT
180 190 200 210 220 230

cry2ab2_820. NYCINTYGRFQGL-NTLHMLFRIY---MFLNVFEYVIMSLF---KYQ-SLLVSSG
230 240 250 260 270
8928012 NYQVEYVITGLNARSGSAIDWLEFFSFRDMLVLDLVAIFPNVPRYPLSTKISLS
240 250 260 270 280 290

cry2ab2_820. ANAYAGSGPQOTV---FQDWPFPYSDQVNSYVINGFSG-ARLSNTFFNIVGLPGSTT
280 290 300 310 320 330
8928012 RKIYTDVGRFTSPSPG---TNTGRTLANFNDLEREVTDSFSLVKWLGDMT
300 310 320 330 340

cry2ab2_820. --THALLAARVNYSG--GIS-SDIGA-----SPNQNNCSFTFLPPLTFPVRSW
340 350 360 370 380
8928012 IYTGADISVRPTSPGDRIGVWYNNIINAVHTSRDVFQRTGQ-TAEDP--STFISNI
350 360 370 380 390

cry2ab2_820. L--DSSGDRGVATVNWOTESFETTLGLRSGE-TARGNSNYPDPYFIRMISGVPLVVR
390 400 410 420 430 440
8928012 LYDDIYKLDLRAAAVSTIQG-AMDTTFGVSSSRFFDIERNQYQSN--FPIPSLPITM
400 410 420 430 440 450

cry2ab2_820. -----NEDLRRPLHYNEIRNIASPSGTGPGGARAYMVSVHNRKKNHAWENSSH
440 450 460 470 480 490
8928012 PPEESSEGANDYSHL-LCDVKTQLQEDSSNICEGRSLLS-HAWTHA-SLDNNHKL-
460 470 480 490 500 510

cry2ab2_820. LAPNDYTGFTISPIHATQVNNQTRTFISEKFGNQSLSRFEQNNITARYTLRGNNSYNL
490 500 510 520 530 540

Final Report

Product Characterization Center

[illegible]

```

8928012      RKIYDVPVGRKTSFG--DW-----INIGRTLANFNDLEREVDTSFLVKVLGDMT
              300      310      320      330      340
cry2ab2_820.  --THALLAARVNYSG---GISGSDIGA-----SPFNQFNCSFTFLPPLLTFFVPSW
              340      350      360      370      380
8928012      IYTGADISYPTSPGDRGVGVYGNINAFYHGTGTDVVMFRQTGD--TAYSDP--STFISNI
              350      360      370      380      390
cry2ab2_820.  L--DSGSDREGVATVNNQTSFETTLGLRSGAF--TARGNSNPFDPYFIRNISGVPLVVR
              380      390      400      410      420      430
8928012      LYDDIYKLDLRAAAVSTIQG-AMDTTEGVSSRRFFDIRGNQLYQSN--KPYPSPILIT
              400      410      420      430      440      450
cry2ab2_820.  -----NEDLRRLHNEIRNIASPGTGCARAYMVSVHNRKNIHVAHENGSMIH
              440      450      460      470      480
8928012      PFGESSEGANDYSHL-LCDVKILQSDNICEGRSSLLS--HAWTHA--SLDRNNTIL-
              460      470      480      490      500      510
cry2ab2_820.  LAPNDYTGFTISPIHATOVNNTFTISEKFGNQGDSLRFFQNNNTARYTLRGNGSYNL
              490      500      510      520      530      540
8928012      --PDEIT--QIPAVTAYELRGNSS--SVVAGPGSTGGLVKMSYVHSWMSFKVYCSLKNYRV
              520      530      540      550      560
cry2ab2_820.  YLRVSSIGNSTIRVTNGRVYATVNTNTTNDGVNDGARFSDINIGNVASSNDVPL
              550      560      570      580      590      600
8928012      RIRYASHGNCQFLMKWPSTGVAPQWARHNVQGTFSNSMRYAFKYDLITFTIPEENN
              570      580      590      600      610      620
cry2ab2_820.  DINVTLSNGTQFDLMIMLVPINISPLY
              610      620      630
8928012      AFTIDLESGGDLFDKIEFIPVSGAFEGYEGKONIEKTKOAVNDLFIN
              630      640      650      660      670
cry2ab2_820.pep
NR04_40278
40278 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]

SCORES      Init1: 128      Initn: 168      Opt: 284      z-score: 317.9 E(): 2.1e-09
>>NR04_40278
      Initn: 168 Init1: 128 Opt: 284 Z-score: 317.9 expect(): 2.1e-09
Smith-Waterman score: 290;      22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820.  FOHKSLDTVQKEWTEWKKNNHSLYLDTPVGRVASFLLKKVGLSVCKRILSELNLFFPSG
              30      40      50      60      70      80
40278      IPYNCLISNPEVLGGERIETGYTPIDISLSTQFLLSFF--VPGAGVFLGLVDIIWGIF
              20      30      40      50      60
90.      100      110      120      130      140
cry2ab2_820.  STNLMQDILRETEKFLNQRLTNDTLARVNAELTGL----QAMVEFNQVDVFNLPNRNA
              :      :      :      :      :
40278      GPSQDAFLVQLEQILNQRLEEFARNQAISRLGSLNLUQIYAESFREWEADPTNP---A
              70      80      90      100      110      120

```


©07

cr2ab2_820. 150 160 170 180 190 200
VPLSITSSVNTMQLFLNRLPFOFOMQGYQLLLPLFAQAANLHLSFIRDIVILNADEWGIS
117536
LREEMRIQFNDMSALTATLPLFAVONYQVPLSVVQAANLHLSVLDRVSVFGORWGF
cr2ab2_820. 210 220 230 240 250
AATLRTYRDYKNNFYDSNYCINTYOSAFK--GNLTHDML---ERTYMFNLVNEY
40278
AATINSYNDLRLTGNVTHAVRWYNTGLERVMGPDSS--DMIRYNQFRRLTILVDI
cr2ab2_820. 260 270 280 290 300 310
VSIWSLFKYGLSVSSGANLVAASGGSGQFTSQDAPFFLYSLFQVNSYLVNGFSGAR
40278
VSLFPNVDSTPIRTVSQL-----TREIYTN---PVLEN-FDGSFRGSAQIGESI
cr2ab2_820. 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510
LSNTFFNVLPGSTTHALLAARVNYSGISGGIDIGASPNQNTCSFSPALL
40278
RS---PHLMDLINSITVTD-AHRGEYIW--SGHQIMASPGV--FSQPTFPLTGVN
cr2ab2_820. 430 440 450 460 470 480
ISGVPLV--VRNEDLRRPLHYNEIRNTASPGTGGARAYMVSVHNEKNNIHAVHENGSM
40278
SGTVDSLDEIPQNNVPPROGFHRLSHVSMFRSGFNSSVSI--IRPDMFVHRSAP
cr2ab2_820. 490 500 510 520 530 540
IHLAPNDYTGFTISPI-HATOVNNQRTFISEKFGNQDGLSRFPQNNNTARTVLRGN---
40278
NNIIPS--SQITQILPTKSTNLGSGTGVKVGPGFTG-GDILRRTPSQGIS--TLRVNNTA
cr2ab2_820. 550 560 570 580 590 600
--GNSVLYLRVSSGNSITRTVINGVYATVNTNNNGVNDNGARPSDINGNVVA
40278
PLSQRYVRIRYASTINLQLHSTIDGRINQGNFATSS--GNSLQSGFRIVGTTFFN
cr2ab2_820. 610 620 630
SSNSDVPDLINV--TLNSGTQFLNMVLPNTISPLV
40278
FNSGSSVFTLISARFVNSGNEVYDIEFVPAETAEAYEDLERAQKAVNELTSSNQIGL
40278
KTDVTDYHIDQVSNLVECLSDFECLDEKSELKVKHAKRLSDERNLLQDPNFRGINRQL
cr2ab2_820. 640 650 660 670 680 690
cr2ab2_820. 690 700 710 720 730 740 750 760 770 780 790 800
cr2ab2_820. 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
cr2ab2_820. 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
cr2ab2_820. 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400
cr2ab2_820. 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
cr2ab2_820. 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800
cr2ab2_820. 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000
cr2ab2_820. 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200
cr2ab2_820. 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400
cr2ab2_820. 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600
cr2ab2_820. 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800
cr2ab2_820. 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000
cr2ab2_820. 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200
cr2ab2_820. 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400
cr2ab2_820. 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600
cr2ab2_820. 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800
cr2ab2_820. 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000
cr2ab2_820. 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200
cr2ab2_820. 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400
cr2ab2_820. 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600
cr2ab2_820. 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800
cr2ab2_820. 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000
cr2ab2_820. 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200
cr2ab2_820. 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400
cr2ab2_820. 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600
cr2ab2_820. 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800
cr2ab2_820. 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000
cr2ab2_820. 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200
cr2ab2_820. 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330

cry2ab2_820.pep
SW:117536

117536 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALINE ENTOMOCIDAL PROTOXIN)." library=NA species=Bacillus thuringiensis serovar


```
cry2ab2_820. --GNSVNLVRYSSIGNSTIRVTINGRVYATNTVNTTNDGVNDNGARFSDINIGNVVA
117536 PLSQRYVRIRYASTTNQLHTSDIGRIINQGNFSATMSS--GSLNQSGLSFRVGTTPFN
520 530 540 550 560 570

cry2ab2_820. SSNSDVPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
117536 FSNQSVFTLSAHVFNSENGEVYIDRIEFVPAEVTPEAEYDLERAKAVNELFTSSNQIGL
580 590 600 610 620 630

117536 KTDVTDYHDQVNLVECLSDPECLDEKSELSEKVKHAKRLSDERNLLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pcp
NRAA:37048803

37048803 source="GENBANK_prot" cryIIA toxin [Bacillus thuringiensis]

SCORES Initl: 159 Initn: 199 Opt: 284 z-score: 317.7 E(): 2.1e-09
>NRAA:37048803
initn: 199 initl: 159 opt: 284 z-score: 317.7 expect(): 2.1e-09
Smith-Waterman score: 290; 22.5% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FQHKSLDTQKEMTKKNNHSLYLDPIVGTVASFLKKVGLVGRKRLSELRLNLIFFPSG
30 40 50 60 70 80
37048803 IPYNCLNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGVGLGLVDILWGIF
20 30 40 50 60

cry2ab2_820. STNLNQDILRETEKFLNQLRNTDITLARVNAELTGL---QANVEEFNRQVDNLFNPNRINA
90 100 110 120 130 140
37048803 GPSQWDAPLQVIOELINQRIEFARNAQAIISRLGLESLNLYQIVAESEFREWEDAPTNP--A
70 80 90 100 110 120

cry2ab2_820. VPLSITSVNTMOQLFNELPQFMQGVQLLLPLFAQANLHLSIFRDVILNADWGIS
150 160 170 180 190 200
37048803 LREEMRIQFNDMNSALTITAIPLFAVONYQVPLLSVYVQAAANLHLSVLDVSVFGQRMGFD
130 140 150 160 170 180

cry2ab2_820. AATLRTYRDVLYKNYTRDYSNCINTYQSAFK--GLNTRLHDML---EFTRYMFLNVFEY
210 220 230 240 250
37048803 AATINSYNDLTBLIGNYTDYAVRWYNTGLERVWGPDSR--DWIRYNGFRRLTLVLDI
190 200 210 220 230 240

cry2ab2_820. VSIWLFKYQSLVSSGANLYASGSGPQQTQSFTSDWPFLYSFLQVNSVNLVNGFSGAR
260 270 280 290 300 310
37048803 VSLFPNYDSRTYPIRTVSQI-----TREIYTN---PVLEN-PDGSFRGSAQIEGSI
250 260 270 280 290

cry2ab2_820. LSNTFPNIVGLPGSTTHALLAARVNYSGGSGDYGASFPNONTNCTFTFPLL-----
320 330 340 350 360 370
37048803 RS---PHIMDLISITTIYTD-AHRGEYTW--SGHQINASFPVG--PSGPEFTFPIYGTWGN
300 310 320 330 340

380 390 400 410 420
```

```
cry2ab2_820. -TPFVR--SWLDSGSDREGVATV--INNOTESFETTLGLRSGAFTARGNSVYFPDYFIRN
37048803 AAPQQRIVAQCGQVYVLTSSLIYLRPPNINQINNOQLSVLDGTEFAFGYSSNLPSAVYRK
350 360 370 380 390 400

cry2ab2_820. ISGVPLIV--VNEDLRRLPHLYNEIRNIASPSGTGPGGARAYMVSVHNRKNINIHAVHENGSM
430 440 450 460 470 480
37048803 SGTVSDLEIIPQNNVPPRQGSFHLSHVMSFRSGFSNSSVSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460

cry2ab2_820. IHLAPNDYGTITSPI--HATQVNNQTRPIFEKFGNOGDSLRFEQNNNTARTITLRGN---
490 500 510 520 530 540
37048803 NNIIIPS--SOITQIPLTKSTNLGSGTSVVKGPGFTG--GDILRTSPGQIS--TLRVNITA
470 480 490 500 510

cry2ab2_820. --GNSVNLVRYSSIGNSTIRVTINGRVYATNTVNTTNDGVNDNGARFSDINIGNVVA
550 560 570 580 590 600
37048803 PLSQRYVRIRYASTTNQLHTSDIGRIINQGNFSATMSS--GSLNQSGLSFRVGTTPFN
520 530 540 550 560 570

cry2ab2_820. SSNSDVPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
610 620 630
37048803 FSNQSVFTLSAHVFNSENGEVYIDRIEFVPAEVTPEAEYDLERAKAVNELFTSSNQIGL
580 590 600 610 620 630

37048803 KTDVTDYHDQVNLVECLSDPECLDEKSELSEKVKHAKRLSDERNLLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pcp
NRAA:58826238

58826238 source="GENBANK_prot" Cry3 delta endotoxin [Bacillus thuringiensis
serovar tenebrionis]

SCORES Initl: 114 Initn: 158 Opt: 280 z-score: 317.6 E(): 2.1e-09
>NRAA:58826238
initn: 158 initl: 114 opt: 280 z-score: 317.6 expect(): 2.1e-09
Smith-Waterman score: 281; 26.5% identity in 249 aa overlap
(36-266:39-286)

cry2ab2_820. NSVLSNGRTTICDAYNVAADHPFSQHKSLDTQKEMTKKNNHSLYLDP-----IV--
10 20 30 40 50
58826238 HDIKITENNEVPTNHVQVPLAETPAPTLEDLNLYKEFLRTADNTNEALDSSSTTKDVIQK
10 20 30 40 50 60

cry2ab2_820. G-TVASFLKKVGLVGRKRLSELRLNLIFFPS--GSTNLMQDILRETEKFLNQLRNTDITLAR
60 70 80 90 100 110
58826238 GISVGDLLGVVGPFPFGALVSVFTNFLTNSWPSEDPMKAFMEQVEALMDQKIADYAKNK
70 80 90 100 110 120

cry2ab2_820. VNAELTGLQANVEEFNRQVDNLFN--NPNNAVPLS---ITSSVNTMOQLFNELPQFMQOG
120 130 140 150 160 170
58826238 ALAELQGLQNVVEDYVSALSSWQKNPVSRRNPHSQGRIRELFSQAESYFRNMPSPFAISG
130 140 150 160 170 180
```


52145404 DPVGVNNLGGYCTTFSNIENIRKPLFDYLLHRIQFHTRRPVGYNDSFNWMSGNVYS
320 330 340 350 360 370

cry2ab2_820.pep
NRAA:8469139

8469139 source="GENBANK_PROT" Pesticidal crystal protein cryIAe (Insecticidal delta-endotoxin CryIA(e)) (Crystalline entomocidal protoxin) (134 kDa crystal protein)gi|142875|gb|AA222410.1| delta-endotoxin

290	300	310	320	330	340
-----	-----	-----	-----	-----	-----

```

SCORES      Init1: 120      Initn: 160      Opt: 283      z-score: 316.6 E(): 2.4e-09
>>NRAD:8469139
      Init1: 120      Initn: 160      Opt: 283      Z-score: 316.6 expect(): 2.4e-09
Smith-Waterman score: 284;    21.4% identity in 602 aa overlap
(60-634:41-610)

```

Smith-Waterman score: 284; 21.4% identity in 602 aa overlap
(60-634:41-610)

	30	40	50	60	70	80
(a) \bar{X}	30	40	50	60	70	80
(b) S^2	90	80	70	60	50	40
(c) σ^2	90	80	70	60	50	40
(d) \bar{S}^2	90	80	70	60	50	40
(e) σ^2	90	80	70	60	50	40
(f) $\bar{\sigma}^2$	90	80	70	60	50	40
(g) \bar{S}^2	90	80	70	60	50	40
(h) σ^2	90	80	70	60	50	40
(i) $\bar{\sigma}^2$	90	80	70	60	50	40
(j) \bar{S}^2	90	80	70	60	50	40
(k) σ^2	90	80	70	60	50	40
(l) $\bar{\sigma}^2$	90	80	70	60	50	40
(m) \bar{S}^2	90	80	70	60	50	40
(n) σ^2	90	80	70	60	50	40
(o) $\bar{\sigma}^2$	90	80	70	60	50	40
(p) \bar{S}^2	90	80	70	60	50	40
(q) σ^2	90	80	70	60	50	40
(r) $\bar{\sigma}^2$	90	80	70	60	50	40
(s) \bar{S}^2	90	80	70	60	50	40
(t) σ^2	90	80	70	60	50	40
(u) $\bar{\sigma}^2$	90	80	70	60	50	40
(v) \bar{S}^2	90	80	70	60	50	40
(w) σ^2	90	80	70	60	50	40
(x) $\bar{\sigma}^2$	90	80	70	60	50	40
(y) \bar{S}^2	90	80	70	60	50	40
(z) σ^2	90	80	70	60	50	40
(aa) $\bar{\sigma}^2$	90	80	70	60	50	40
(ab) \bar{S}^2	90	80	70	60	50	40
(ac) σ^2	90	80	70	60	50	40
(ad) $\bar{\sigma}^2$	90	80	70	60	50	40
(ae) \bar{S}^2	90	80	70	60	50	40
(af) σ^2	90	80	70	60	50	40
(ag) $\bar{\sigma}^2$	90	80	70	60	50	40
(ah) \bar{S}^2	90	80	70	60	50	40
(ai) σ^2	90	80	70	60	50	40
(aj) $\bar{\sigma}^2$	90	80	70	60	50	40
(ak) \bar{S}^2	90	80	70	60	50	40
(al) σ^2	90	80	70	60	50	40
(am) $\bar{\sigma}^2$	90	80	70	60	50	40
(an) \bar{S}^2	90	80	70	60	50	40
(ao) σ^2	90	80	70	60	50	40
(ap) $\bar{\sigma}^2$	90	80	70	60	50	40
(aq) \bar{S}^2	90	80	70	60	50	40
(ar) σ^2	90	80	70	60	50	40
(as) $\bar{\sigma}^2$	90	80	70	60	50	40
(at) \bar{S}^2	90	80	70	60	50	40
(au) σ^2	90	80	70	60	50	40
(av) $\bar{\sigma}^2$	90	80	70	60	50	40
(aw) \bar{S}^2	90	80	70	60	50	40
(ax) σ^2	90	80	70	60	50	40
(ay) $\bar{\sigma}^2$	90	80	70	60	50	40
(az) \bar{S}^2	90	80	70	60	50	40
(ba) σ^2	90	80	70	60	50	40
(bb) $\bar{\sigma}^2$	90	80	70	60	50	40
(bc) \bar{S}^2	90	80	70	60	50	40
(bd) σ^2	90	80	70	60	50	40
(be) $\bar{\sigma}^2$	90	80	70	60	50	40
(bf) \bar{S}^2	90	80	70	60	50	40
(bg) σ^2	90	80	70	60	50	40
(bh) $\bar{\sigma}^2$	90	80	70	60	50	40
(bi) \bar{S}^2	90	80	70	60	50	40
(bj) σ^2	90	80	70	60	50	40
(bk						

cry2ab2_820. FQHKSLDTVQKEWTWKNNHSLYLDPIVGTVASFLKKVGSVGVKRIILSELNLIFFSPG

8469139 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLIDLNGFV

[illegible]

90 100 110 120 130 140
 CTCTGAC 820. STNNMQDILRETEKFLNQRLNTDTLARVNAELTGL----QANVEEFNRQVDNFLNPNRNAR

GPSONDAFLVOIEOLISORIEEFARNOASRLEGLSNLYOIVAEAFREWEADPTNP----

Year	1950	1955	1960	1965	1970	1975	1980	1985	1990	1995	2000
Population (millions)	1.5	1.6	1.7	1.8	1.9	2.0	2.1	2.2	2.3	2.4	2.5
GDP (billions of dollars)	100	150	200	250	300	350	400	450	500	550	600

CITY AND DISTRICT OF COLUMBIA

8469339 GREENRIQNDMSALITAIPLFTVQNYQVPLESVYQAVNLHLSVLRDVSFQGRWGD
126 140 150 160 170 180

210 220 230 240 250

~~cry2ab2_820 ATATCTGTDYLNKYTRDTSNYCINTYQSAFK--GLNTRLHDML---EFRTYMFLNFVEE~~

8469139
VAINSNANDLTRA1610TDYAVRWYNGSLERWVGPSR--DWRYNQFRRELITLTVLDI
180 190 200 210 220 230 240

0517 0007 017 027 032 047

260 270 280 290 300 310
cry2ab2.820. VSIWSLFKYQSLNLSGNL--X-VASGGQQQTQSFTSODWFFLYSLFQVNSNYYVINGFF

8469139
VSLFPNDVRTYPIRTVSSNTRRLTYNWDENRGSFRGSMORFQSIRSPHMLMDINSL

250 260 270 280 290 300

320 330 340 350 360 370

[illegible]

8469139
T-----LYTDAHGYYVWSGHQIMASVPGSGFFIIPLYGIMGMAAPQRI-----
310 320 330 340 350

380 390 400 410 420 430

cry2ab2_820. PLLTPFVRSWLDSGSDREGVATVTNWQTESPTTLGLRSGAFTAGNSNYFPDQFTRAS

8469139 QLGGVPT-LSTFYRNPFIINNQR-----LSVLDGTEFAGSSSNLPNAVRRKSG

360 370 380 390 400

cry2ab2 820. GVPLV--VRNEDLRPLHYNEIRNIASPSGTPGGRAYMVSVHNRKNNIHAVHENGSMIN

8469139 TVDLSLDELPPODNNVPPROGFSHRLSHVSMFRSGFSNSSVSI-IPAPMFSWIHRSAEENN

Study No. 06-01-62-01

MSL No. 20307

Page 238 of 361

[illegible]


```

SCORES      Initl: 128      Initn: 168      Opt: 278      z-score: 315.6 E(): 2.8e-09
>>NRAA:36244769
Initn: 168 initl: 128 opt: 278 z-score: 315.6 expect(): 2.8e-09
Smith-Waterman score: 284;    22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FQHKSLDTVQKEWTEKKNNHSLYLDPIVGTVASFLFKKVKLSLGVGRKRLLSENLNLPFSG
30      40      50      60      70      80
IPNCILSNPEVEVLGGERIETGYTPDDISLSITQFLISEP--VPGAGFVLGLVDIIWGIF
20      30      40      50      60
cry2ab2_820. STNLMODILRETEKFANORINTDTLARVNAELTGL----QANVEFNQRVDNFAPNPNRA
90      100     110     120     130     140
GPSOWDAFLVQIEQLINRIEEFAARQAQSRLEGLSNLYQIYAESFREWEADPTNP--A-A
70      80      90     100     110     120
cry2ab2_820. VPLSISSVTNTMOQLFLNFLPGFCOMOGYOLLHLPLFAQANLHLSFTIRVDILNADMGVIS
150     160     170     180     190     200
LRBEMRIQFDNMNSALTATPLFVAQYQVLPILLSVVOQANLHLSVLRDVSVFQGQWGF
130     140     150     160     170     180
cry2ab2_820. AATLTTRVDYLKNYTRDYSNYCINTQSAPK--GLNTRLHDML---EFTYMFNLNVFEY
210     220     230     240     250
36244769 KATINSRYNDLTRLGNGYTDHAVRWYNTGLERVMGPDSR--DMTRYNQFRRELITLVLDI
190     200     210     220     230     240
cry2ab2_820. VSIVSLRKQSLVLSGANLVSAGSQOQTOSTQDPWFFLYSFQVNSVNLVNGFSGAR
260     270     280     290     300     310
36244769 VELPFENYRTYTIPIRLISOL-----TREIYTIN--PVLEN-FDGSPFGSAQGLEGI
250     260     270     280     290
cry2ab2_820. LSTNTPFNIVGLRPSATHALLARVNVSIGGISGDIAGSPNQNFNCSTLEPLL-----
320     330     340     350     360     370
36244769 RS--PMIMDLANSITLVDRHRGEYTW--SCHOLMASPGV--FSGPEFTPLYCYTMGN
300     310     320     330     340
cry2ab2_820. TPVPR--SWIDSGSDRGKGVTV--TNQEPSETTLGRSQTARTAGNSNFPDYFIRN
380     390     400     410     420
36244769 AAPQQRIVAQLGGVVYRLTSSTLRYPFNIGLNQNSVLDGTTFATCTSSNLPFSAVVRKK
350     360     370     380     390     400
cry2ab2_820. TSGVPLV--VRNEDLRRPLUHYNEIRNIASSPGDGRQAYVWSVVMKWIHAHEMSRM
430     440     450     460     470     480
36244769 SCTVDLSDEIIPPQNNVPPROGFSHRLSHVSMFSGFNSSLSI--IRA PAFMFIHSRAAE
410     420     430     440     450     460
cry2ab2_820. IHLAPNDYTGFTISPI-HATQVNNQOTRFISERKFGNQGSULRFQNNHTVARTKNG--
490     500     510     520     530     540
36244769 NNIIIPS--SQITQIPLTIKSTNLGSGTSVWVGPGFTG-GDILRRYSPGOIS--LRVMTA
470     480     490     500     510
cry2ab2_820. --GNSYNLYLRVSSIGNISRTVINGRVYTATWNTTTINDGDVNDGARSQDINIANGV
550     560     570     580     590     600

```

NRAA: 36244769

362444769 source="GENBANK PROT" Crv1abl [synthetic construct]

Study No. 06-01-62-01
MSL No. 20307
Page 240 of 361

Smith-Waterman score: 277; 27.4% identity in 219 aa overlap
(60-266:24-239)

crv2ab2_820. FQHKSLDTVQKEWTEKKNHSLYLDPIVGTVASFLKKKGSLVGRKILS---ELRNLIFF
 30 40 50 60 70 80
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
312848 MTADNNTALDSSITKDVIQKGISVVGGDLIGVGFPFGGALVSFYTNFLTIIW
 10 20 30 40 50

crv2ab2_820. PSGSTNLMDILIRETEKFANRLNTDTLARVNAELTGQANVEEFNRQVDNFL-NPNRNA
 90 100 110 120 130 140
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
312848 PS--EDPWKAFMQEVAALMDOKIADYAKNALAEQLQGNNVEDYVSALSSWKQNPVSSR
 60 70 80 90 100 110

crv2ab2_820. VPLS---ITSVNNTMQQLFNRLPFQMOMGYQLLLPFAQAANLHSIFRDVLINADEW
 150 160 170 180 190 200
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
312848 NPHSQGRIRLEFSQAESHFRNSMPSFAISGYEVLFITTYAQAANTHLFLKKDAQIYGEEW
 120 130 140 150 160 170

crv2ab2_820. GISAAIT-RYRIDLYNKLTDRYSNYCINTYQSAFKGL-NTRLHDMLEFRTY---MFLNVF
 210 220 230 240 250
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
312848 GYEKEDIAEYFKQLK-LTQEYTDHCVKAVNGLKRGSSVESWNENRYRRMTLVL
 180 190 200 210 220 230

crv2ab2_820. EYVSIWLSFYQSLLVSSGANLYASGGPGQTOSTSDMPFLSYLQVNSNYINGFSG
 260 270 280 290 300 310
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
312848 DLIALFLPYDVRLYPKVETELTRDVLTDPIGVGNLNLRGYGTTFSTNIENYIKRPHLFDYL
 240 250 260 270 280 290

crv2ab2_820.pep
NRRA:471281

471281 source="GENBANK_PROT" CrviIIIA insecticidal crystal protein [synthetic construct]

SCORES Init1: 114 Initn: 158 Opt: 277 Z-score: 314.6 E(): 3.2e-09
>>NRRA:471281
Initn: 158 Init1: 114 opt: 277 Z-score: 314.6 expect(): 3.2e-09
Smith-Waterman score: 277; 27.4% identity in 219 aa overlap
(60-266:24-239)

crv2ab2_820. FQHKSLDTVQKEWTEKKNHSLYLDPIVGTVASFLKKKGSLVGRKILS---ELRNLIFF
 30 40 50 60 70 80
 :::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
471281 MAADNNTALDSSITKDVIQKGISVVGGDLIGVGFPFGGALVSFYTNFLTIIW
 10 20 30 40 50

crv2ab2_820. PSGSTNLMDILIRETEKFANRLNTDTLARVNAELTGQANVEEFNRQVDNFL-NPNRNA
 90 100 110 120 130 140
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
471281 PS--EDPWKAFMQEVAALMDOKIADYAKNALAEQLQGNNVEDYVSALSSWKQNPVSSR
 60 70 80 90 100 110

crv2ab2_820. VPLS---ITSVNNTMQQLFNRLPFQMOMGYQLLLPFAQAANLHSIFRDVLINADEW
 150 160 170 180 190 200
 || : : : : | : : : | : : : | : : : | : : : | : : : | : : : |
471281 NPHSQGRIRLEFSQAESHFRNSMPSFAISGYEVLFITTYAQAANTHLFLKKDAQIYGEEW
 120 130 140 150 160 170

©01

cry2ab2_820 GIQAATLFLYDYLKNTKSYNYCYQAFKGL-NTRLHDMLEFRTY---MFLNVF
471281 GYKEDIAEYFQK-LTQETDNRKWNVGLDKRGSSYSWNFNRYRREMTLVL
180 190 200 210 220 230

cry2ab2_820 EYVINSLSLQSLVSSGNIASGSGPQOQSISQSDWPFYLSLQVNSNVLNGFSG
471281 DLIALPFLVDVLYPKVETELRPMTHIVGVNNGGRTTFSNIENYKRPKLPDYL
260 270 280 290

cry2ab2_820.ppep
NRAA:40253

40253 source="GENBANK PROT" unnamed protein product [Bacillus thuringiensis
thuringiensis]gi|142736|gb|AA50255.1| crystal protein [Bacillus thuringiensis
serovar morrison]gi|61221658|sp|P0A380|C3A3A.BACTM.Pesticidal crystal protein
cry3Aa precursor (insecticidal delta-endotoxin CryIIIA(a)) (73 kDa crystal
entomocidal protoxin) (73 kDa crystal protein)gi|61221658|sp|P0A380|C3A3A.BACTM
Pesticidal crystal protein cry3Aa precursor (insecticidal delta-endotoxin)

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 314.2 E(): 3.3e-09
>>NRAA:40253
initn: 158 initl: 114 opt: 277 z-score: 314.2 expect(): 3.3e-09
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:39-286)

cry2ab2_820 ARVNAELTGLQANVEEFNRQVDNEL-NPNRNVPLS---ITSSVNTMOQLFLNRLPOFQM
40253 HDTIKTTENNEVPNTNHVQVPLAETPNPTLEDLNYKEFLRMATADNTEALDSSTTKDVIQK
10 20 30 40 50 60

cry2ab2_820 G-TVASFLKKVGLVGRKILS---ELRNLIFFSGSTNLMQDILRETEKFLNRLPQFOM
40253 GISVVGDLGVGFPFGGALVSFYTNFTIMWS--EDPWKAFMEQVEALMDQKIADYAK
70 80 90 100 110 120

cry2ab2_820 QGYQLLLPLFAQANHLHSFRDVLNADWEGISAAITL-RTYRDYLNKNTYRDSNYCIN
40253 NKALAELOQGNVEDYVSALSSQKPNFVSRNPHSQGRIRLFQSAEHSFNSMPSFAI
130 140 150 160 170 180

cry2ab2_820 QGYQLLLPLFAQANHLHSFRDVLNADWEGISAAITL-RTYRDYLNKNTYRDSNYCIN
40253 SGYVFLTYAQANHLFLDKDAQYGEWGYEKEDIAEFYKQRLK-LTQEYTDHCVK
190 200 210 220 230 240

cry2ab2_820 TYQSAFKGL-NTRLHDMLEFRTY---MFLNVFEVVSWSFKYQSLVSSGNLYASGSG
40253 WYNVGLDKRGSSYSWNFNRYRREMTLVLDLIAFLFYDVRLYPKVETELTRDVL
250 260 270 280 290 300

cry2ab2_820 PQOTSQTSQDWPFYLSLQVNSNVLNGFSGARLSNTFPNIVGLFGSTTTTHALLARVN

40253 DPIVGVNVLRGYGTTFSTFNIENYKRPKLPDYLHRIQFHTRFQFGYGNDSFNWWSGNVVS
310 320 330 340 350 360
cry2ab2_820.ppep
SW:61221657

61221657 description="Pesticidal crystal protein cry3Aa precursor (insecticidal
delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar tenebrionis"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 114 Initn: 158 Opt: 277 z-score: 314.2 E(): 3.3e-09
>>SW:61221657
initn: 158 initl: 114 opt: 277 z-score: 314.2 expect(): 3.3e-09
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266:39-286)

cry2ab2_820 NSVLNSGRTTICDAYNVAADHPFQHKSLDTVQKEWTKNNHSLYLDP-----IV--
61221657 HDTIKTTENNEVPNTNHVQVPLAETPNPTLEDLNYKEFLRMATADNTEALDSSTTKDVIQK
10 20 30 40 50 60

cry2ab2_820 G-TVASFLKKVGLVGRKILS---ELRNLIFFSGSTNLMQDILRETEKFLNRLPQFOM
61221657 GISVVGDLGVGFPFGGALVSFYTNFTIMWS--EDPWKAFMEQVEALMDQKIADYAK
70 80 90 100 110 120

cry2ab2_820 ARVNAELTGLQANVEEFNRQVDNEL-NPNRNVPLS---ITSSVNTMOQLFLNRLPQFOM
61221657 NKALAELOQGNVEDYVSALSSQKPNFVSRNPHSQGRIRLFQSAEHSFNSMPSFAI
130 140 150 160 170 180

cry2ab2_820 QGYQLLLPLFAQANHLHSFRDVLNADWEGISAAITL-RTYRDYLNKNTYRDSNYCIN
61221657 SGYVFLTYAQANHLFLDKDAQYGEWGYEKEDIAEFYKQRLK-LTQEYTDHCVK
190 200 210 220 230 240

cry2ab2_820 TYQSAFKGL-NTRLHDMLEFRTY---MFLNVFEVVSWSFKYQSLVSSGNLYASGSG
61221657 WYNVGLDKRGSSYSWNFNRYRREMTLVLDLIAFLFYDVRLYPKVETELTRDVL
250 260 270 280 290 300

cry2ab2_820 PQOTSQTSQDWPFYLSLQVNSNVLNGFSGARLSNTFPNIVGLFGSTTTTHALLARVN
61221657 DPIVGVNVLRGYGTTFSTFNIENYKRPKLPDYLHRIQFHTRFQFGYGNDSFNWWSGNVVS
310 320 330 340 350 360

cry2ab2_820.ppep
SW:61221658
61221658 description="Pesticidal crystal protein cry3Aa precursor (insecticidal
delta-endotoxin CryIIIA(a)) (Crystalline entomocidal protoxin) (73 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar morrison"
source="swissprot_prot" version="NA type="PRT

Study No. 06-01-62-01
MSL No. 20307
Page 242 of 361

```

10      20      30      40      50
cry2ab2_820.  NSVLNSGRITTCDAYNVAADPPSFQKSLDVTQKEWTEWKNNHSLYLDP-----IV--
                                         |  || :  || :  ||
61221658     HDTKITENNEVPTNHVOYPLAETPNPTLEDLNYKEFLRMADNNTEALDSSITKDVIOK

```

```

cy2ab2_820.  ARVNAELTGLQANVEEFNRQVDNPL-NNRNNAVPLS---ITTSVNTVQQLFNRLNPQFQM
              120   130   140   150   160   170   180
61221658      NKALAEGLQNNVEDYVSALLSKWKNPVYSNNPHISQGRITELPSQAESHFNSPSTAI
              130   140   150   160   170   180

```

```

cry2ab2_820..:YQSFAFKGL-NITLHDMLEFPTY---MFLNVEYYSINSLFKYQSLIVSSGANLVAASGG
61221658WYVGLDKLGGSSYWNFNRYREMTLVLDLALFLFDVLDPYFKPEVKYKTELTRDVLVT
230240250260270280290300

```

cry2ab2_820.pep
NRAA:143084

SCORES Init1: 114 Initn: 158 Opt: 277 z-score: 314.2 E(): 3.3e-09
>>NRAA:143084
Initn: 158 Init1: 114 Opt: 277 Z-score: 314.2 expect(): 3.3e-09 (644 aa)
Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
(36-266;39-286)

CXV2362	820	G-TYASEI I KKVCSI VSKBII S--E I BNI JEP SGSTNI MOD IL RET EKEFI NOR INTDTI.
	60	
	70	
	80	
	90	
	100	
	110	

crY2ab2_820. ARVNAELTGLANVEEFNRQVDNFL--NPNRNAVPLS---ITSSVNTMQGLFNLKLPQFQM
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
NKALAEQLQGNVEDYVYSALSGWQKNPVSSNPHISQGRITRELFSGAQRSHFNSMPSEAI
143084

cyt2ab2_820. TYQSAFKGI-NTRLHDMLEFRTY---MFLNVEYYSIWSLTKYQSLVSSGANLYASGSG
143084 WYNYGLDKLRGSSSYESWNNFRNRRYREMTLLDLALPPLYDRLVLPKVKVETELTRQVLVT

cry2ab2_820.pep
SW:117325

```

SCORES      Init1: 114      Initn: 158      Opt: 277      z-score: 314.2 E(): 3.3e-09
>>SW:117325                                     (164 aa)
      Init1: 158      Initn: 114      Opt: 277      z-score: 314.2      expect(): 3.3e-09
Smith-Waterman score: 278;      26.7% identity in 251 aa overlap
(36-266;39-286)

```

```

cry2ab2_820.  NSVLSNGRTTICDAYNVAADPFQKSDLTQVEKWTENKKNHSLYLDP-----IV-
                                     10  20  30  40  50
117325        HDTKTTENNEVPTNHVQVPAETPNPTEDLNLYKEFURMTADNNTAEDLSSTTKDVIQK
                                     10  20  30  40  50  60

```

[illegible]

cry2ab2_820. ARVNAELTG:QANVEEFNRQVDNLF--NPNRNAVPLS---ITSSVNTWQQLQFLNRLPQFQM
 120 130 140 150 160
 117325 NKALAEQLGQNNVEDYVSALLSQWKPNVPSNRNPHSQCRIRELFSQAESHFRNSPSPFAI
 130 140 150 160 170 180

180 190 200 210 220
 crv2ab2 820. OGYOLLPLFAOAAHLHFIRDVILNADEWGISAATL-RTYRDYLKNYTRDYSNYCIN

~~Product Characterization Center~~

```

1117325      196      200      210      220      230      240
SGYVQLPHTTAAQANNTNMLFLKDAQIYGEENGKEKEDIAEAFYKRLK-LTQETDHCVK

cry2ab2_820  290      260      270      280
TTSQAKGL-NKALHMLEFRIV-MFLNFEVYSIWSLFKYQSLLVSSGANLYASGSG
WYNYGLDKLRSGSYESWAFNRVREMTLVLDLALFFLYDVLRYPKVKVKTLLTRDVLTI
250      260      270      280      290      300

cry2ab2_820  290      300      310      320      330      340
PQQTQSFTSQDWPFLLYSFQNSVYLNFGSGARLSNTFNITGLPGSTTHALLAARVN
DPIGVGNLRLRGVGTTFNSNIENYARKKALFDYNGFQPIRFPQFQVGNASFNYSNGNVYS
310      320      330      340      350      360

cry2ab2_820  260      270      280      290      300      310
NSVLSGRITICDAYNVAADPFPSFOHKSJLTVQEWENTKKNKNSLYLDP-----IV-
10      20      30      40      50
HDTIKTTENNEVPTNHVQVPAETPNFTLEDLNYKEFLRMTDADNTNEALDSSSTTKDVQIK
10      20      30      40      50      60

cry2ab2_820  60      70      80      90      100      110
G-TVASFLKKVGSIVGKRILS---ELRNLIFFSGSTNLMODILREKFLNQLRNTDITL
GISVVGDLGVGFPGGALVSYFTNLTWPS--EDPKAFVEQVEALMDQKADYAK
70      80      90      100      110      120

cry2ab2_820  120      130      140      150      160      170      180
ARVNAELTGLQANVEFNRQVDNFL-NPNNNAVPLS---ITSSVNTWQQLFLNRLPQFQM
130      140      150      160      170      180
NKALAEQLGQLNNVEDYVSALSSQKPNVSRNPHSQGRIRELFSQAEFRNMSPSFAI
190      200      210      220      230      240

cry2ab2_820  180      190      200      210      220
QGYQLLLPLPFAQANLHLSPFROVLINADGWSIAATL-RYRDYDLKNTYDRYSNYCIN
190      200      210      220      230      240
SGYVEFLTTTAAQANLHLKDAQIYGEENGKEKEDIAEAFYKRLK-LTQETDHCVK
190      200      210      220      230      240

cry2ab2_820  230      240      250      260      270      280
TYQSAFKL-NTRLHDMLEFRIV--MFLNFEVYSIWSLFKYQSLLVSSGANLYASGSG
250      260      270      280      290      300

61221659      250      260      270      280      290      300
WYNYGLDKLRSGSYESWAFNRVREMTLVLDLALFFLYDVLRYPKVKVKTLLTRDVLTI
290      300      310      320      330      340

cry2ab2_820  290      300      310      320      330      340
PQQTQSFTSQDWPFLLYSFQNSVYLNFGSGARLSNTFNITGLPGSTTHALLAARVN

```

DPTVGVNNLRGVGTTFTFSNIENIRKPHFLFDYLHRIQIHFTRFQFGYGGNDSPFYMSGVNVV
 310 320 330 340 350 360
 cry2ab2_820.pep
 NRRAA:4688623
 4688623 source="GENBANK_PROT" Cry3Aa protein [Bacillus
 thuringiensis]gi|142734|gb|AAA22336.1| delta-endotoxin
 Initln: 114 Initn: 158 Opt: 277 z-score: 314.1 E(): 3.4e-09
 (652 aa)
 >>NRRA:4688623
 Initln: 158 Initl: 114 opt: 277 z-score: 314.1 expect(): 3.4e-09
 Smith-Waterman score: 278; 26.7% identity in 251 aa overlap
 (36-266:47-294)
 cry2ab2_820. NSVLNIGRTTICDAYNVAADHPFSQHKSLDTQKEMTEKKNHSLYLDP-----IV-
 10 20 30 40 50 60 70 80 90 100 110
 4688623 HDTIKITTENVEVPIHHVGYPLAETPNPTLEDLNVYKFLFETADNTEALDSSITTKVDVQIK
 20 30 40 50 60 70
 cry2ab2_820. G-TVASFLKKVGLSVGKRIIS---ELRNLIFFSGSTNLMDILRETEFLKRNLTDTLL
 60 70 80 90 100 110
 4688623 GISVGDGLGVGVFPFGGALVSFVTLNTIWS--EDPWKAFNEQVEALMOOKTADYAK
 80 90 100 110 120 130
 cry2ab2_820. ARVNAELNIGLQANVEEFNRQVDNPLNPNRNVAFLS---ITSSVNTMQQLFNLRLPQFQM
 120 130 140 150 160 170 180 190
 4688623 NKALAEIQSQQNVEDYVYSALSSWKQNPVSSRNPHSQGRIRLEFSQAESHFRNSMPSFAI
 160 170 180 190
 cry2ab2_820. CPTQLLPLFLPQAQNLHDSFTRVILNADENWIGISAATL-RTYRDYLNKNTYRDYSNYCIN
 200 210 220 230 240 250
 4688623 SGVGVGLTIYAAQVLAHFLIKRSQVIGEEGWYKEDIAFVKQKQ-LTQYIDHCVK
 220 230 240 250
 cry2ab2_820. TYQSAFQGLNTRSDHMLDEFTYVIFLNVEFVNSLKFQYGLSVSSGANLYASGG
 230 240 250 260 270 280
 4688623 WYNVGLDLRGSSYSWVNFNNVYREWGVVIALPLFDYDLQYLPKEVKTELTLDVLT
 260 270 280 290 300 310 320 330 340 350 360 370 380 390
 cry2ab2_820. PQQTQSTSDQWPFLLYSVLPQVNSVNLNPSQSRASNTFPPVGLPQSTVTHALLAARN
 280 300 310 320 330 340
 4688623 DPTVGVNNLRGVGTTFTFSNIENIRKPHFLFDYLHRIQIHFTRFQFGYGGNDSPFYMSGVNVV
 320 330 340 350 360 370 380 390
 cry2ab2_820.pep
 NRRAA:45934892
 45934892 source="GENBANK_PROT" insecticidal crystal protein [Bacillus
 thuringiensis]
 Initl: 114 Initn: 158 Opt: 277 z-score: 314.1 E(): 3.4e-09
 >NRRA:45934892

Study No. 06-01-62-01
MSL No. 20307
Page 244 of 361

[illegible]

Study No. 06-01-62-01

MSL No. 20307

Page 245 of 361

B469142
NONGIGTERQIRQ-PLHMDFFNTMTWTSYNRRREYVWSGLEMTAYFTGTGAGQVSPFLAG
290 290 300 310 320 330 340

```

370      380      390      400      410      420
cry2ab2_820.  FLPLLTFF-VRSMLDGSOREGAVTVNWQTESFETTLGLRSGATARGNSYPPDVFVI
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
8469142  TRGDAAPPNVRFSVND-----GIYIL--SAPPYSAFLGTSVLGSGRGEFMPA---L
350      360      370      380

```

```

ccry2ab2_820. 390 400 410 420 430 440 450 460 470 480
NNISGVLV-VRNEDLRRLHYNEIRNIASPGTGGARVMYSVNRKNHIAVHENG
NNISPPSARVYRNEGTVDLSLVPQDNVPPHRGSSHRLSHTVMNRSPFIWHTRSAT

```

cyab2_820. MIHLA^NDYGTGTSPIHAQVNNQTRFISEKFGNGDSLRFEQNNTTARTVTLRGNSG
490 500 510 520 530 540
TTNRINS^VVIIT-QIPMWKANLHAGATVVVRGGFTG-GDLIRTSGMWV--TLRADASA
884649142

450 460 470 480 490 500

CRY2AB 820. -----NLYLRYVSSIGNSTIRVTINGRVYATNVNTTNNNDGVNDGARFSDINIGTVVA

04-6942 VRNORIRFRYAATSNFYFVW- RGNLGVNGREIMTKMTSGELKASVF--LGERIT
510 520 530 540 550 560

846943 PPFEEVOPLOIEIETQSIFGGEVYLKIEFTPATITFEAEYDLERQAQVNALITSTIN 620

846942 RGNVDVTDYNDQNSNLVECLSDFECLDEKSELYKHAKRLSDERNLLQDPNFTSIN 680

cry2ab2.820.pep
 SW:8469142

library=NA species="Bacillus thuringiensis" source="swissprot.p
version=NA type=PRT

intn: 209 in1: 153 opt: 280 z-score: 113.2 expect: 3.7e-09
Smith-Waterman score: 325; 21.6% identity in 607 aa overlap
(54-634:32-598)

8469142	10	20	30	40	50
EINNOQCIYPNCLSNPEEVLIDGERILPDIDPLEVMSLLQFLNIF-VPGGASISL					

8469142
FDKINGALRPSDWELFLAQIEQLDQRIEATVRKNAEGLGRSQLVVVEAPEWEEET
60 70 80 90 100 110

Study No. 06-01-62-01
MSL No. 20307
Page 246 of 361

```

protein). " library=NA species="Bacillus thuringiensis serovar kurstaki"
source="swissprot_prot" version=NA type=PRT

SCORES   Init1: 206      Initn: 233      Opt: 280      z-score: 312.9 E(): 3.9e-09
>>SW:61221651
initn: 233 init1: 206 opt: 280 z-score: 312.9 expect(): 3.9e-09
Smith-Waterman score: 284;    25.9% identity in 251 aa overlap
(56-297:68-303)

cry2ab2_820. DPFSFOHKS LDTVQKEWTEWKNNHS LYLDPDVGTVASFLKKVLGSLGVKRLISELNLNI
30          40          50          60          70          80
-->SW:61221651
EGNNDIPFVSASTVTQTGINIAGRILGLVGPFAQLASFY----SFLVGE-----L-L
40          50          60          70
cry2ab2_820. FPGSGNLMDQILRETEKFNLORNLTDTLARLNVAELTGLQANVEENRQVDNFLNPRNA
90          100         110         120         130         140
-->SW:61221651
WPGRG-DQWEIFLEHVQLINQITENRANTALARGLOGDSFRAYQQSLDWLEDNRDDA
90          100         110         120         130         140
cry2ab2_820. VPLSITSSVNTMOOL-FINLPPOFGOYQLLLPLFAQAANIHLISFDRIVLNADGWGI
150         160         170         180         190         200
-->SW:61221651
RTSRVLYTQYALELDLFNAMLPFAIRNQEVFLMWYAQAANLHLLLRDASLFCSEFGL
150         160         170         180         190         200
cry2ab2_820. SIWSLPFKGOYLSLVSGANL---YASGGPQQTOSTSDWPELYSLFQVNSVNLNGFS
210         220         230         240         250         260
-->SW:61221651
TSOEIQRYVERQERTRDYSDYCVENYTGSLNLRGTNAASWRYNQRFRODLITLGVLIDLVL
210         220         230         240         250         260
cry2ab2_820. ALFPSYDIETYPINTSAQLTRREVYDAIGATGV-NMASMMWNYNAPSFAIEAAAIRSP
270         280         290         300         310         320
-->SW:61221651
GARKLSMTFNFIIVGLPGSTTHALLAARNVYSGGISGDIGASPQNFCNSTFPPLPLLT
330         340         350         360         370         380
HLILDLEQLTIFFSASSRNTRHWYWRGHITQSRPIGGGLNTSHGATNTSNIPVTLRF
330         340         350         360         370         380
cry2ab2_820.pdp
NRAA-14486714

cry2ab2_820. DPFSFOHKS LDTVQKEWTEWKNNHS LYLDPDVGTVASFLKKVLGSLGVKRLISELNLNI
30          40          50          60          70          80
-->SW:61221651
EGNNDIPFVSASTVTQTGINIAGRILGLVGPFAQLASFY----SFLVGE-----L-L
30          40          50          60          70          80

```

61221651 description="Pesticidal crystal protein crylBa (Insecticidal delta-endotoxin CryIB(a)) (Crystalline entomocidal protoxin) (140 kDa crystal


```

crry2ab2.820. 210 220 230 240 250
SAAATATYRDYKUNTYRDYKNYCI---NTYQAFKGLNT-RLMDMLIEFTYFWLNVFYY
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
TSEIQRYRYQVERQVTDYSDYCVENYNTGLNSLFGTNAASWRYNQFRDITLGVLDLV
580949 210 220 230 240 250

```

[illegible]

cy2ab2_820. GARLSNFTFNIVGLFGSTTTALLAARVNSGGISSGDIGASPNFONFCSTFLPPLLTP
320 330 340 350 360 370
HLLDFLEQLTISASSAWSNTRHWTWYRGHTTQSPPTGGGINTSTGTAINTSINPVTLLRF
320 330 340 350 360 370

crv2ab2_820.pep
SW:134562

```
DATA-ENDOTOXIN CRVB(A) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (140 KDA CRYSTAL-  
LIZING PROTEIN)." library=NA species=Bacillus thuringiensis serovar entomocidus  
source=swissprot_prot" version=NA type=PR
```

SCORES INFLIR 206 inltn: 213 opt: 280 2-score: 312.9 E(I): 3.9e-00
 5.56W 15842 inltn: 213 inltn: 283 inltn: 206 opt: 280 2-score: 312.9 E(I): 3.9e-00
 Smith-Waterman score: 384 25.9% identity in 251 aa overlap
 (56-297:58-303)

cry2ab2_820 DPSPFQSLDIDVQKRWTKNNHSIYLDPIGVGTVASFLKKVGSIVGKRLISERNLI 30 40 50 60 70 80
 1345842 EGNIDPFVASTTITNAGRLVGLVGPFGOLASFY-----SFLVGE 50 60 70

~~cry2ab2_820.FPSSGNTLMQSLITKFNFOINTDIARNNALIGLOANTVEENRVDNFLPNENA~~

: :

1345942.WPRGR-DOWEIELEECGNOCIOINAEATLAFGLCSGSFVAVCOUSLEDWLNRRDA

90 100 110 120 130 140

```
cry2ab2_820. VPISTISSVNTMOOI-FLNLFPOFGVOLLILLAFANLHLS-TIDNLTINADENGI  
: : | | | | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
RTSRVLYTOYIALELDNFAMPUPFARNQOGLDNYACRANLHLILRLDASLDFSGEGL
```

ccry2ab2_820. SAALLTYDYLYKNTYRDYSNYCI---NTYQSFAKGLNT-RHJHDLEPRHTYHTEFYV
:
TSOEIRYYVERQVERTDYSDYCVENWTGSLRGJTNAAWSRYNFOFNDLTLLSJDJW
210 220 230 240 250 260

ccry2ab2_820. SWSLKFYKQSLVSGANL---YASGSGPQOTQSTSQDWPFYLSLFQVNSNYDNGFS
11345842 ALPFSYDTFTYPTSQQLTRVYTDIGATGV-NMAGMWHYNNAPSFSAIEAAAIRSP

cry2ab2_820.	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	
46409861	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
1345842	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
cry2ab2_820.pap	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
46409861	10	20	30	40	50	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
46409861	10	20	30	40																																																																																																

©01

```
cry2ab2_820. 190 200 210 220 230 240
260 270 280 290 300 310
cry2ab2_820. VSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLLYSLFQVNSVYLVNGFSGAR
61221643 VSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLLYSLFQVNSVYLVNGFSGAR
250 260 270 280 290
cry2ab2_820. 320 330 340 350 360 370
380 390 400 410 420 430
cry2ab2_820. LSNTPFNVLGSGSTTHALLAARVYVGGISSGQGNAPFNQFNCSFTLPPLL-----
61221643 RS---PHEMDILNSITITVD-AHRGEYV--SGHOIMASVPG--FSGPEFTFLYGTMGV
300 310 320 330 340 350 360 370 380 390 400 410 420 430
cry2ab2_820. 430 440 450 460 470 480 490 500 510 520 530 540
550 560 570 580 590 600
cry2ab2_820. --TPFVR--VNEDELRRPLHNEIKNIASPSGTPGGRAYMVSVHNRKNHIAVHENGSM
61221643 SGTVDSLDEIPQNNVPPROGFSHRJSHVSMFRSGFNSSVSI--IRAPMFSWIHRSAREF
410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600
cry2ab2_820. 490 500 510 520 530 540 550 560 570 580 590 600
61221643 NNIIIPS--SQITQIPLTKSTNLGSGTSVVGKPGFTG--GDILARTSPGQIS--TLRVNITA
470 480 490 500 510 520 530 540 550 560 570 580 590 600
cry2ab2_820. 550 560 570 580 590 600 610 620 630
61221643 PLSQRYRVRIRYASTTNLOFHTSIDGRPNQGNFSATMS--GSNLSQSGSFTVGFITPFN
520 530 540 550 560 570 580 590 600 610 620 630
cry2ab2_820. 610 620 630
61221643 KTDVTDYHIDQVNLVECLSDFCLEKKELSEKVKHAKLSDERNLLQDPNFRGINRQL
640 650 660 670 680 690
cry2ab2_820.pep
SW:61221650
```

delta-endotoxin CryIIA(b)) (Crystalline entomocidal protein) (130 kDa crystal protein)." library=NA species="Bacillus thuringiensis serovar aizawai" sources="swissprot_prot" version=NA type=PRT

SCORES Initl: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>>SW:61221650
initn: 168 initl: 128 opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

```
cry2ab2_820. FOHSLDVTQKEWTEMKNNHSLYLDPIVGTVAFLKKVGLVGRILSELRLNLIFFSG
61221650 IPYNCLSNPEVEVLGGRIETGYTPIIDISLSLTQFLSEF--VPGAGFVLGLVDLIWGIF
20 30 40 50 60
cry2ab2_820. 90 100 110 120 130 140
150 160 170 180 190 200
61221650 STNLMODILRETEFLNRLNLTDTLARNVAELTGL-----QANVEEFNRQVDNLFNPNRNA
70 80 90 100 110 120 130 140 150 160 170 180 190 200
cry2ab2_820. 150 160 170 180 190 200
210 220 230 240 250
61221650 LAEEMRIQFNDMNSALTITAIPLFAVQNVQVPLLSVYVQAANLHLSVLRDVSFVGORGFD
130 140 150 160 170 180 190 200 210 220 230 240 250
cry2ab2_820. 210 220 230 240 250
260 270 280 290 300 310
61221650 AATLRTRDYLNKTRDYSNCINTVQSAFK---GLNIRLHML---EPTYMFNLNVEFY
190 200 210 220 230 240 250
cry2ab2_820. 260 270 280 290 300 310
320 330 340 350 360 370 380 390 400
61221650 VSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFLLYSLFQVNSVYLVNGFSGAR
250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
cry2ab2_820. 430 440 450 460 470 480
490 500 510 520 530 540 550 560 570 580 590 600
61221650 PLSQRYRVRIRYASTTNLOFHTSIDGRPNQGNFSATMS--GSNLSQSGSFTVGFITPFN
520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
```



```
61221650 KTDVTDYHIDQVSNLVECLDSECLDEKKEKSEKVKHAKSLDERNLLODPNFRGINRQL
640 650 660 670 680 690

cry2ab2_820.pep
SW:117533
117533 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAB (INSECTICIDAL
DELTA-ENDOTOXIN CRYIA(B)) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (130 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version="NA type="PRT

SCORES Init1: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>>SW:117533
Initn: 168 Init1: 128 Opt: 278 Z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHKSLEDTQKEWTEWKNNHSLYLDPIVGTVASFLKKVGLVKRILSELNLIFFPSG
30 40 50 60 70 80
cry2ab2_820. STNLMDILRETEKFLNQLNTDTILARVNAELTGL---QANVEEFNRQVDNFIENRVA
90 100 110 120 130 140
117533 GPSQWDAFLVQIQEQLINQRIEFARNOAISRLGLESLNLYQIYAESFREWEADTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQQLFNLRFQOMQGYQLLLPLFAQANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200
117533 LREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF
130 140 150 160 170 180

cry2ab2_820. VSIWLSFKYQSLVSSGANLVASGGPQQTCSFTSQDWPFLYSLFOVNSVNLGFGSGAR
260 270 280 290 300 310
117533 VSLFPNYDSRTYPIRTVSQI-----TREIYTN---PVLEN-FDGSFRGSAQGIIEGSI
250 260 270 280 290

cry2ab2_820. LSNTFPNVLPGSITTHALAAARVNSGGISGDIAGFPNQFNCSFTFLPPL-----
320 330 340 350 360 370
117533 RS---PHLMDILNSITITD-AHRGEYWM--SGHQIMASFPV--PSGPEFTFLYGTMGN
300 310 320 330 340

cry2ab2_820. --TPPVR--SWLDSGSDREGVATV--TNWQTESFETTLIGRSAGFTARGNSYFPDFIRN
380 390 400 410 420
117533 AAPQQRVAQLGQGVYRTLSLTVRRPFNIGINNQQSLVLDGTEFAYGTSNLPSPAVYRK
350 360 370 380 390 400

cry2ab2_820. ISGVPLV--VRNEDLRPLHYNEIRNIASPSGTPGCGARAYMYSVHNKKNHIAHENGSM
430 440 450 460 470 480
```

```
117533 SGTVDLSDEIPQNNVPPRQSGFSLSHVMSFSGSNSSVSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460

cry2ab2_820. IHLAPNDYGTITSPI-HATQVNNQRTFISEKFGNOGDSLRFEQNNITARYLGRN---
490 500 510 520 530 540
117533 NNIIPS--SQITQIPLTKSTNLGSGTSVVKGPGFTG-GDILRRTSPGIS--TLRVNITA
470 480 490 500 510

cry2ab2_820. --GNSNLYLKVSSIGNSITRVINGRVYATNNTINNDGVNDGARFSDINIGNVVA
550 560 570 580 590 600
117533 PLSQRYRVIRIYASTTNLQHTSIDGRPINQGNFSATMSS--GSNLOSQSFRTVGTPTFFN
520 530 540 550 560 570

cry2ab2_820. SSNSDVPDLINVTLSNGTQFDLMNIMLVPTNISPLY
610 620 630
117533 FNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGL
580 590 600 610 620 630

117533 KTDVTDYHIDQVSNLVECLDSECLDEKKEKSEKVKHAKSLDERNLLODPNFRGINRQL
640 650 660 670 680 690

cry2ab2_820.pep
NFAA:40273
40273 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|216280|dbj|BAA00071.1| delta-endotoxin [Bacillus thuringiensis
serovar kurstaki]gi|3746545|gb|AAC64003.1| crystal protein [Bacillus
thuringiensis serovar kurstaki]gi|27436100|gb|AAO33302.1| crystal endotoxin
CryIAb [Bacillus thuringiensis]gi|2590352|gb|AANT6494.1| insecticidal protein P
[Bacillus thuringiensis]gi|61221643|sp|P0A370|CRLAB_BACTK_Pesticidal crystal
...

SCORES Init1: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>>NRAA:40273
Initn: 168 Init1: 128 Opt: 278 Z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHKSLEDTQKEWTEWKNNHSLYLDPIVGTVASFLKKVGLVKRILSELNLIFFPSG
30 40 50 60 70 80
40273 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEF--VPGAGFVLGLVDIIWGIF
20 30 40 50 60

cry2ab2_820. STNLMDILRETEKFLNQLNTDTILARVNAELTGL---QANVEEFNRQVDNFIENRVA
90 100 110 120 130 140
40273 GPSQWDAFLVQIQEQLINQRIEFARNOAISRLGLESLNLYQIYAESFREWEADTNP---A
70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQQLFNLRFQOMQGYQLLLPLFAQANLHLSFIRDVILNADEWGIS
150 160 170 180 190 200
40273 LREEMRIQFNDMNSALTATPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF
130 140 150 160 170 180

cry2ab2_820. AATLRTRYDLYKNTVDYNSVNCINTYQSAFK--GLNTRLHMDL---EFTYMFNLVFEY
210 220 230 240 250
```


Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 251 of 361

40273 AATINRYNDRLNLSNYTDHVRWYNTGLERVMPGDSR--DWIRYNQFRRLTLVLVDI
190 200 210 220 230 240
cry2ab2_820. VSMWLFVRLVSSGNYVSGSPQOTSQDMPFLYSLSFVNSYLVNGFSGAR
250 260 270 280 290 300 310
40273 VSLFNYDSRTIPRTVSOQ-----TREIYTN---PVLEN-FDGSFRGSAQGIESI
250 260 270 280 290 300 310
cry2ab2_820. LSNTPFNIVGLPGSTTHALLAARVNGSGSSGDIASPNQNFNCSTFLPPLL-----
320 330 340 350 360 370 380
40273 RS---PHLMDIINSITITVD--AHGGEYVW--SGHQIMASPVG--FSGPEFTFPLYGTMGN
300 310 320 330 340 350 360
cry2ab2_820. -TFPVR--SWLDSGSDREGVATV--TNWQTESFETTLGLRSGAFTAGNSYFFDIERN
370 380 390 400 410 420 430
40273 AAPQQRIVAQOGGVYRTLSLTYRRPFNIGINNOQLSWDGTETAYGSSNLPASVYRK
350 360 370 380 390 400 410
cry2ab2_820. ISGVPLV--VRNEDLRPLVHNEIRNIASPGTGGARAYMVSVHNRKNNIHAVHENGSM
430 440 450 460 470 480 490
40273 SGTVDSLDEIPQNNVFPQGSFRLSHVSMFRSGFSNVSYSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460 470
cry2ab2_820. IHLAPNDYGTFTISPI--HATQVNNQTRTISEKFGNQGSRLRPQNNITARTLGRN---
490 500 510 520 530 540 550
40273 NNIIIPS--SQITQIPLTKSTNLGSGTSVVKGPFGTG--GDILRRTPSQGIS--TLRVNITA
470 480 490 500 510 520 530
cry2ab2_820. --GNSYLVLRVSSIGNSITRTVINGRYVATNTVNTTNDGVNDNGARSDINIGNVVA
550 560 570 580 590 600 610
40273 PLSQRYVRIRYASTNLIQFTSIDGRPNQGNFSATMSS--GSNLQSGSFRTVGFTTFPN
520 530 540 550 560 570 580
cry2ab2_820. SSNSDVPDLINV--TLNSGTQFDLMNIMLVPTNISPLY
610 620 630 640
40273 FSGSSVFTLSARHVFNSGNEVYIDRIEFVPAEVTFEAEVDLERAKQAVNELFTSSNQIGL
580 590 600 610 620 630 640
40273 KTDVTDYHIDQVSNLVECLSDFECLDEKSELSEKVKHAKRLSDERNLLQDPNFRGINROL
640 650 660 670 680 690 700
cry2ab2_820.pcp
SW:61221646
61221646 description="Pesticidal crystal protein cryIAb (Insecticidal
delta-endotoxin CryIA(b)) (crystalline entomocidal protoxin) (130 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar berliner"
source="swissprot_prot" version="NA type="PRT
SCORES Init: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>SW:61221646
Initn: 168 init: 128 opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

30 40 50 60 70 80
cry2ab2_820. FOHKSLSLTVQKEWTEWKNKNSLVLDDIVGTIVASFLKKVGLVKGKILSELNLIFPFG
90 100 110 120 130 140
61221646 IPYNCLSNPGEVILGGERIETGYTPIDISLSLTQFLLEF--VPGAGVILGLVDIIWGIF
20 30 40 50 60 70
cry2ab2_820. STNLMQDILRETEKFLNQLNTDTLARNVAELTGL-----QANVEFNQVDNLFNENRNA
90 100 110 120 130 140
61221646 GFSQWDAFLVQIQEQLNQIRIEFARNQAIKSLGLEGLNLYQIYAESFREMEADPTNP--A
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVNTMQQLFNLPQFOMQGYQLLLPLFAQAANLHLSFRDVLNADWGIS
150 160 170 180 190 200
61221646 LREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRLDVSFQRMGFD
130 140 150 160 170 180
cry2ab2_820. AATLRTYRDYKNTDYNSYNTYQSAFK---GLNTRLHML---EFRTYMLNVEFY
210 220 230 240 250 260
61221646 AATINSRYNDLTRIGNYTOHARWYNTGLERVMPGDSR--DWIRYNQFRRLTLVLVDI
190 200 210 220 230 240
cry2ab2_820. VSMWLFVRLVSSGNYVSGSPQOTSQDMPFLYSLSFVNSYLVNGFSGAR
260 270 280 290 300 310
61221646 VSLFNYDSRTIPRTVSOQ-----TREIYTN---PVLEN-FDGSFRGSAQGIESI
250 260 270 280 290 300
cry2ab2_820. LSNTPFNIVGLPGSTTHALLAARVNGSGSSGDIASPNQNFNCSTFLPPLL-----
320 330 340 350 360 370
61221646 RS---PHLMDIINSITITVD--AHGGEYVW--SGHQIMASPVG--FSGPEFTFPLYGTMGN
300 310 320 330 340 350
cry2ab2_820. -TFPVR--SWLDSGSDREGVATV--TNWQTESFETTLGLRSGAFTAGNSYFFDIERN
370 380 390 400 410 420
61221646 AAPQQRIVAQOGGVYRTLSLTYRRPFNIGINNOQLSWDGTETAYGSSNLPASVYRK
350 360 370 380 390 400 410
cry2ab2_820. ISGVPLV--VRNEDLRPLVHNEIRNIASPGTGGARAYMVSVHNRKNNIHAVHENGSM
430 440 450 460 470 480 490
61221646 SGTVDSLDEIPQNNVFPQGSFRLSHVSMFRSGFSNVSYSI--IRAPMFSWIHRSAEF
410 420 430 440 450 460 470
cry2ab2_820. IHLAPNDYGTFTISPI--HATQVNNQTRTISEKFGNQGSRLRPQNNITARTLGRN---
490 500 510 520 530 540 550
61221646 NNIIIPS--SQITQIPLTKSTNLGSGTSVVKGPFGTG--GDILRRTPSQGIS--TLRVNITA
470 480 490 500 510 520 530
cry2ab2_820. --GNSYLVLRVSSIGNSITRTVINGRYVATNTVNTTNDGVNDNGARSDINIGNVVA
550 560 570 580 590 600 610
61221646 PLSQRYVRIRYASTNLIQFTSIDGRPNQGNFSATMSS--GSNLQSGSFRTVGFTTFPN
520 530 540 550 560 570 580
cry2ab2_820. SSNSDVPDLINV--TLNSGTQFDLMNIMLVPTNISPLY
610 620 630 640
61221646 FSGSSVFTLSARHVFNSGNEVYIDRIEFVPAEVTFEAEVDLERAKQAVNELFTSSNQIGL
580 590 600 610 620 630 640
61221646 KTDVTDYHIDQVSNLVECLSDFECLDEKSELSEKVKHAKRLSDERNLLQDPNFRGINROL
640 650 660 670 680 690 700
cry2ab2_820.pcp
SW:61221646
61221646 description="Pesticidal crystal protein cryIAb (Insecticidal
delta-endotoxin CryIA(b)) (crystalline entomocidal protoxin) (130 kDa crystal
protein)." library="NA species="Bacillus thuringiensis serovar berliner"
source="swissprot_prot" version="NA type="PRT
SCORES Init: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>SW:61221646
Initn: 168 init: 128 opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)


```
61221646 KTDVTDYHIDQVSNLVECLDFECLDEKELSEKVKHAKRLSDERNLLQDPNFRGINRQL
640 590 600 610 620 630
580 590 600 610 620 630
cry2ab2_820.pcp
NRAA:10440886
10440886 source="GENBANK_PROT" delta endotoxin [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>>NRAA:10440886
initn: 168 initl: 128 opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)
cry2ab2_820. FQKSLDVTQKTEWTKNNHSLYLDPIVGTVASFLKKVGLSKRLSELNLIFFSG
30 40 50 60 70 80
cry2ab2_820. STNLMDILRETEKFLNQLRTDILARVNAELTGL---QANVEEFNRQVDFNLFPNRNA
90 100 110 120 130 140
10440886 GPSQWDALFVQIEQLINQRIEFARNAQISRLGLSNLYQVYAESFREWADPTNP--A
70 80 90 100 110 120
cry2ab2_820. VPSITSSVNTMQQLFLNRLPQFMQGYQLLLPLPFAQAANLHLSFIRDVILNADWGIS
150 160 170 180 190 200
10440886 LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAANLHLSVLRDVSFGQWGF
130 140 150 160 170 180
cry2ab2_820. VSIWLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFYLSFQVNSVYLNFGSGAR
260 270 280 290 300 310
10440886 VSLFPNYSRTPYPIRTVSQL-----TREIYTN---PVLEN-FDGSFRGSAQGIIEGI
250 260 270 280 290
cry2ab2_820. LSNTFPNVLPGSTTHALLAARNVYSGGSDIGASPFPNQFNCSITFLPLL-----
320 330 340 350 360 370
10440886 RS---PHLMDILNSITITVD-AHRGEYV--SGHQIMASPVG--FSGPEFTFLYITGMN
300 310 320 330 340
cry2ab2_820. -TPFVR--SWLDGSDREGVATV--TNWQTESFETTLGRSCAPTAGNSNYFPDYFIEN
380 390 400 410 420
10440886 AAPQQRVAQLGQGVYRTLSLTFRPFNIGINNQLSLVDGTFTYSSNLPSSAVYFK
350 360 370 380 390 400
cry2ab2_820. ISGVPLV--VRNEDLRRPLHYNEIRNIATSPGTPGCGARAYVSHNRKNHIAVHENGSM
430 440 450 460 470 480
10440886 SGTVDSDLEITPQNNVFPFQGFHRLSHVSMFRSFSNSSVSI-IRAPMFSIHRSAEF
430 440 450 460 470 480
cry2ab2_820. IHLAPNDYTGFTSPY-HATQVNNQTRTFISEKFGNQSLSRFEQNNITARYLRGN---
490 500 510 520 530 540
10440886 NNIIPS--SQITQIPITKTNLGSCTSVKGPFTG-GDILARTSPGOIS--TLRVNITA
470 480 490 500 510
cry2ab2_820. --GNSYNYLVRVSSIGNSTIRTVYATVNTTNDGVNDNGARFSDINIGNVVA
550 560 570 580 590 600
10440886 PUSQRYRIRYATSTNLQPHSIDGRFINQCNFSAIMSS--GSNLQSGSFRTVGTTFPFN
520 530 540 550 560 570
cry2ab2_820. SSNSDVPDLIDNV-TLNSGTQFQDLNIMLVPNTISPLY
610 620 630
10440886 FNGSSVFTLSARVNSGNEVVDRIEFVPAEVTFEAEYDLERAAQKAVNELFTSSNOIGL
580 590 600 610 620 630
10440886 KTDVTDYHIDQVSNLVECLDFECLDEKELSEKVKHAKRLSDERNLLQDPNFRGINRQL
640 650 660 670 680 690
cry2ab2_820.pcp
NRAA:40255
40255 source="GENBANK_PROT" unnamed protein product [Bacillus thuringiensis]
SCORES Initl: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>>NRAA:40255
initn: 168 initl: 128 opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)
cry2ab2_820. FQKSLDVTQKTEWTKNNHSLYLDPIVGTVASFLKKVGLSKRLSELNLIFFSG
30 40 50 60 70 80
40255 IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLLEF--VFGAGFVLGLVDLIWGF
20 30 40 50 60
cry2ab2_820. STNLMDILRETEKFLNQLRTDILARVNAELTGL---QANVEEFNRQVDFNLFPNRNA
90 100 110 120 130 140
40255 GPSQWDALFVQIEQLINQRIEFARNAQISRLGLSNLYQVYAESFREWADPTNP--A
70 80 90 100 110 120
cry2ab2_820. VPSITSSVNTMQQLFLNRLPQFMQGYQLLLPLPFAQAANLHLSFIRDVILNADWGIS
150 160 170 180 190 200
40255 LREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAANLHLSVLRDVSFGQWGF
130 140 150 160 170 180
cry2ab2_820. AATLRTYRDKNYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFTYMFNLVFEY
210 220 230 240 250
40255 AATINSYNDLTRIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRELTLVLDI
190 200 210 220 230 240
cry2ab2_820. AATLRTYRDKNYTRDYSNYCINTYQSAFK---GLNTRLHDML---EFTYMFNLVFEY
210 220 230 240 250
40255 AATINSYNDLTRIGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRELTLVLDI
190 200 210 220 230 240
cry2ab2_820. VSIWLFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFYLSFQVNSVYLNFGSGAR
260 270 280 290 300 310
40255 VSLFPNYSRTPYPIRTVSQL-----TREIYTN---PVLEN-FDGSFRGSAQGIIEGI
250 260 270 280 290
```


CRY2AB2_820. VFLSITSSVNTMOQLFNLKPOFGQYQVQLLLPLFAQANLHLSFIRDVILNADWGIS
225669 LREENRIQFNDMMNSALTATPLFAVONYVPLLSVYVQAANLHLSVLDVSVFGQWGF
CRY2AB2_820. RATLRTYDYLKNTYDYSNYCINTYQSAFK--GLNTRLHDM--EFTYMLNVFEY
225669 AATINRSYNDLTLLIGNYDTHAVRWYNGIERVWGPDSR--DWIRYNOFARELTLTLDI
CRY2AB2_820. VSIWELFYQSLVSSCANLYASGSGPQQTOSTQDMPFLYSLFQVNSNYVLNFGSGAR
225669 VSLFPNYSRTPYRTVSQ--TREIYTN--PVLEN--PDGSGFRGSAQIGESI
CRY2AB2_820. LNTFPNVLPGSGTTHALLAARVNYSGGSSGDIAGSPFNQNCSTFLPPL--
225669 RS---PHLMDILANSITTYD--AHRGEYTW--SGHQIMASVPG--FSGPEFTFLYGTMGN
CRY2AB2_820. TPFVLR--SWLDSGSDREGVATV--TNNOTESFETTLGLRSGAFTARGNSNYFPDYFIRN
225669 ANQORIVAQCGQVIRTLSSLYRPNINNOQLSVLDGTETAYGTSSNLPSAVYRK
CRY2AB2_820. ISGVPLV--VRNEDLRRLPHVNEIRNIASPSGTPGGARAYMVSVHNRKNHIAVHENGSM
225669 SGVDSLEIPQNNVPPROGFSHRLSHVSMRSGNSSVSI--IRAPMFESWIHRSAEF
CRY2AB2_820. IHSAPNVTGFTIPI--HATQVNNOTRIFISEKFGNQGDSLRFPQNNITARYTIRN--
225669 NNIIPS--SQITQIPLTSTNLGSGTSVWKGPGFTG--GDILRRTPSGQS--TLRVNITA
CRY2AB2_820. --GNSNLYLRVSSIGNSLRTINGR--TNTNTTINDGVNDNGARFSDINIGNVVA
225669 PLSQRYVRIRYASTTNLQPHIS--DGRINQNMSP--SS--GSMQSGFRTVGTFTPFN
CRY2AB2_820. SSNSDVPDLINV--TLNSGTQFDLMNIMLVPTNISPLI
225669 FNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEVLEAQAQAVNLFSSNQIGL
CRY2AB2_820. KTDVTDYHDQVSNLVECLSDPEFCLDEKSEKVKHAKRLSDERNLQDPNFRGINROL
225669 IPYNCNLSPEVVEGLGERIETGYTPTDISLSLTQFLLSSEF--VPGAGFVLGLVDIIGWIF
CRY2AB2_820. FOHKSILTQKTEWKKNNHSLYLDIPVGTVASFLIKKVGSLVCKRILSELNLIFFSG
225669 IPYNCNLSPEVVEGLGERIETGYTPTDISLSLTQFLLSSEF--VPGAGFVLGLVDIIGWIF
CRY2AB2_820. STNLMQDLIRETEKFLNQLNTDILARVNAELTCL---QANVESFNEQVDFNPNRVA
225669 GPSQWDAPLQVQIEFQINQRIEFARNQAIKRLGCLSNLYQIYAESFREWADPNP---A

CRY2AB2_820. VFLSITSSVNTMOQLFNLKPOFGQYQVQLLLPLFAQANLHLSFIRDVILNADWGIS
225669 LREENRIQFNDMMNSALTATPLFAVONYVPLLSVYVQAANLHLSVLDVSVFGQWGF
CRY2AB2_820. RATLRTYDYLKNTYDYSNYCINTYQSAFK--GLNTRLHDM--EFTYMLNVFEY
225669 AATINRSYNDLTLLIGNYDTHAVRWYNGIERVWGPDSR--DWIRYNOFARELTLTLDI
CRY2AB2_820. VSIWELFYQSLVSSCANLYASGSGPQQTOSTQDMPFLYSLFQVNSNYVLNFGSGAR
225669 VSLFPNYSRTPYRTVSQ--TREIYTN--PVLEN--PDGSGFRGSAQIGESI
CRY2AB2_820. LNTFPNVLPGSGTTHALLAARVNYSGGSSGDIAGSPFNQNCSTFLPPL--
225669 RS---PHLMDILANSITTYD--AHRGEYTW--SGHQIMASVPG--FSGPEFTFLYGTMGN
CRY2AB2_820. TPFVLR--SWLDSGSDREGVATV--TNNOTESFETTLGLRSGAFTARGNSNYFPDYFIRN
225669 ANQORIVAQCGQVIRTLSSLYRPNINNOQLSVLDGTETAYGTSSNLPSAVYRK
CRY2AB2_820. ISGVPLV--VRNEDLRRLPHVNEIRNIASPSGTPGGARAYMVSVHNRKNHIAVHENGSM
225669 SGVDSLEIPQNNVPPROGFSHRLSHVSMRSGNSSVSI--IRAPMFESWIHRSAEF
CRY2AB2_820. IHSAPNVTGFTIPI--HATQVNNOTRIFISEKFGNQGDSLRFPQNNITARYTIRN--
225669 NNIIPS--SQITQIPLTSTNLGSGTSVWKGPGFTG--GDILRRTPSGQS--TLRVNITA
CRY2AB2_820. --GNSNLYLRVSSIGNSLRTINGR--TNTNTTINDGVNDNGARFSDINIGNVVA
225669 PLSQRYVRIRYASTTNLQPHIS--DGRINQNMSP--SS--GSMQSGFRTVGTFTPFN
CRY2AB2_820. SSNSDVPDLINV--TLNSGTQFDLMNIMLVPTNISPLI
225669 FNSGSSVFTLSAHVFNSGNEVYIDRIEFVPAEVTFEAEVLEAQAQAVNLFSSNQIGL
CRY2AB2_820. KTDVTDYHDQVSNLVECLSDPEFCLDEKSEKVKHAKRLSDERNLQDPNFRGINROL
225669 IPYNCNLSPEVVEGLGERIETGYTPTDISLSLTQFLLSSEF--VPGAGFVLGLVDIIGWIF
CRY2AB2_820. FOHKSILTQKTEWKKNNHSLYLDIPVGTVASFLIKKVGSLVCKRILSELNLIFFSG
225669 IPYNCNLSPEVVEGLGERIETGYTPTDISLSLTQFLLSSEF--VPGAGFVLGLVDIIGWIF
CRY2AB2_820. STNLMQDLIRETEKFLNQLNTDILARVNAELTCL---QANVESFNEQVDFNPNRVA
225669 GPSQWDAPLQVQIEFQINQRIEFARNQAIKRLGCLSNLYQIYAESFREWADPNP---A

225669 source="GENBANK_PROT" insect control protein

SCORES Initl: 128 Initn: 168 Opt: 278 z-score: 311.1 E(): 4.9e-09
>NRAA:225669
Initn: 168 Initl: 128 Opt: 278 z-score: 311.1 expect(): 4.9e-09
Smith-Waterman score: 284; 22.4% identity in 604 aa overlap
(60-634:41-610)

CRY2AB2_820. FOHKSILTQKTEWKKNNHSLYLDIPVGTVASFLIKKVGSLVCKRILSELNLIFFSG
225669 IPYNCNLSPEVVEGLGERIETGYTPTDISLSLTQFLLSSEF--VPGAGFVLGLVDIIGWIF

CRY2AB2_820. STNLMQDLIRETEKFLNQLNTDILARVNAELTCL---QANVESFNEQVDFNPNRVA
225669 GPSQWDAPLQVQIEFQINQRIEFARNQAIKRLGCLSNLYQIYAESFREWADPNP---A

CRY2AB2_820.pep
SW:117543

117543 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE

[illegible][illegible]

©01

cry2ab2_820. -TPFVR--SWLDSGSDREGVATV--TNWQTESFETTLGSRGAGTARGNSYFPDYFIRN
142886 AAOQRIYVAGOGVYRVLSSLYRPFNIGINNOQLSVLDTEFAYGTSSNLPFSAYVRK
350 360 370 380 390 400

cry2ab2_820. ISGVPLV--VRNEDLRRPLHYNEIRNTASPSGTPGGARAYMVSVHNRKNIHVAHENGSM
142886 SGTVDLSDEIPPONNVPPROGFSHLSHVMSFSGNSSSVSI--IRAPMFSWIHSANF
410 420 430 440 450 460

cry2ab2_820. IHLAPNDYTGFTISPI--HATOVNNDRTFISEKFGNQGDSLRFEQNNTARYTLRGN---
142886 NNLIIS--SQITQIPLTSTKSLGSGTSVWVGPGFTG--GDLIRTSFGQIS--TLRVNITA
470 480 490 500 510 520 530 540

cry2ab2_820. --GNSYLYLRVSSIGNSITRVINGVYATNTVNTTNNQDNGNDNGARFSDINIGNVVA
142886 PLSQRYRIRYASTTNLOPHTSIHGRPINQGNFSATMSS--GNSLQSGSPRHLGFTTIPFN
520 530 540 550 560 570 580 590 600

cry2ab2_820. SENSVDPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
142886 FNSGVSFTLSAHVFNSGNEVYIDRIEFVPAEVFAEYDLERAQKAVNELFTSSNQIGL
610 620 630 640 650 660 670 680 690

142886 KTDVTDYHIDQVSNLVECLDFECLDEKEELSEKVKHANGLSDERNLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pep
SW:117539

117539 description="130 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE
ENTOMOCIDAL PROTOXIN) (5.3 CLASS)." library=NA species="Bacillus thuringiensis
serovar kurstaki" source="swissprot_prot" version=NA type=PRT

SCORES Init1: 128 Initn: 128 Opt: 277 z-score: 309.9 E(): 5.7e-09
>>SW:117539
Initn: 128 init1: 128 opt: 277 z-score: 309.9 expect(): 5.7e-09
Smith-Waterman score: 283; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHSLDITVQKEWTEWKNHSLYLDPIVGTIVASFLKKVGLSKRIISLRNLIPIPSG
117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

cry2ab2_820. STNLMQDILIRETEKFLNQRLNTDILARVNAELTGL----QANVEFNQVDNPLPNRNA
117539 GPSQWDAFLVQLEQLINQRIEFAFNQAISRLGLSNLYQIYAESFEWEADPTNP---A
150 160 170 180 190 200

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

117539 IPYCNLSNPEVEVLGGERIETGVTPIIDISLTLQELSEF--VPGAGFVLGLVDIIMGIF
70 80 90 100 110 120 130 140

cry2ab2_820. AATLRVRYLKNYTRDYSNVCINTQSAPK--GLNRLHDML---ERTYMFNLVFEY
117539 AATINSRYNDLRGLNIGNYTHARVWYNTGLERWVGPDNR--DWIRYNQFRRELTIVLDI
190 200 210 220 230 240

cry2ab2_820. VSIWFLFKVQSLVSSGANLYASGSGPQQTQSFTSODWPFYLSLFOVNSYVNLGFSGAR
117539 VSLFPNDKRTPIRTIVSQL-----TREIYTN---PVLEN--FGSGFSGSAQIGESI
250 260 270 280 290 300 310

cry2ab2_820. LSNTFPNIVGLPGSTTHALLAARVYNSGGISGDIAGSPFNQNFNCSTFLPELL-----
117539 RS---PHLMDILNITIVTD--AHRGEYV--SGHQIMASVPG--FSGPEFTFLYGTMCN
320 330 340 350 360 370 380 390 400

cry2ab2_820. -TPFVR--SWLDSGSDREGVATV--TNWQTESFETTLGSRGAGTARGNSYFPDYFIRN
117539 AAOQRIYVAGOGVYRVLSSLYRPFNIGINNOQLSVLDTEFAYGTSSNLPFSAYVRK
350 360 370 380 390 400

cry2ab2_820. ISGVPLV--VRNEDLRRPLHYNEIRNTASPSGTPGGARAYMVSVHNRKNIHVAHENGSM
117539 SGTVDLSDEIPPONNVPPROGFSHLSHVMSFSGNSSSVSI--IRAPMFSWIHSANF
410 420 430 440 450 460

cry2ab2_820. IHLAPNDYTGFTISPI--HATOVNNDRTFISEKFGNQGDSLRFEQNNTARYTLRGN---
117539 NNLIIS--SQITQIPLTSTKSLGSGTSVWVGPGFTG--GDLIRTSFGQIS--TLRVNITA
470 480 490 500 510 520 530 540

cry2ab2_820. SENSVDPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
117539 FNSGVSFTLSAHVFNSGNEVYIDRIEFVPAEVFAEYDLERAQKAVNELFTSSNQIGL
610 620 630 640 650 660 670 680 690

117539 KTDVTDYHIDQVSNLVECLDFECLDEKEELSEKVKHANGLSDERNLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pep
NRAA:143099

143099 source="GENBANK_PROT" insecticidal protein

SCORES Init1: 128 Initn: 168 Opt: 277 z-score: 309.9 E(): 5.7e-09
>>NRAA:143099
Initn: 168 init1: 128 opt: 277 z-score: 309.9 expect(): 5.7e-09
Smith-Waterman score: 288; 22.4% identity in 604 aa overlap

cry2ab2_820. SENSVDPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
117539 FNSGVSFTLSAHVFNSGNEVYIDRIEFVPAEVFAEYDLERAQKAVNELFTSSNQIGL
610 620 630 640 650 660 670 680 690

117539 KTDVTDYHIDQVSNLVECLDFECLDEKEELSEKVKHANGLSDERNLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pep
NRAA:143099

143099 source="GENBANK_PROT" insecticidal protein

SCORES Init1: 128 Initn: 168 Opt: 277 z-score: 309.9 E(): 5.7e-09
>>NRAA:143099
Initn: 168 init1: 128 opt: 277 z-score: 309.9 expect(): 5.7e-09
Smith-Waterman score: 288; 22.4% identity in 604 aa overlap

cry2ab2_820. SENSVDPLDINV--TLNSGTQFDLMNIMLVPTNISPLY
117539 FNSGVSFTLSAHVFNSGNEVYIDRIEFVPAEVFAEYDLERAQKAVNELFTSSNQIGL
610 620 630 640 650 660 670 680 690

117539 KTDVTDYHIDQVSNLVECLDFECLDEKEELSEKVKHANGLSDERNLQDPNFRGINROL
640 650 660 670 680 690

cry2ab2_820.pep
NRAA:143099

143099 source="GENBANK_PROT" insecticidal protein

(60-634:41-610)

cry2ab2_820. FQKSLDTVQKEMTEWKNHSLYLDPIVGTVASFLKKVGLSKVILSELNLIFFPG 30 40 50 60 70 80

143099 IPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLESEF--VPGAGFVLGLVDIIWGIF 20 30 40 50 60

cry2ab2_820. SINLMQDILRETEKFLNORLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPNRA 90 100 110 120 130 140

143099 GPSQWDAFLVQLEQLNQRIEFPARNQAISRLGLESLNLYQIYAESFREWADPTNP---A 70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGIS 150 160 170 180 190 200

143099 LREEMRIQFNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF 130 140 150 160 170 180

cry2ab2_820. AATLRTRDYLNKNTIRDYSNYCINTYQSAFK---GLNTRLHDM---EFRTYMFANVFEY 210 220 230 240 250

143099 AATINSRYNDLTRIGNYTDHAVRWYNTGLERVMGPDSE--DWIRYNQFRRELTLTVLDI 190 200 210 220 230 240

cry2ab2_820. VSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQVNSYVNLGFSGAR 260 270 280 290 300 310

143099 VSLFPNYSRTYPIRTVSQI-----TREIYTN---PVLEN-FDGSFALAQGIESI 250 260 270 280 290

cry2ab2_820. LSNTPFNIVGLPGSTTHALLAARVNSGGISGSDIGASPNQFNCSITFLPPL----- 320 330 340 350 360

143099 RS---PHLMDILNSITITVD-AHRGEYV--SGHQIMASPVG--FSGPEFTFLYGTMG 300 310 320 330 340

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

143099 AAPQORIVAQLGQGVYRTLSLTLYRRFNGINNOQLSVLDGTETFAFGTSSNLPSSAVYRK 350 360 370 380 390 400

cry2ab2_820. ISGVPLV--VRNEDLRRLPHVNEIRNIATSPSGTPGGARAYMVSVHNNKNIHVAHENGSM 430 440 450 460 470 480

143099 SGTVDLSDEIPQNNVPPROGFSRHLSHVSMRSGSNSVSI-IRAPMFSWIHRSAEF 410 420 430 440 450 460

cry2ab2_820. IHLAPNDYTGFTLSPI-HATQVNNQRTFISEKFGNQGSURFQNNNTIARYLRGN--- 490 500 510 520 530

143099 NNIIPS--SQITQIPLTKSTNLGSGTSVVKGPQFTG-GDILRRTSPQGIS--TLRVNITA 470 480 490 500 510

cry2ab2_820. --GNSINLYLRVSSIGNSIIRVTINGRVYATATVNTTNNQGVNDNGARSDINIGNVVA 550 560 570 580 590 600

143099 PLSORVIRVASTINLQFTSIDGRPINQGNFSATMS--GSNLQSGSFRTYGTTPFN 520 530 540 550 560 570

cry2ab2_820. SSNSDVPDLINV-TLNSGTQFDLNMIVETNISPLY 610 620 630

143099 FNGSSVTLARHVFNSGNEVIDRIEFVFAEYTFEAYEDLEPRAQKAVNELFTSSNQIGL 580 590 600 610 620 630

143099 KIDVTYHIDQVSNLECLSEDFCLDEKXELSEKVKHAKELSDERNLLQDPNFRGINRQL 640 650 660 670 680 690

cry2ab2_820.pap
NPAA:13173238

13173238 source="GENBANK_PROT" insecticidal crystal protein BTRX24 [Bacillus thuringiensis serovar kunthalarX24]

SCORES Init1: 128 Initn: 168 Opt: 276 z-score: 309.0 E(): 6.4e-09
>NPAA:13173238
Initn: 168 init1: 128 opt: 276 z-score: 309.0 expect(): 6.4e-09
Smith-Waterman score: 282; 22.4% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FQKSLDTVQKEMTEWKNHSLYLDPIVGTVASFLKKVGLSKVILSELNLIFFPG 30 40 50 60 70 80

13173238 IPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLESEF--VPGAGFVLGLVDIIWGIF 20 30 40 50 60

cry2ab2_820. SINLMQDILRETEKFLNORLNTDILARVNAELTGL---QANVEEFNRQVDNLFNPNRA 90 100 110 120 130 140

13173238 GPSQWDAFLVQLEQLNQRIEFPARNQAISRLGLESLNLYQIYAESFREWADPTNP---A 70 80 90 100 110 120

cry2ab2_820. VPLSITSSVNTMQQLFNRLPQFMQGYQLLLPLFAQAANLHLSFIRDVILNADWEGIS 150 160 170 180 190 200

13173238 LREEMRIQFNDMNSALITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGF 130 140 150 160 170 180

cry2ab2_820. AATLRTRDYLNKNTIRDYSNYCINTYQSAFK---GLNTRLHDM---EFRTYMFANVFEY 210 220 230 240 250

13173238 AATINSRYNDLTRIGNYTDHAVRWYNTGLERVMGPDSE--DWIRYNQFRRELTLTVLDI 190 200 210 220 230 240

cry2ab2_820. VSIWLSFKYQSLVSSGANLYASGSGPQQTQSFTSQDWPFYLSLFQVNSYVNLGFSGAR 260 270 280 290 300 310

13173238 VSLFPNYSRTYPIRTVSQI-----TREIYTN---PVLEN-FDGSFALAQGIESI 250 260 270 280 290

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

13173238 RS---PHLMDILNSITITVD-AHRGEYV--SGHQIMASPVG--FSGPEFTFLYGTMG 300 310 320 330 340

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

13173238 AAPQORIVAQLGQGVYRTLSLTLYRRFNGINNOQLSVLDGTETFAFGTSSNLPSSAVYRK 350 360 370 380 390 400

CRY2AB2_820. ISGVAV--VNEDERRPLHYNEIRNIASPGTGGARAYMVSVHNRKNNIHAVHENGSM
SGTQSDLPQNNPPQNGFSGHLSVMSFRSGNSGVSII-IRAPMFSWIHRSAEF
13173238 410 420 430 440 450 460

CRY2AB2_820. IHKRNNDVGTFTPTIATOVNNQNTTFSEKFGNQGDLSRFEQNTTARTYILRGN---
NNIIPS--SQTCTPLTKSNLGGTSVVKGGPGG-GLILRRISPGQIS--TLRVNITA
13173238 470 480 490 500 510

CRY2AB2_820. --GNSVNLVRSVSGTSTSTVAVNGRVKATNTTTNNDSVNDGARFSDINIGNVVA
PLSQRYVRIRYASTTLMQFHTSIRGPANOGNFSNMS--GSLQSGGRTVGTGTFPPN
13173238 520 530 540 550 560 570

CRY2AB2_820. SSSNDVPLDINV--TLNSGTQFDLMNIMLVPTNISMIY
FMSGSSVFTLSAHVFNSEVYIDRIETFEVPAEVTPEAEYDNERAQAVNKLFSSSAGL
13173238 580 590 600 610 620 630

13173238 KTDVTDYHQDVSNLVECLSDFECLDEKELSEKYNKAKRLSDERLDDPDERGINQD
640 650 660 670 680 690

CRY2AB2_820.pep
SW:8469147

8469147 description="PESTICIDIAL CRYSTAL PROTEIN CRY2AB (INSECTICIDIAL
DELTA-ENDOTOXIN CRY2AB(b)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (131 KDA CRYSTAL
PROTEIN) * library-NA species="Bacillus thuringiensis" source="swissprot_prot"
version-NA type=PRT

SCORES Initl: 152 Initn: 176 Opt: 275 z-score: 307.6 E(): 7.7e-09
>>SW:8469147
initn: 176 initl: 152 opt: 275 z-score: 307.6 expect(): 7.7e-09
Smith-Waterman score: 275; 23.4% identity in 286 aa overlap
(70-349:54-321)

CRY2AB2_820. QLFNLRLPQFMQSCYQILLPLPACQWHLSTFARQDNLNADENGISAATLRYDYLNK
8469147 DAERLETGNVADISGLINFLYSNFPVGGGFVIG--LLELWGFVGPQO---WEIFLA
30 40 50 60 70

CRY2AB2_820. ETEKFNQNLQNTDITLARVNAELTGLQANVEEFNRQVDNLF--NPNRNAVPLSITSSVNTMQ
8469147 QIEQLISQRIEFAFNQAISFLEGLSNVEIYETTFRAWEKDPSPNPALEEMRTQFNVMN
80 90 100 110 120 130 140 150

CRY2AB2_820. QLFNLRLPQFMQSCYQILLPLPACQWHLSTFARQDNLNADENGISAATLRYDYLNK
8469147 SALIAAIPLLRVNVEVALLSVYQAANLHLSVLKDVSVYQVQGRGDFPATVNSRYSDLTR
160 170 180 190 200 210

CRY2AB2_820. YTRDYSNCINTYQSAFKGLN--TRLHDML---EFTRYMFLNVEFVNSLWFKYQLSLLVS
8469147 LIHVTYDHCVDYNDGLNLEGRSLSDWVYVNRFRRLTISVLDIAFFPNYDIEAYPIQ
220 230 240 250 260 270

CRY2AB2_820. SGANLYASGSGPOQTGFTSDQWDFLYSLFOVNSVYLNGFSGARLSNTF--PNIVGLPGS
8469147 TAS-----QLTREVYLDLPVNETLSPASVPT--FSAAESALIRSPHLVDPLNS
280 290 300 310 320 330 340 350 360

CRY2AB2_820. TTHALLAARVNSGGISGGIDIGASFPNQFNCSITFLPPLTFPVRSMWLDGSGDREGVAT
8469147 FTIYTDSLASYAVWGGHLVNSFRGTGTTNLRSLRSLYXGREGNTERPVTISASPSVPIFRTL
310 320 330 340 350 360

CRY2AB2_820.pep
NRAA:295864

295864 source="GENBANK_PROT" crystal protein [Bacillus
thuringiensis]gi|8469147|sp|Q45747|CribD BACTU Pesticidal crystal protein
cry1Db (Insecticidal delta-endotoxin Cry1D(b)) (Crystalline entomocidal protoxin)
(131 kDa crystal protein)

SCORES Initl: 152 Initn: 176 Opt: 275 z-score: 307.6 E(): 7.7e-09
>>NRAA:295864
initn: 176 initl: 152 opt: 275 z-score: 307.6 expect(): 7.7e-09
Smith-Waterman score: 275; 23.4% identity in 286 aa overlap
(70-349:54-321)

CRY2AB2_820. KEWTEWKNHSLYLDPIVGTVASFLKVKVSLGVKRLSELNLIFFSGSTNLMQDILR
295864 DAERLETGNVADISGLINFLYSNFPVGGGFVIG--LLELWGFVGPQO---WEIFLA
30 40 50 60 70

CRY2AB2_820. ETEKFNQNLQNTDITLARVNAELTGLQANVEEFNRQVDNLF--NPNRNAVPLSITSSVNTMQ
295864 QIEQLISQRIEFAFNQAISFLEGLSNVEIYETTFRAWEKDPSPNPALEEMRTQFNVMN
80 90 100 110 120 130 140 150

CRY2AB2_820. QLFNLRLPQFMQSCYQILLPLPACQWHLSTFARQDNLNADENGISAATLRYDYLNK
295864 SALIAAIPLLRVNVEVALLSVYQAANLHLSVLKDVSVYQVQGRGDFPATVNSRYSDLTR
160 170 180 190 200 210

CRY2AB2_820. YTRDYSNCINTYQSAFKGLN--TRLHDML---EFTRYMFLNVEFVNSLWFKYQLSLLVS
295864 LIHVTYDHCVDYNDGLNLEGRSLSDWVYVNRFRRLTISVLDIAFFPNYDIEAYPIQ
220 230 240 250 260 270

CRY2AB2_820. SGANLYASGSGPOQTGFTSDQWDFLYSLFOVNSVYLNGFSGARLSNTF--PNIVGLPGS
295864 TAS-----QLTREVYLDLPVNETLSPASVPT--FSAAESALIRSPHLVDPLNS
280 290 300 310 320 330 340 350 360

CRY2AB2_820. TTHALLAARVNSGGISGGIDIGASFPNQFNCSITFLPPLTFPVRSMWLDGSGDREGVAT
295864 FTIYTDSLASYAVWGGHLVNSFRGTGTTNLRSLRSLYXGREGNTERPVTISASPSVPIFRTL
310 320 330 340 350 360

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 258 of 361

```

310      320      330      340      350      360
cry2ab2_820.pcp
NR000:13899010
13899010 source="GENBANK_PROT" insecticidal crystal protein [Bacillus
thuringiensis]
SCORES      Initl: 152      Initn: 176      Opt: 275      Z-score: 307.6 E(): 7.7e-09
>NR000:13899010
Initn: 176 Initl: 152 Opt: 275 Z-score: 307.6 expect(): 7.7e-09
Smith-Waterman score: 275; 23.4% identity in 286 aa overlap
(70-349:54-321)

310      320      330      340      350      360
cry2ab2_820. KWTWKNNHSLVLDPIVGTVASFLKKVGLVGRKILSELNRNLIFFSGSTNLMQDILR
13899010      DAERLETGNTVADISGLINFLYNFVPGGFIVG--LLELIWGFVGSQ---WEIFLA
80      90      100      110      120      130      140      150
cry2ab2_820. ETEKFLNORLNTDLARVNAELTGLQANVEEFNQVDNLF--NPNRNVPLSITSSVNTMQ
13899010      QIEQLISORIEEFARNQALSRLEGLSNYEIYETTFRAMEKDFSPNPAUREEMRTQFNVMN
80      90      100      110      120      130      140      150
cry2ab2_820. QLFNLRFQFQMGQYQLLLPLFAQAANLHLSFIRDVILNADWGISATLRTYRDYLNK
13899010      SALIAAIPLLRVRNVEVALLSVYVQAANLHLSFIRDVSVYVQGVGDFPATVNSRYSDLTR
140      150      160      170      180      190      200      210
cry2ab2_820. YRDYSNYCINTVQSAFKGLN--TRLHML---EFRTYMFNFYEVSVISLKYQSLVLS
13899010      LTHVYTDHCVDTYNDGLKNLEGRSLDWMVYVNRFRRLTISVLDIIAFPPNYDIEAYPIQ
200      210      220      230      240      250      260      270
cry2ab2_820. SGANLYASGSGPQQTQSFTSQDWPEFLYSLFQVNSNYVINGFGSGLSNTP--PNIYGLPGS
13899010      TAS-----QLTREVIYLDLPFVNETHSPASVPT--FSAEASAIIRSPHLVDPLNS
260      270      280      290      300      310      320      330
cry2ab2_820. TTTALLAARVNSGSGISGSDIGASFPNQFNCGSTFLPPLLTPFVRSWLDSDREGVAT
13899010      FTIYDLSASYAVWGGLVNSFRGTITNLIRSLPLYGREGNTERPVTISASPSVPIFRL
310      320      330      340      350      360
cry2ab2_820.pcp
NR000:8469144
8469144 source="GENBANK_PROT" Pesticidal crystal protein cryIIa (Insecticidal
delta-endotoxin CryIIa(a)) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)gi|474892|gb|AA22341.1| crystal protein
SCORES      Initl: 150      Initn: 203      Opt: 275      Z-score: 307.6 E(): 7.7e-09
>NR000:8469144
Initn: 203 Initl: 150 Opt: 275 Z-score: 307.6 expect(): 7.7e-09
(1167 aa)
```

```

Smith-Waterman score: 337; 21.2% identity in 598 aa overlap
(54-634:32-597)
30      40      50      60      70      80
cry2ab2_820. AHDPFQHKSLDVTQKTEWKNNHSLYLDP--IVGTVASFLKKVGLVGRKILSEL
8469144      EINNQKQICPEYCNLSNPEEVLDDGERILPDIDPLEVLSLSLQFLNNF--VPGGGFISGL
10      20      30      40      50
cry2ab2_820. RNLIFFSGSTNLMQDILPETEKFLNORLNTDLARVNAELTGLQANVEEFNQVDNLF--N
8469144      VDKIWGALPSEWDLFLAQIERLIDQRIEATVRAKAITTELEGICGRNQYIYAAFAKWESED
60      70      80      90      100      110
cry2ab2_820. PNRNAVPLSITSSVNTMQFLNRFQFQMGYQLLLPLFAQAANLHLSFIRDVILNAD
8469144      PDNEAAKSRVIDRFRILDLGLIEANIPSRILIGFEVPLLSVYVQAANLHALLRDSVIFGE
120      130      140      150      160      170
cry2ab2_820. EWGISAATLRTYRDYLNKYNTRDYSNYCINTVQSAFKGLNTRLHMLPEFRITYMFLNVFYV
8469144      RWGLITKNVNDIYNRQRIEIHYSNHCVDYNTLELGRF--SLAQWRIY--NOFRRE
180      190      200      210      220      230
cry2ab2_820. SIWSLFKYOSLVSANLYASGSGPQQTQSFTSQDWPEFLYSLFQVNSNYVINGFGSAR
8469144      LTVLVDIVLVALPNDRLYPIOTFSQLTREIVTSPVSEFYGV--INSGNIITGLTTEQQ
240      250      260      270      280      290
cry2ab2_820. LSNTPFNVGLPGSTTTTHALLAARVNSGSGIS-----SGDIGAS---PQNQFNCGSTFLP
8469144      IRR--PHLMDPNSMIMYTDNRREHNSGLEMTAYFTGTAGAQVSPFLVGTGESA--P
300      310      320      330      340
cry2ab2_820. PLTTPFVRSWLDSDREGVATVTNMQTESFETTLGLRSGAFTAGNSNYFPDYFIRNIS
8469144      PLT---VRSVND-----GIYRIL---SAPPFYSAFFLGTIVLGRGCK--F-DPALNNIS
350      360      370      380      390
cry2ab2_820. GVP-LVVRNEDRLRPLHYNIRNIASPSGTGCGARATVSVHNRKNIHNVHENGSMTH-
8469144      PPSTIYRHPGTVDLSVLPQDNSVPPHSGSSHRLSHVTMRASSPIFWHTRSATITNT
400      410      420      430      440      450
cry2ab2_820. LAPNDYGTFTSPIHATQVANNQTRTFISEKFGNQGDSLRFEONNTTA--RYTLRGN-GNS
8469144      INPNAL--IQIPLVKAFNLHSGATVVRGPGFTG-GDILRRTNIGTFADMRVNTGTPUSQR
460      470      480      490      500      510
cry2ab2_820. XNLYLRVSSIGNSTIRVTINGRVTATNVNTTINNDGVNDMGARFSDINIGNVASSNSD
8469144      YVRVIRYASTIDLOQFFRTRINGTSVNGQNFQRTMNR--GDNLSEGNFRTAGSTPFFSNAQ
520      530      540      550      560
610      620      630
```


cry2ab2_820.	GVP-LVVRNEDLRRLPHYNEYNRTNTPASGTPGGAAYMVSVHNRKNHIVHENGSMIH	400	410	420	430	440	450
8469144	PPPTIYRHPGTVDGLSVIPPDQNSUPPHRGSSHLSHVTHRASSPIFPHWTHRSATTNT	400	410	420	430	440	450
cry2ab2_820.	LAPNDYTGTFISPIHATOVNMQTRTFISEKFGNQGSDFRFEQNNMTA--RYTLRGN-GNS	490	500	510	520	530	540
8469144	INPNAI--IQIPLVAFNLHSGAVVRGCGFTG-GDILRRNTGTFADRMVNIITGELSOR	460	470	480	490	500	510
cry2ab2_820.	YNLYRVSSIGSNSTRVINGRVYATNVNNTTNDGVNDGNARFSDINTGNVVASNSD	550	560	570	580	590	600
8469144	YRVAIRVASTDLQFPFRINGTSVQNGNQFQRTMNR-GNLESGNFRTAGFTSPFVSFNAQ	520	530	540	550	560	570
cry2ab2_820.	VPLDINVLTNSGTQFDLMNIMLVPTNISPLY	610	620	630			
8469144	STFTLTGQASNQEVVIDRIEFPVAVTPEASDLERAQKAVNALFTSTNQLGLKTDVTD	570	580	590	600	610	620
cry2ab2_820.pep							
NC_015988322							

```

cry2ab2_820. AHDPSFQHKSLDTVQKEWTEWKNHNSLYDPP--IVGTVASFLIKKVGSLVGVKNKSLPSE
               50      40      30      20      10      0
               |||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||:::
84691144      EINNQKQICYPNCLSNPEEVLLDGERILPDIDPLEVLSLSLLQFLNPF--VGGGCFISGL

```

~~1598832 source="GENBANK_PROT" Chain A, Crystal Structure Of The Insecticidal Bacterial Del Endotoxin Cry3bb1 Bacillus Thuringiensis~~

SCORES Initi: 154 Opt: 270 z-score: 306.9 E(): 8.5e-09
 > NRRA1:558-322
 Initi: 192 Initi: 154 Opt: 270 z-score: 306.9 expect(): 8.5e-09
 Smith-Waterman score: 286 20% identity in 534 aa overlap
 (81-282,334-538)

```

cry2ab2_820.  WLDRIWGVASFLGKSLSELNLFFPGSGTNLMQDILRETKFJUNQSLNTD
              70      80      90      100      110
15988322      GTGISWQGLGVGKPGKALTSYFASFTNTPSDA-DPWKAFMAQVEVLDDKKIEEY
              10      20      30      40      50

```

[illegible]

```
cry2ab2_820. RLPQWOGVQLLLPLFAQAANLHLFSFIVTINADENGSAAITRTYRDUKNTRDY  
      :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|: :|:  
159868322 SWSFSAKSVKEVLFTPYAQAANTHLLLLKKDAVPFEENSYSSEDAEFTHROLKPKOON
```

```

cry2ab2_820.  SNYCINTYQSAQKGLNLRHLDML---EFTYTMFLNVEFYVSINLKYSLIVSSVANA
                230      240      250      260      270
15988322      TDHCYNWNVNGLANGLSGSYDAWKFNFRFRETTLVLDLVLVLPFFDIR-LYKGVKVT
                180      190      200      210      220      230

```

```
cir2ab2_820. YASG--SGPQQTSTSDWPFVLSLQF VNSNVLNGFSGARLNTF PNVJLPGS-
```


Study No. 06-01-62-01

MSL No. 20307

Page 260 of 361

8928007 DPKSTGNLSTLVTKTALDSDFNGAIRVTNNQSGPGYELLLLPVYAQAIALNLHLHLLLRDA
160 170 180 190 200 210

cry2ab2_820 LNADEMGISAALT-TYRDYLKNVTRDYSNYCINTYQSAFKGLNT--RLHDLMLEFRTYMF
200 210 220 230 240 250

8928007 IYGDKWSANARDNYIOLEKTEYECINWYKGLNDFTAGOVWFNRVRREMT
220 230 240 250 260 270

cry2ab2_820 LNVFEYVISWSLFK--YQSILVSSGANLYASGSPQOTQFTSISQDWPF--LYLSFQVNS
260 270 280 290 300

8928007 LTVLDIISMPPIYDARLPYTBVKTELTRYTSVDINGEIVGYLGMTPYFSFEKAESLY-TRA
280 290 300 310 320 330

cry2ab2_820 MYLVNGSFGARL-SNTFPNIYGLPGSTTHALLAARVNYSGGI--SSGDIGASFPNQNFN
310 320 330 340 350 360

8928007 PHLTFLKLGRFRTVINSIISWTFLSGGONKYSYTNNSSINEGSRGQDTDYGGFSSTINIP
340 350 360 370 380 390

cry2ab2_820 CSTFLPLLTP---FVRSWLSDGSDRGVATVNNMOTESPETTLGL-RSCGAFTARGSNY
370 380 390 400 410 420

8928007 SNSVYNLWNTENVEYIYPWGDPVNITEMNFSVTD--NNSKKELIYCAHRINKPKVPVRTDFD-
400 410 420 430 440 450

cry2ab2_820 PFDYFIENISGPVLVVRNEDLRPLHYNEIRNIASPSTGCGAAYMVSVHNRKNNIHAV
430 440 450 460 470 480

8928007 ---FLNKEGTELAKYND-----YNHILSVMLINGETTFGQRKHGYSFAPTHSS--VV
460 470 480 490 500

cry2ab2_820 HENGSMTHLAPNDYTGFTSLPIAHQTANNORTRFISEKFNGQDSLAFQNUN--TTARTIL
490 500 510 520 530 540

8928007 DPNNTI---AANKITOIFV-AVKASSINGSISIEKGPGFTG-GDLVKMRADSGLTRMFKFA
510 520 530 540 550

cry2ab2_820 RGNGNSVNLVRVS-SIGNSTRIVTINGRVYTAIVNTNNDCVNDGARSDSIGNV
550 560 570 580 590

8928007 ELLDKYRVIRVRYKCNYSKULLRKWKGEYIQOOIHNIISTYGA-----FSYLESPTFI
560 570 580 590 600

cry2ab2_820 VASSNSDVPLDINVTLNGSTGF--DLNMIML-----VPTNISPLY
600 610 620 630

8928007 TTENI-FDLTMEVTPYVGROFVEDIPSLLDKIEFLPTIN
610 620 630 640

cry2ab2_820.pgp
NRAA:2624005

2624005 source="GENBANK PROT" mosquitocidal toxin [Bacillus thuringiensis]gi|8928007|sp|32307|Cl9AA BACTY pesticidial crystal protein cry19a [Insecticidal delta-endotoxin CryXIX(a)] (Crystalline entomocidal protoxin) (75 kDa crystal protein)

SCORES Initi: 135 Initn: 135 Opt: 270 z-score: 306.2 E(): 9.3e-09
>NRAA:2624005 (648 aa)
Initn: 135 Initi: 135 opt: 270 Z-score: 306.2 expect(): 9.3e-09

Smith-Waterman score: 282. 21.3% identity in 610 aa overlap
(57-632, 74-648)

```
cry2ab2_820. PPSFOHKS...DVOKEWTKKHS...LYDPVGTVASFLKKVSGSLVGKRI--LSELNRL      30      40      50      60      70      80
2624005. YKDNVNVCGHIL...RDEE...EVRAGLQKGLGSLVIVGFG---GSIIDTICLFQVISEL      50      60      70      80      90      100

cry2ab2_820. IPFSGSTNLM--QDNRESEKFLNLT...TTLARVNA--EKLQANVEEFNRQVDNFLN      90      100      110      120      130      140
2624005. LWFEDDTQYTQWQIMNHVPSLLDKRI--TWTIRNAIRTLASLQKQVDVDNNMLKKWKD      110      120      130      140      150      160

cry2ab2_820. PNRNAVPLS--ITSSVNTWQOLFNLRLPQFQDQ--GYQLLPLFAQANLHLSFTRDVI      150      160      170      180      190      200
2624005. DPKSTGNSTLVFTALDSDFNGAIRTVNNGGSPSEVELLLPVYQVQANLHLLLRQ      160      170      180      190      200      210

cry2ab2_820. LNADEWGISAAFLR--TYRVDYLNKVTSDYSNYCINTYQSAFKGLNT--RNDMLSESTME      200      210      220      230      240      250
2624005. IYGDKWSANARADNYIOLEKTEYECINWYKGLNDFRTAGQVWYKNGRREMT      220      230      240      250      260      270

cry2ab2_820. LNVFEVYSIWSLFK---YQSLVSSGANLYASGSPQQTQSFTSQDWPFF--LYSLFQVNS      260      270      280      290      300      310
2624005. LTVLDIISMFPIYDARLYPTEVAKTELTRIYSVDVINGEIVGLMTPVFSFEKAESELY-TRA      280      290      300      310      320      330

cry2ab2_820. NYVLNFGSGLRL--SNTFPNIVGLPGSTITTHALLAARVNSGGI--SSGDIGASPNQNFN      310      320      330      340      350      360
2624005. PHLFTWLKGFRTVNSISYWTFLSGGQNKYSYTNNSINSGSRGQDTDYGTSTINIP      330      340      350      360      370      380

cry2ab2_820. CSTFLPPLTLP---FVRSWLDGSGDREGVATVNTWQTESFETTLGL--RSGAFTARGNSNY      370      380      390      400      410      420
2624005. SNSVYVNLWTEVYIYPWGDPNITKMFNSVTD--NNSSKELIVGAHRINKPVVITDFD-      390      400      410      420      430      440

cry2ab2_820. FPDYFIRNLSGVPLVNRNEDLRPLHYNEIRNIAPSCTPGGARAYMVSVHNRKKNIHAV      430      440      450      460      470      480
2624005. ---FLTNEGTELAKYND-----YNHLSYMLINGETPGQKRHGSYFATSHS--V      450      460      470      480      490      500

cry2ab2_820. HENGSMIHLAPNDVTGTFTSPIHATQVNNQTRTFISEKFGNCGSLRPFQNN--TIARTYL      490      500      510      520      530      540
2624005. DPNNTI---AANKITQIPV--VRASSINGSISIEKPGPGFTG--GDLVNRADSGLTWRFA      510      520      530      540      550      560

cry2ab2_820. RGNGSVNLILAVS--SIGNSTIRVTINGRVYATVNTVNTTNNQGVNDNGARSDINIGV      550      560      570      580      590      600
2624005. ELDDKXYRIRYIKCNYSKLLILRKWKGEGYIQOQIHNSIPTYCA-----FSYLESTFI      560      570      580      590      600      610

600      610      620      630
```

```
cry2ab2_820. VASNSDVPLDINVLNSGTQF--DLNMIML-----VPTNISPLY
2624005. ITTENI--FDLTMEVTPYGRQGFVEDIFSLILDKIEFLPTN
610      620      630      640
```

cry2ab2_820.pep
SW:8469161

8469161 description="PESTICIDIAL CRYSTAL PROTEIN CRY3CA (INSECTICIDAL DELTA-ENDOTOXIN CRYIIIC(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (73 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis serovar kurstaki" source="swissprot_prot" version=NA type=PRT

SCORES Initl: 118 Initn: 146 Opt: 270 Z-score: 306.2 E(): 9.3e-09
>>SW:8469161
Smith: 146 Initl: 118 opt: 270 Z-score: 306.2 expect(): 9.3e-09
Smith-Waterman score: 271; 23.4% identity in 304 aa overlap
(70-361:84-355)

```
cry2ab2_820. KEWTEWKKNNHSLYLDPIVGTVASFLKKVSGSLVGKRIILSELNLIIPFSGSTNLMQDIILR      40      50      60      70      80      90
8469161. ALDSSTTKDAIQKGISILIGDLLGVVGFPGYGGALVS--FVTNLLNTIWPQ--EDPLKAFWQ      60      70      80      90      100
```

```
cry2ab2_820. ETEKFLNQRINTDTTLARVNAELTQLQANVEEFNRQVDNPNRNNAVPLSITSSVNTMOQ      100      110      120      130      140      150
8469161. QVEALIDQKIADYAKDAETAEQLQKKNVFKDYVSALDSW---DKTFLTLRDGSGQRIRE      110      120      130      140      150      160
```

```
cry2ab2_820. LRF-----LNR-LPFGOMQGVOLLILLPLFAQANLHLSFIRDVILNADENWGISAAFLRTY      160      170      180      190      200      210
8469161. LPSQAESFRRSMPSPVSGVEVFLPFIYAQAANTHLLLLKDAQIYGTDMGYSTIDDLNEF      170      180      190      200      210      220
```

```
cry2ab2_820. RQYLNKNTSNYSNYQNTYSAPFKGLNTTS--HDMLEFRY---MFLNVFEVYSIWSLFKY      230      240      250      260      270      280
8469161. HTKOKDLTIE--TNPKAKWYKMGVJMLRGSYTFEWAQFNRYRREMILTVDLIDLTILFLYDV      230      240      250      260      270      280
```

```
cry2ab2_820. QSLIVSSGANLYASGSPQQTQSFTSQDWPFF--LYSLFQVNS      270      280      290      300      310      320
8469161. RT-----YTKGVKTELTREDVLND--ATV---LAVPTI--MNGI-GTAFSN-IENYI      290      300      310      320      330      340
```

```
cry2ab2_820. GLPGSTT--THALLAARVNSGSGISGGIDIGASPNQNNCTFLPALTPTPERSWLDSSD      330      340      350      360      370      380
8469161. RXPHLFDYLHA-----IQPHSRLOQGFPGIDSFNYSWGNVSTRSIGSDLTFPEYKGN      330      340      350      360      370      380
```

```
cry2ab2_820. REGVATVNTWQTESFETTLGLRSGAFTARGNSNYFFDYFIRNISGVPLVNRNEDLRPLH      390      400      410      420      430      440
8469161. KSTLLDNQLEENGKVFRAVANGNLAWVPVGTGSGTKIHSGVTKVQFQSOYNDRKDEVAIOI      390      400      410      420      430      440
```


Study No. 06-01-62-01
MSL No. 20307
Page 262 of 361

```
version=NA type=PRT
```

```

SCORES      Init1: 154      Initn: 192      Opt: 270      z-score: 306.1      E(): 9.3e-09
>SW:8469155
initn: 192      init1: 154      opt: 270      z-score: 306.1      expect(): 9.3e-09
Smith-Waterman score: 286;    20.8% identity in 534 aa overlap
(83-582;97-601)

```

520	530	540	550	560	570
560	570	580	590	600	610

**Monsanto Company
Final Report**

Study No. 06-01-62-01
MSL No. 20307
Page 264 of 361

```

290      380      390      400      410      420      430      340
cry2ab2_820.  RSWLDGSDREGVATVNWNTESFETTLGSRGAGTARGNSYPPDYFIRNLSGVLVWR
      : : : : : : : : : : : : : : : : : : : : : : : :
46409863      R--NNG--EGIVRIL---SDTFYSAPLGTSGVLGSGEGEFAFASNTTISLPST--IYR
      350      360      370      380      390
cry2ab2_820.  440      450      460      470      480      490
      NEDLRRLPHYNEINRTIASPGTGGARAYMVSVNRKNINHAHENGSMIH-LAPNDYTG
      : : : : : : : : : : : : : : : : : : : : : : : :
46409863      NRGTVDSLVSPIDQGVSPVPHRGYSHLLSHVTWNSSPFHWTHRSATPRNTIDPSIT-
      400      410      420      430      440      450
      500      510      520      530      540      550
cry2ab2_820.  FTISPIHATOWNQOTRTFISEAFNGQDGLURFQNN--TTARYTLRGNG-NSYNLYLRVSS
      : : : : : : : : : : : : : : : : : : : : : : : :
46409863      -QIPAVGAYFINSP--VITGFGHTGGDIIRFNPNTQNNIRIPFHSNAVORYAIRWYAA
      460      470      480      490      500
      560      570      580      590      600
cry2ab2_820.  IGNSITRVTN-----GRVYATATVNTT--TNNDGVNDNGARFSDINIGNVASSNSDVL
      : : : : : : : : : : : : : : : : : : : : : : : :
46409863      EADCIIESGVNTVTCAGVYTERPIKATVPGSPLYYSFOYADLANI--NLTAIPRPNFV
      510      520      530      540      550      560
      610      620      630
cry2ab2_820.  DINVTLSNGTQFDLMNLMVPTNISPLY
      : : : : : : : : : : : : : : : : : : : : : : : :
46409863      SIFRSNQFNLY-IDRIEFIP--IDPIREAEHLERAKAVNALFTSSNQLGKTDVTDY
      570      580      590      600      610      620
      30      40      50      60      70
cry2ab2_820.  PFSFOHKSJLTDVOKETWKNHSLYLDPIVGTVASFLKKVGS-LVGKRLISLRNLI
      30      40      50      60      70
1334252      KDYLKMGSEGDYDSINPGVNRVTGLQTGDIIVAVVGVALGPGVGILTG--FLSTLFGFL
      30      40      50      60      70
      90      100      110      120      130      140
cry2ab2_820.  FPGSGTNLMQDILRETEKFLNQRNLNTDITLAKVNAELTGLQANVEEFNRQVDFNLN--PNRN
      : : : : : : : : : : : : : : : : : : : : : : : :
1334252      WFSNQDAWAEAFIEQMBELTEORISDQVVRALDDLTGIONYNQYLAKWEERENG
      80      90      100      110      120      130
      150      160      170      180      190
cry2ab2_820.  AVPLSITSSVNTMQQLFLNRLPQFO---MGVQLLLPLFAQRANLHLSFIRDVILNAD
      : : : : : : : : : : : : : : : : : : : : : : : :
334252      RANL-VLQREIFLHALFVSSMFSFGSGFGSFOAQLLVYAAQANLHLLULADAEKYGA
      140      150      160      170      180      190
      210      220      230      240      250

```

```

cry2ab2_820.  EMGISAATL-RTYRDYLKNTYRDYNYCINTYOSAFKGL-NTRLHDMWL---EFRTYFWLNL
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          RWGLRESQIGNLYFNELOTRDVTYCHVYNNYAGLAGTSAESWLKYHQPFEATLML
          200      210      220      230      240      250

cry2ab2_820.  VFEYVSWSLFWKYQSLLVSSGAML-YASGSGFQQTQSTQDWFFLYSL-FQVNNVVLNL
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          AMDJIALFFYNYTRYPIANNPOLREVTYDPLGVPSSESLFPELRLCLRWQETSAMTSL
          260      270      280      290      300      310

cry2ab2_820.  GFSGARLS-----NTFFPNIVGLFGSTTH---ALLAARNVYSGGISGDIASP---FNQ
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          NLNENALISPHLEFTINLMLVTGFSVHLTNQLIEGWIGHS--VTSSLASGPTIVLRLR
          320      330      340      350      360      370

cry2ab2_820.  NFNCSTFLPLLTPFVRSLDGSREGVATVNMQTESFETTLGLRSGAFTAGNSNYF
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          NYGSTT-----SLVNYF-----SFNDRD---VQVINTSL-HTGLGFONAPLFGITRAQFY
          380      390      400      410      420

cry2ab2_820.  PDYFIRNISGVPLVWNEDLRRPLHYNETRNATASPGTGPGARAYVMVSVHNNKNIHAVH
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          P-----GCTYSVTQNALTCQNYNSIDELPSLDPNPISYSYSHRLSHITSYSLHRLV
          430      440      450      460      470

cry2ab2_820.  ENGSMHLAPNDYTGFTISPHATQVNNQTRFISEFGNQGSURFQNNNTARYTLRG
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          TIDGI-----NIYSGNLPTVYVWTHRDVLTNTIADRLTQLPLVKVSFEIPAGTT--VWRG
          480      490      500      510      520

cry2ab2_820.  NGNSNLYLRVSSIGN-STIRVTINGRYVYATNVNTTNNQDVGNDGARSDFNIGNVVA
1334252      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          PGFTGDLIRLTGVTGFTIRVYRTAPLTQRYRIRFFASTNLFIGRIGVDRQNVYDF
          530      540      550      560      570      580

cry2ab2_820.pcp
NR04:19386614

19386614 source="GENBANK_PROT" mosquitoicidal toxin [Bacillus thuringiensis
serovar aizawai]

SCORES      Initl: 122      Inltn: 155      Opt: 269      Z-score: 304.9 E(): 1.1e-08
>>NR04:19386614
Initl: 155 Initl: 122 Opt: 269 Z-score: 304.9 expect(): 1.1e-08 (660 aa)
Smith-Waterman score: 278, 21.7% identity in 604 aa overlap
(58-636:68-639)

cry2ab2_820.  FSFOHKSLLDTVQKEWTEWKNNHSLYLDPIVGTGTVASFLKKVGSIVLGKRI--LSERNLII
19386614      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          MQNTNYKDWLTWCBDRTDITDVLSSRGAVSTGVGMSTLISLFGIPLIGEGIDLLGGAADFL
          40      50      60      70      80      90

cry2ab2_820.  FPG---SGSTNLMQDILRETEKFLNRLTDTLAFRNAELTGQANVEEFNRQVDNLF-NP
19386614      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
          90      100      110      120      130      140

```



```

©01
CRY2AB2.820. STIRVINGRVYTAIVNTTTINQVNDNGARFSDINICNVVASSNDSVDPLDINVTLNSG
: : : : : | : |
LRLQNSQNDFLVIYINPNKKDDLLTYQTFDLATNSMCGSCDKNELIIGAESFVN
8469155 480 390 610 630
CRY2AB2.820.pep
NR04:8469155
8469155 source="GENBANK:BC07_Pesticide crystal protein cry3Bb (Insecticidal
delta-endotoxin CryIIIB(b)) (Crystalline delta-endotoxin) (74 kDa crystal
protein)gi|142730|gb|AAA22334.1|c|CryIIIB2
SCORES Init1: 154 Initn: 192 Opt: 270 Z-score: 306.1 E(-): 9.3e-09
>>NR04:8469155
initn: 192 init1: 154 opt: 270 Z-score: 306.1 E(-): 9.3e-09
Smith-Waterman score: 286; 20.8% identity to 584 aa overlap
(83-582:97-601)

```

cry2ab2_820_	YLDPIVGTVASFLKKVGSVLGKRIILSELNRILFFPSGSTMLOKQVILNTEFLAFNANQDND	60	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000
8469155	GTGISVVGQILGVGVVPFAGALITFYQSFINTIMPSDA-DPWFAPFAQVEYDNDKXIEY	70	80	90	100	110	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	
cry2ab2_820_	TLIARVNABELTQLOANVEEFNRQVNFENPRNNAVLSTIS--SVNTMOQLEF-----N	120	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000						
8469155	AKSKALAELOQLOQNNFEDIV-----NANLNSWKKT-PLSLRSKRSDRIRELFSQAESHFN	130	140	150	160	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000							
cry2ab2_820_	RLPQFOMQGYQLLLPLPFAQAANHLSPIDRVILNADWEGISRAATLTVRDLYKNKYTRDY	170	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000											
8469155	SMPSFAVSKEFLVLPFYAQAANTHLLKDAQVGEENGWSSVEDVAFVHQLKLTQOY	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370																																																																												

[illegible]

19386614 WPESTGHGYWEDLNHHELMERLETERKITTALDRLGLKALLGLFRDAFDSWEKNO
100 110 120 130 140 150
cry2ab2_820. NRRVPLSTSVNTMOQLFDELPO FOMQYQQLLLPLFAQANLHLSFIRDVLNAD
160 170 180 190 200
19386614 NDFPARNVAGGYFVUTINFKDMASFSFANVYVLLLPVYQAANLHLLDREGVIYS
160 170 180 190 200 210
cry2ab2_820. EWCISATLRTVRLKNTVTRDYSFNSNWSAFKSNLHLMLEFRTYMFNFVEYV
210 220 230 240 250 260
19386614 RWGIAPAA-DFHOLLKYLALINHCVAUNNN-GLAQOELPAKSPNNRNFAYRRD
220 230 240 250 260 270
cry2ab2_820. SIWSLFQYOSLLVSSGANLYASGSGPQQTSTQDMWFFLYSLFQVNSYKINGCSGAR
270 280 290 300 310 320 330
19386614 MTITVDIITALPFTYDARLVTKPIKTELTRYISNLSNLDVYGVQOITLKNREAPF--R
280 290 300 310 320 330
cry2ab2_820. LSNFTFNIVGLPGSTTH----ALLAARVNYSGGSSGDIGASPMQNNC--STPDR
320 330 340 350 360 370 380
19386614 SPLVTLRLRGDFYTRTRYAYWRYLAGHNYFSTFGNGTIYSSFNWIDCMKSTINL
340 350 360 370 380 390
cry2ab2_820. PLITPFRVSWLSDGSDREGVATVNWQTESFETTLGRSGAFTARGNSYFPDYIRNIS
380 390 400 410 420 430
19386614 PDYANIYKLTWKSNTNISPYTDPVGISOMQFSLT--NNQOLTYYTGISA--PKYPVRETF
400 410 420 430 440
cry2ab2_820. GVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVH--NRK--NNIHAVHENG
440 450 460 470 480
19386614 ---FEIPPTD-EKPLTYENYSHILS-----YMTSAQHFGDKKIGYTFAMHESVD
450 460 470 480 490
cry2ab2_820. MIHLAPNDYTGFTISPIHATQVNNQTRTFISEKFGNOG-DSLRPEQNNITARTYLRNGN
490 500 510 520 530 540
19386614 FDNVRDPPD---KITOIPAVKGVLYQYVKGQPGHGTGDLVSMIRTDRLGINVYFPQL
500 510 520 530 540
cry2ab2_820. SYNLILRVSSIGNSTRV-TINGRVYATVNTTNNQDGNVND-NGARFSDINTGNVASS
550 560 570 580 590 600
19386614 DYRIRIYSTSSNGLYIYSPNTKI---VYLPTTLVDGQPTDFDMPFSAFRVEVPASF
550 560 570 580 590 600
cry2ab2_820. NSDVPDLINVTLSNGT-QFDLMNIMLVPTNISPLY
610 620 630
19386614 RASVAGYTNFTIEAGFPVYIDKIEFIPDNTTILEYEGGRDLEKTKNAVNDLFTN
610 620 630 640 650 660
cry2ab2_820.pep
NRAA:56900936
56900936 source="GENBANK_PROT" CryIab (Bacillus thuringiensis)

SCORES Initl: 128 Initn: 168 Opt: 272 Z-score: 304.2 E(): 1.2e-08
>NRAA:56900936
Initn: 168 opt: 272 Z-score: 304.2 expect(): 1.2e-08
Smith-Waterman score: 280; 21.4% identity in 604 aa overlap
(60-634:41-610)
cry2ab2_820. FQHKSLTVQKEWTMKNNHSLYDLPVIGTVASFLLKKVSLVGVKRIILSELRLNLIFFPSG
30 40 50 60 70 80
56900936 IPYNCNLPNPEVGLGERIEGTGTPIDISLSLTQFLSEF--VFGAGFVLGLVDLIWGIF
20 30 40 50 60
cry2ab2_820. STNLMOQILRETEKFLNQLNTDILARVNAELTGL----QANVEEFNRQVDFNLNPNRRA
90 100 110 120 130 140
56900936 GPSQWDAFLVQIEQLINQRIEFARNOAISRLGLESLNLYQIYAESFREWEADTNP---A
70 80 90 100 110 120
cry2ab2_820. VPLSITSSVNTMOQLFNLPLPOFQMOGQVQLLLPLFAQANLHLSFIRDVLNADWGLS
150 160 170 180 190 200
56900936 LREERNRIQFNDMNSALTITAPLFAVONYQVPLLSVYVQAANLHLSVLDRDVSFVGORGFD
130 140 150 160 170 180
cry2ab2_820. AATLTEDYLVKNYTRDYSNYCYQSAFK--GLNTRLHDML---EFRTYMFNLVNFY
210 220 230 240 250
56900936 AATINSRNDLTILIGNYTHAVRYNTGLERVWGPDSR--DWIRYNOFRRELTTLVLDI
190 200 210 220 230 240
cry2ab2_820. VSNSLDRYQQLVSSGANL----YASGSGPQQTSTQDMWFFLYSLFQVNSYVNLGF
260 270 280 290 300 310
56900936 VSLFPNYDRIRTRITVQSOLTREIYTNFVLENFDSGPRGSAQGIQSIRSPHLMIDILNSI
250 260 270 280 290 300
cry2ab2_820. SGARLSGTFPNIIVGCPSTTHALLAARVNYSGGIS--GDIGASFPNQNFNCST---
320 330 340 350 360
56900936 T-----HYTDARFAYMSEGHQVLRNRYVGFSGPEFTFFLYGTMGNAAPQQRIVIAQLGQG
310 320 330 340 350
cry2ab2_820. FLPPLLTFFVSNLSDSDRECVANNNNOTE--FEVTLGRSGAFTARGNSYFPDYFI
370 380 390 400 410 420
56900936 VYRTLSSTLYARPENIGNNQOLSVLDTTFEAVGTSNLLPAAVYRKSGTVDLSLEIPP
360 370 380 390 400 410
cry2ab2_820. RNISGVPLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVSVHNRKNIILHENGSM
430 440 450 460 470 480
56900936 QN--NNVP--PROGFSHRLSHVSMFRSGFSNSN-SLRAPMFSW-----LRSSEF
420 430 440 450 460 470
cry2ab2_820. IHLAPNDYTGFTISPI-HATQVNNQTRTFISEKFGNOGDSLRPEQNNITARTYLRNGN
490 500 510 520 530 540
56900936 NNIIIPS--SQITQIPLTKSNVSGTSVVKGPGFTG-DGILRTTSPQGS--TLRNNTY
470 480 490 500 510 520
cry2ab2_820. --GNSNLYLRVSSIGNSTRVTINGRVYATVNTTNNQDGNVNDNGARFSDINTGNVAA
550 560 570 580 590 600
56900936 PLSQRYVRIRYASTNINLQFHTSIDGRFPINQGNFSAITMSS--GSNLSGSGFRVTVGFTTFPN
550 560 570 580 590 600

**Monsanto Company
Final Report
Product Characterization**

```

520      530      540      550      560      570
cry2ab2_820. SSNSDVLPLDIINV-TLNSGTQFLIMLVLTSPLY          610      630
||||| : :::: ||||| : ::|||:::
FSGSGSVFTLSAHVFNSEGVNIDRIEFVPAEVTFAEYDLERAQAKVNELTFSNQIGL
580      590      600      610      620      630
KTDVTDYHIDOVSNLVECLSDFECDLDEKKELSKEVKHKARISDERNLLODPNFRGINQL
640      650      660      670      680      690
cry2ab2_820.pep
NR0A:14190061
14190061 source="GENBANK_PROT" CryIabi6 [Bacillus thuringiensis]

SCORES   Init1: 116   Initn: 156   Opt: 272   z-score: 304.2 E(): 1.2e-08
>NPAA:14190061
inintn: 156 inintl: 116 opt: 272 z-score: 304.2 expect(): 1.2e-08
Smith-Waterman score: 278; 22.0% identity in 604 aa overlap
(60-634:41-610)

cry2ab2_820. FOHKSLDTVQKEWTENKNHSLYLDFIVGTVASFLKLKKGSLVGKRILSELRLNLPFGS
30      40      50      60      70      80
14190061 IFYNCLSNPEVEVLGERIETGYTPDISLSUTQFLSEP--VFAGFVLGLVDIIWGIF
20      30      40      50      60
90      100     110     120     130     140
cry2ab2_820. STNLMDILRETEKFNLORNTDTLARVAELTGL---QANVEENRQVONFLNPNRA
||||| : :::: ||||| : ::|||:::
GPSOWDAFLVQLEOLINQRIEFARQAQSRLGLESLNYQIYAESFREWEADPNP---A
70      80      90     100     110     120
150     160     170     180     190     200
cry2ab2_820. VPLSITSSVNTWQQFLNRLPFQMOMQGYQLLLPLFAQANHLHSIRDTVINADEGIS
||||| : :::: ||||| : ::|||:::
LRMEIQFNDMNSALITAIPLFAVQNVRPLSVVQAVNLHLSVLDRDLVFGORGFD
130     140     150     160     170     180
210     220     230     240     250
cry2ab2_820. AATLTYRDYALKMYTRDYSNYCINTYQSAFK---GLNIRUHDML--EFRTYMFLENVFFY
||||| : :::: ||||| : ::|||:::
AATINSRYNDLTRILGNITHVARVNTGLSERVNGPDSR--DWIRYNGFBRELTLVDLI
190     200     210     220     230     240
260     270     280     290     300
cry2ab2_820. VSNIWSLFKYQSLLVSSGANILYASGSPQQTGSTSQDWPPFLYLFQVNSYVLNGFSGAR
||||| : :::: ||||| : ::|||:::
VSFLFPNYSRTVPYRTVSQ-----TRIYYTN---PVLEN-FDGSRFGSAQGIEGI
250     260     270     280     290
320     330     340     350     360     370
cry2ab2_820. LSNTFNVIUGLPGSTTHALLAARNVYSGGISGDIGAFPNQNFNCSTLPLPLL-----
||||| : :::: ||||| : ::|||:::
RS---PHLMIDLINSITIYTD-AHRGEYYW--SGHOIMASPVG--PSGPETFPLYCYTMGN
300     310     320     330     340
380     390     400     410     420
cry2ab2_820. -TPFVR-SWLDDSSDREGVATV--TNMQTESFETTLGURSGAFTARGNSYFPDYFIRN
||||| : :::: ||||| : ::|||:::
AACQQRIVAQGGQGYRTLSLTYLRPFNNIGNNQQLSVLDGTEFAYGTSNLPASVYRK

```

```

350      360      370      380      390      400
cry2ab2_820.  ISGVPLV--VRNEDLRRLPLHAYNEIRNIASPSTGGARAYMVSVHNEKNHIAHVHENGSM
14190061      SGTVDLSDEIPPNNVPPQGFSGHRLSHVSMFSGFSNVSVI--IRAPMFSWIHRSAF
410      420      430      440      450      460
490      500      510      520      530      540
cry2ab2_820.  IHLAPNDYTGFTISPI-HATQVNNQTRFTISEKFGNQSGLRFQNNNTIARTVLRGN--
14190061      NNIPS--SQITQIPKTKSTNLGSGTSVVGPGFTG-GDILRRTPSQGIS--TLRVNITA
470      480      490      500      510      520
cry2ab2_820.  --GNSNVLLRVSSGINSIRVTNGRYVYATVNTIINNQVNDGNGARFSDINTGNVVA
14190061      PLSQRVRIYATSTNLQHTSIDGRPIQNGFSATWS--GSLNAGSGSFRVTGFTTFPN
520      530      540      550      560      570
cry2ab2_820.  610      620      630
>NSNSDVPDIDNV-TLNSGTFQDLNIMLIVTISPLY
14190061      FNGSGSVFTLSARVENSNGEYIDRIEFVPAEYFPEABYDLERAQKAVNELETSSNQIGL
580      590      600      610      620      630
14190061      KTDVTDYHIDQVSNLVECLDSDEFCLDEKKEKSEKVKHAKRLSDERNLLQDPNFRGINQL
640      650      660      670      680      690
cry2ab2_820.pep
NF001:940200
940200 source="GENBANK_PROT" Cyt3Bb2

SCORES   Init1: 154   Initn: 154   Opt: 268   Z-score: 303.9   E(): 1.2e-08
Initn: 154   Init1: 154   Opt: 268   Z-score: 303.9   expect(): 1.2e-08
Smith-Waterman score: 276;   23.1% identity in 295 aa overlap
(83-360:97-381)

cry2ab2_820.  YLDPITGVTVASFLLKKVGSGLVKGRILSEURNLIPFGSGTNLMQDLIRETKFLNQRLNTD
940200      GTGSIVVGQILGVGVPPAGALTSFYQSFLDTIPSDA-DPMKAFMAQVFLVDIKKIEEY
70      80      90      100      110      120
60      70      80      90      100      110
cry2ab2_820.  TLARVNAELTGLQANVEFNRQVDNFINRNNAVPLSITS--SVNTMQQLFL-----N
120      130      140      150      160      170
940200      AKSKALAEALQGLQNNFEDYV-----NALNSWKT-PLSLRKSQDRIRHELFPSQAESHFRN
130      140      150      160      170      180
cry2ab2_820.  RLPOFQNGVQLLLFLUPAQANLHLSITRDVIINADWGISAAFLTRYDYLKNTRYD
170      180      190      200      210      220
940200      SMPSFAVSFEVLFLPTYAQAAANTHLLLKDAQVGEENGYSSEDVAEFYHRQLKLTQOY
190      200      210      220      230      240
cry2ab2_820.  SNYCINTYSAFKGLNTRLDHML-----EPRTYMLNVFFYVSIMSLFYQSLLVSSGANL
230      240      250      260      270
940200      TDHCWNVNVNGLNGLSRGSTYDAWKNFRFEMTLTVLDLIVLFFPYDVR--LYSGVKYT
250      260      270

```


©07

```

cy2ab2_820      250      260      270      280      290
          300      310      320      330
--S-SPQDTQSFTSQRPPTKYSLFQ-VNSNYLVGFGSGARLSTFNINVLGSGSTT
            :   :   :   :   :   :   :   :   :   :   :   :
ELERDAFTDPIGLANTAOEYGPFTFSLNFKPHFLVDLGIEFHTRLOP -GYSGKDS
            :   :   :   :   :   :   :   :   :   :   :   :
          340      350      360      370      380      390
THALLAARNVSYGGISGGDGMCPFFMNCSTFPRDLATPFVRWLDGSDGREGVATVT
            :   :   :   :   :   :   :   :   :   :   :   :
PNYMSGNVYETRFPSIGSSATTSIPFFYGDKAFKKVHTTANTIDVAAMPNGK
            :   :   :   :   :   :   :   :   :   :   :   :
          360      370      380      390      400      410

cy2ab2_820.pep
NRAA:48734426

48734426 source="GENBANK_PROT" parasporal crystal protein (Basillus
thuringiensis)

SCORES      Initl: 122      Inltn: 162      Opt: 264      Z-score: 295.1 EN: 3.8e-08
>>NRAA:48734426
inltn: 162 initl: 122 opt: 264 Z-score: 295.1 expect(): 3.8e-08
Smith-Waterman score: 270;      22.0% identity in 604 aa overlap
(60-634:41-610)

```

[illegible][illegible]

```

cry2ab2_820.pep
  >>NRAA:8469159
  8469159 source: "GENENK PROT" Pesticidal crystal protein cry8Ca (Insecticidal
  delta-endotoxin CxvIIIIC(a)) (crystalline insecticidal protoxin) (130 kDa crystal
  protein) gi|53254184|gb|AAA21211.1| cryII delta-endotoxinsi|1096647|prf||2112230A
  delta-endotoxin
  SCORES Init1: 152 Init2: 162 Opt: 263 Z-score: 294.0 E(): 4.4e-08
  >>NRAA:8469159
  Init1: 152 Init2: 152 Opt: 263 Z-score: 294.0 E(): 4.4e-08
  Smith-Waterman score: 277; 22.7% identity in 618 aa overlap
  (56-632:87-659)
  30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200
  cry2ab2_820. DPFSFQHKSLDTVQKEWTENWKNNHSLYLDPLVGVWASELKKYGVSLNGKRISEENLI
  8469159 SRNPGCTFISQADAVGTGDIIVSTIISSGLGIPVLGVETSL-----GSAIG-----SL
  90 100 110 120 130 140 150 160 170 180 190 200
  cry2ab2_820. PFPSGSLNMQDILRETEKFLNQRNLNMTDITLARVNAELTGLQANVEFNRQDNELVNER
  8469159 WFSNNENWQIIFMNRVEELIDOKILDSVRSFATADLANSRVAVEYYQNALEWERNKPHST
  110 120 130 140 150 160 170 180 190 200

```


Product Characterization Center

```

initn: 164 initl: 140 opt: 263 Z-score: 293.5 expect(): 4.7e-08
Smith-Waterman score: 314; 23.5% identity in 622 aa overlap
(56-623:73-652)

cry2ab2_820. DPFSQHKSLDTQKTEWKNNHSLYLDPIGVTVASFLLKKGSLVKRILLSELRLNI
30 40 50 60 70 80
22213635 EVNVIDPFVASTVQTGINAGRIILGVLGVPFAGQALAFV---SFLVGE-----L
50 60 70 80

cry2ab2_820. FPGSGTNLMODILRETEKFLNLTNDTLARVNAELTGLQANVEFNRQVDNPELNPNNA
90 100 110 120 130 140
22213635 WPSGR-DPWELFIEHVEQLIRQOVTVENTRTALRGLEGGRGYRYSQQALETWLDNRNDA
100 110 120 130 140

cry2ab2_820. VPLSTTSVNIMQOL-FLNRLPQFQMOMGYQLLLPLPFAQANHLHSFIRDVILNADEWI
150 160 170 180 190 200
22213635 RRSRIILERVVALELDITTAIPLFRIENREVPVLMVYQAANLHLRLDASLFGSEWGM
150 160 170 180 190 200

cry2ab2_820. SAATLRTYRDLKNNYTRDYSVNCINTYOSAFKGL-NTRLHDML---EFRTYMFVNFVYV
210 220 230 240 250 260
22213635 ASSDQNYQYQEQIRYITEEYSHCHQWYNTGLNLRGTAESWLRYNQFRDRLTLGLVLDV
210 220 230 240 250 260

cry2ab2_820. SIWSLFKYQSLVYSSCANL---YASGSGPQQTQS-FTSQDW-----
270 280 290 300 310 320
22213635 ALFYSYTRYPINTSAQTRIERYTDPFGRTWAPSGFASNTWNNFNAPSFAIEAAIRPF
270 280 290 300 310 320

cry2ab2_820. -----PFLYSLFQVNSNVV---LNGFSGARLSNTEFNIVGLPGSTTHALLA-ARVN-
330 340 350 360 370 380
22213635 PHLLDPFEQLTIYSASSWSSTQHMVYWGHL-NFRP--IGGTLNTSTQGLTNNTISNP
330 340 350 360 370 380

cry2ab2_820. YSGSIGSGDIGASPQNFGNFCSTPLPLLPFVR-SWLDSGSDREGVATVNMQTESFET
390 400 410 420 430 440
22213635 VTLOFTSRDYYTESNAGTNILFTTPVNGVPWDFRFINQNIYERGATTIYSPQYG--V
390 400 410 420 430 440

cry2ab2_820. TLGRSGATARGNSVFPDY--FINISGVPLVRNEDRLPHNEIRNAPSPTGP
450 460 470 480 490 500
22213635 GIQLFQSETLPTPTERPNEYSYSHRSLHGLIGNT-LRAPV-YSMTHSARDNTIG
450 460 470 480 490 500

cry2ab2_820. GARAYMV-SVNRKNNIHAVHENGSMIHLANDYTGFTTSPHIAQVNNQTRTFISEKGF
510 520 530 540 550 560
22213635 PNRIITQPAVGR-----FLFNGSVIS-GFG-FTGGDVVRLNRNNGNIQRGVIEVP--
510 520 530 540 550 560

cry2ab2_820. NOGDSLRFEQNITTARTLGRNGSV-NLYLRVSSIGNSTIRVTNGRVYATVNVNTTN
570 580 590 600
22213635 -----IQF--TSTIRTVRVRYASVTSEIILNVN-LGNSSIFT--NTLPATAASLONLGS
570 580 590 600

```

[illegible]

cy2ab2_820. VPIJSTSSVNTMOOL-FLNRLPQFMOGYOLLLLPLFQAANLHLFSFIRDFVFLNADSWG

Study No. 06-01-62-01
MSL No. 20307
Page 274 of 361

```

SCORES   Init1: 128   Initn: 168   Opt: 261   z-score: 293.3 E(): 4.8e-08
>>SW:61252381
initn: 168 init1: 128 opt: 261 Z-score: 293.3 expect(): 4.8e-08
Smith-Waterman score: 292; 22.2% identity in 600 aa overlap
(60-634:41-609)

cry2ab2_820.  FOHSLDVTQKEWTEWKKNNHSLYLDPIVGTVASFLFKKKVSLGKRIISLRNLNLFPSG
161252381  IPYNCLSNPEVEVLGGERIETGYTIPDISLSLTQFLLSEF--VPGAGFVLGLVDIWIIGF
20 30 40 50 60 70 80

cry2ab2_820.  STNLMDILRETEKFLNQRLNLTDLIARNAELTGL----QANVEEFNRQVDNFIAPNRNA
161252381  GFSQMDAPLVOIQELINRIEFAFNQASIRLEGSLSNYIAYAESFREMEADPTNP--A--
70 80 90 100 110 120 130 140

cry2ab2_820.  VPLSITTSVNTMOQLFNRLPQOMQGYQLLLPLFAQAANLHLSFDRVILNADMGWIS
161252381  LFEEMRIQFNDMSALTALPLFAVQNYQVPLSVYQAANLHLSVLDRVSVFGQWGFED
130 140 150 160 170 180 190 200

cry2ab2_820.  AATUTRYDYLNKNTYRDSYNCINTYOSAFK--GLNTRLHDML---EERTYMYLNFVEY
161252381  AATINSYNDLTRLIGNYTDYAVRWYNTGLERWGFQDSR--DMVRYNQFRRELTITLVID
190 200 210 220 230 240 250

cry2ab2_820.  VSIWSLF---KYQSLVSS--GANIYASGSPQQTOSTSQDWPLSLFQVNSNVNLNGF
161252381  VALPSNDSRRYPIRTVSQLTREIYTNVPLENFDGSPFGMAQRIEQNRIPHLMDLIN--
250 260 270 280 290 300 310

cry2ab2_820.  SGARLSNFFNIYGLPGSTTTTHALLAARVNYSGISS---GDIG--ASPPNQFNCSFT
161252381  --RIT-IYTDVHRGFNMYGSHOITASPVGSGPEFAFLFGNAGNAAPFLVLSLTGLGI
310 320 330 340 350 360

cry2ab2_820.  LPPLLTFPVRSM--LDSGDREGAVITNNQTESFET--TLGURSAFTARGNSYPPDYFI
161252381  FRTLSSPLRYEILGSGNNQEL--FVLDDGTESFASLTNLPSTIYRQGRVDSLS--DVIP
360 370 380 390 400 410

cry2ab2_820.  ENISGVLVVRNEDLRPLHNYEINIAFSGTFCGAPAYNVSHVRKNKHIVHNGSM
161252381  PQDMNSVP--PRAGFGRRLSH---VTMLSOAGAVTYLRAFTSWQHSAEFNIIIPSQI
420 430 440 450 460 470 480

cry2ab2_820.  --IHLAPNDYTGFTTSPHATQVNNQTRFISEKEGNGDGLSFEQNNTIYARTLGRNGN
161252381  TQIPLTKSTNLGSGTSVVKGPGFTGGD--ILRSTFGQISTLAV---NITAPLSOR---
480 490 500 510 520 530 540

cry2ab2_820.  SYNLIYLRVSGISNTIRVTINGRVYTTANVTNTDNCQWDNGAREFSINIGNVASNS
161252381  -YRVIRYASTNLTNLFSTIDGRPIQGNFSAITMS--GSNLSGSGFTVGTFTTTPNSG
550 560 570 580 590 600

```

61252381 description="Pesticidal 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

~~Product Characterization Center~~

©07

```

cry2ab2_820.evldlnr  TANGSTOFDDANINVTNISPLY
                        6%      620      630
                        : : : : : : : : : :
SSVFSSAVFPGHGVWIDRIEFVAPATEAEVDLERAKAVNELFTSSNQIGLKTDV
6161252381          580      590      600      610      620      630

cry2ab2_820.pep
NEAA:61252381
61252381 source="GENBANK PROT" Peptide: crystal protein cryIAa (Insecticidal
delta-endotoxin CryIA(a)) (Crystalline entomotoxin) (333 kDa crystal
protein)[gi|1551713|gb|AAA22552.1| insecticidal cryIAa
protein][224474|prf||1106181A protein, insecticidal crystal

```

SCORES In1L: 128 Opt: 261 Z-score: 293.3 expected: 4.8e-06
 --NNAAG:61952381
 In1n: 168 In1L: 128 Opt: 261 Z-score: 293.3 expected: 4.8e-06
 Smith-Waterman score: 292
 2.62% identity in 600 aa overlap
 (60-634:41-609)

30 40 50 60 70 80
 cry2ab2_820. FQKSLDTQKQEWTEWKKNNHSLYLDPVIGTVASFLKKYVGSVGRKRIUSELRNIPSSG
 IPNCLSNPEVEVLGERIEFGTYPTDILSLTQFLSEF--VPGAGFVGLVDVIINGTF
 61252381

[illegible]

```

150      160      170      180      190      200
cry2ab2_820. VPLSITSSVNTTQQQLFINRLPQFMQYQQLLLPLFAQAANLHLSFIRDVILNADGWGIS
61252381 IREMRTOFDNMNSALTTTALPLFVANYQVPLLSVQAANLHLSLVRDVSFVFGQWGFED

```

cyt2ab2_820. AATLRTYRDYLNKVFEDSYNCINTYQSAFK--GINTRLHDML--EFFYMFNLNVEFY 250

260
270
280
290
300
310
cry2ab2_820. VSIWSLP---KYSLLVSS--GANLYVSSGPGQTQSTFTSDWPFYLSLFQVNSNYLVNCF

61252361
VALGRAND..... 250 260 270 280 290 300
civ2ab2 020. SCARLUNTFNVLPGSTTHLLAARVNSGISS---GDIG--ASPQNQNCSTF
320 330 340 350 360

61252381
---RIT-IYTDVHRGNYNSHQITASVPVGSFPEAFILFGNAGMAAPVVLNSLGLG
370 380 390 400 410 420
TTCGSGAFTARGNSVFFDYF

61252381
FRTLSPLYRRIILGSGNNQEL-FVLDGTEFSPASLTNLPSTYRGRGVDSL-DVITE

360	370	380	390	400	410
PNTSGVTVNEDLRPLRYNEINIASPSGTPGGARAYMVSVHNKXNIHVAHNSGM					
430	440	450	460	470	480
.....					
970					

61252381
PQNSVP--PRAGFSLRH---VTMLSQAGAVTYLTAPFMSQCHESAENFIIPSSQI
420 430 440 450 460 470
490 500 510 520 530 540
-----PNSGCGGATDCAVNTATATACN

6125281
TQPLTKSTNIGSGTSVVKPGFTGD---ILRRTSPQGLTUV---NITAPLSQR----

```

c9y2ab2_820. SYNLXLRVSSGSLIKLVINGKVIARIVALLNGQREGLN...!!!:
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~!!:
61252381 -YVRVTRASTINLQFHTSIDGRPNQNQNFSAITMSS-GENLOSGSFRTVGTTFPFNSMG
              530       540       550       560       570

```

```

cry2ab2_820. DVPIDINV-TLNSGTQDLMNINLVPTNISPLY
      : ::::: |::::: |::::: |::::: |:::::
SSVFTLSAHSVNGNEVVIDRIFEAPEAYDEJERAKAVNELTSSNQGLKTDV
125381          580    590    600    610    620    630

```

crystallization of 130 kD crystal protein (delta endotoxin) (crystalline
cry2ab2.820.pgp
SW 147534

ENTOMOLOGICAL PROCEEDINGS, 1982, 103, 103-104
 Sotto" swissprot prot" version=NA type=PRT
 SCORES Init1: 128 Init2: 100 Opt: 261 z-score: 293.3 E(): 4.8e-08

initn: 160 initli: 168 opt: 261 g score: 293.3 expect(): 4.8e-08
Smith-Waterman score: 292: 22.2% identity in 600 aa overlap
(60-634:41-609)

cy2ab2_820. FOHSLDUIVUNWISNPKNNWSA D UO I V I S T O P L E F F - V P G A G F V I G L A V D I W C I F
117534 TPYNCLSNPEVEIGRINTGVZPZLSITOTPLEFF --VPGAGFVLGLAVDIWICIF

20 30 40 50 60

[illegible]

cry2ab_820. VFLSITSVNTMOQLFNLFPQFMQGVLHLLPFAQAANHLSTSRDYLKAPANGIS
150 160 170 180

:
LREWRVFNDFMSAULTAIPIFAVNQYQIVPLLSVVYQQANHLSTSRDYLVFGGQFEI
190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400

```

cry2ab_820.  AATLRTYRDLKNYTRDYSNCINTYQAFK---GNTLTHDML---EFTYMFNLNEYF
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
AATINSRVNDLTRLGNITDYAVRWNTGLERVGWGFDSR-DWRYNQFRRLTLVLLDI
|||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::

```


**Monsanto Company
Final Report
Product Characterization Center**

Study No. 06-01-62-01
MSL No. 20307
Page 276 of 361

```

cyy2ab2_820. VSIWELF---KYOSLLVSS-GANLYASGSPQOQTOSTSDWPFFLYSLFOVNSVLNFG
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 VALFNDSRRYPIRTVSOLTREITYTVPLENFDCSGFMGAQLIQEINRPHLMDILN--
250      260      270      280      290      300

cyy2ab2_820. SGARLNTEFNIVGLPGSTTTTHALLAARNVNYGGISS-----GDIG-ASPQNQFNCGSTP
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 ---RLT-IYDVHURGFNWGSQHGTATSPGVGFSPEFAFLPFNGMAGNAAPPVLIVSLTLGLI
310      320      330      340      350

cyy2ab2_820. LPPLLTLPFRWSM-LDGSDDRGVAIVTNMQTESPET-TLGURSCAFARGNSNFPDYFI
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 FRTLSSPLYRIIRITLGGPNDEL-FVLDTGEESFASLTNLPTSYIRQGVVDLS-DVIP
360      370      380      390      400      410      420

cyy2ab2_820. RNIISGPLVVRNEDLRRPLHYNELRNIAPSGPFGGARAYMSVHNKNNITHAVENGSM
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 PQDNVP--PRAGFSHRLSH---VTMLSOAGAVALTRAPFTSQHRSAEPNFLIPSSOI
420      430      440      450      460      470

cyy2ab2_820. --IHLPNDYTGFTTSPIATHAQVNQTRTFISEKFNGOGDSLRFQONNTARIYLGRGN
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 TQILTKSNLNGSGLSVVKPGFTGCD--LIERTSPQISTLRV---NITAPLSQR----
480      490      500      510      520      530      540

cyy2ab2_820. SYNLRYLVSSIGNSTRIRVTINGRVYTAIVNTMTNDGVNDGNARFSDINIGNVASSNS
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
117534 -YRVIKYASTINN-QFTHSIDGRPINQGNGFSAFTMSS-GSNLGSFRTVGFTTPFNMSG
530      540      550      560      570

cyy2ab2_820. DVLPLDINV-TLNSGTOFDLMNLMLVPTNISPLY
||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
580      590      600      610      620      630

cyy2ab2_820.pwp
SW:8927981

8927981 description= "PESTICIDIAL CRYSTAL PROTEIN CRYLIC (INSECTICIDAL DELTA-ENDOTOXIN CRYII(C)) (CRYSTALLINE ENTOMOCIDAL PROTIOXIN) (B1 KDA CRYSTAL PROTEIN)." library=NA species="Bacillus thuringiensis" source="swissprot_prot" version=NA type=PRT

SCORES   Initl: 185       Inltln: 247       Opt: 259       z-score: 292.9 E((): 5.1e-08
inltln: 247 inltl: 185 opt: 259 Z-score: 292.9 expect((): 5.1e-08
Smith-Waterman score: 273;    21.3% identity in 616 aa overlap
(57-634:70-646)

cyy2ab2_820. PFSFHKSILTVOKEWTWKNNHSLYLDPIPVGTASFLLKKVSGVKGKRILSELRLNLF
          30           40           50           60           70           80
8927981 EDYLEMHSEHSIDPPFVASSTIQTGITACKIKLGLTGVDPFGQIASLYS-FILGEL---WW
          40           50           60           70           80           90

```

```

90      100      110      120      130      140
cry2ab2_820.  PSGSTNLMQDITRETEKFLNORLNTDTLARNVAELTLQANVEEFNRQVDNPLNPRNAV
8927981      PKGASQ--WEIFMEHVEALINRKISTYARNKALTDLKGLDALAVYSHLESLESWGNRRNTIR
          100      110      120      130      140      150

150      160      170      180      190      200
cry2ab2_820.  PLSIT--SSVNTWQQLFLNRLPQOMOGYQLLLPLPFAQANLHSLFIRDVINADEWGIS
8927981      ARSVKNQYIATLELMFVOKLPFSANSGEEVPLPPTYQAANLHLLLRDASIFEFKNGLS
          160      170      180      190      200      210

210      220      230      240      250      260
cry2ab2_820.  AATLRTYRDYLNKYTRDYSNYCI--NTYQSFAFKLNTLR-LHDMLEFRIYFMFLNVPEYVS
8927981      ASESTIFYNRQVETRDYSVHCYKWNNTGLNKLKATQGSQSVRYNQFRKDIELMVLVDLVR
          220      230      240      250      260      270

270      280      290      300      310      320
cry2ab2_820.  IWSLFYQSLLVSSGAML----YASGSGP-QOTQSFSTQDMPFLYSLFQVNSNVNLNGFS
8927981      VFPXYDILVPYIKTISQTLREVYDAIGTVDPNQAARSTIW--YN---NNAPSPSAIE
          280      290      300      310      320      330

330      340      350      360      370      380
cry2ab2_820.  GARLSNTFNTVGLPGSTTTTHALLA-----ARVNYSGG--ISSGDIG-ASFPNQNFNCST
8927981      AAVIRS--PHLLDLEKVTIYLSLGRWNTQYMMGMGHRLESREIGGALNTSTQGSTNT
          330      340      350      360      370      380

370      380      390      400      410      420      430
cry2ab2_820.  FLPLPLTPFV-----RSM----LDGSGDREGVATVTL-NWOTSEFTTLGLSGAFTAR
8927981      SINPVLTOFTSRDYRTESWAGLNLFLTPQVNGVPRVDFHWK--FFT-LPIASDNF--
          390      400      410      420      430      440

440      450      460      470      480
cry2ab2_820.  GNSNYFPDYFIRNLSGVPLVVRNEDRLRPHYNEINIASPGTPGGARAYMVYVHNRNK
8927981      ---XYLYC-----AGVGTQLODSENELPPTETGQPNVESYSHRL--SHIGLITSGSHVKA
          440      450      460      470      480

480      490      500      510      520      530
cry2ab2_820.  NIHA-VHENGSMIH-LAPNDYGTFTPIPHATQVNTQRTFISEKFGNQGDSIRPEQNTT
8927981      LVYWSMTHRSADRNTIETPNSITQPL--VKAFNLGSGAAVVRGPGFTG-CHILRRTKSGT
          480      490      500      510      520      530      540

540      550      560      570      580      590
cry2ab2_820.  TARYTLRGN--GNSNLYLVRVSSGINSTIRVINGRYVTATNNVTNNQVNDNGARF
8927981      PCHIRVNINPFAQRYVRMSYASTDLOFHTSINGKAINQNGFSATMNR-CEDLJYKTF
          540      550      560      570      580      590      600

600      610      620      630      640      650      660
cry2ab2_820.  SDINIGNVWASSNSVPLDINV---TLNSGTQFDLMNIMLVPTNISPLY
8927981      R--TVGFTTFPSFDVQSTFIYGANWFFSGNSVEYIGRIEFVPEVTEYAEYDFEKAQEKV
          610      620      630      640      650      660      670

670      680      690      700      710
927981      TALTSTINPGLKTDVQHDIDQVSNLVSDESLEYLDEKRELFVYKQAQIHERNM
          670      680      690      700      710

```


Study No. 06-01-62-01
MSL No. 20307
Page 278 of 361

[illegible]

crystal 820 pep
NNEA:3334431

SCORES Initl: 128 Inltn: 168 Opt: 262 z-score: 392.7 E(I): 5.2e-08
>>NRAA:32344731
inltn: 168 Inltn: 128 Opt: 262 z-score: 292.7 E(I): 5.2e-08
Smith-Waterman score: 293; 22.0% identity in 600 aa overlap
(60-633,41-609)

~~cry2ab2_820. FQHSLLDTVQXEWTEWKNNHSLYLDPIVGTVASLKLKWSGLVKGR/LSELRNLITPSSG
32344731 IPYNCLSNPEVEVLGGRIETGYTPIDISLSLTQFILLSEP-VPGAGVGSGVDNDXNGIF~~

cy2ab2_820 STNLMQDILRETEKELINQRLNLTDLARVNAETGL-----QANVEFNQRQVQNFENRRA
GPSQWDFAFLVQIQQLINQRIEFPARNQATSRLEGLSNLVQIYAESFPEWAEPTNR--A
32344731 90 100 110 120 130 140

```

150      160      170      180      190      200
cry2ab2_820. VPLSITSVNTMOQLFLNRLQFQWQYQLLLPLFAQANLHLSFIRDVILNADEMGIS
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
LREWRQTFQNDMSALTIAIPLFAVQYQVPLLSVYQAANLHLSVRDVSVFGRGWGF
32344731
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :
              : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

cry2ab2_820.  AATRTYRDYLNKYRDYSNCINYSAFK---GLNRLDHML---EFTYMFNLNVFEY
|||: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
AATINSRNDLTLLIGNYTDYAVRWYNTGLERWVGPDSE-DWRYNQCFRELLTFLVDI
23244731      200    200    200    220    220    240    250

```

```

cry2ab2_820. VQINSLF--KQSLLVSS-GANLYASGSGPQTOSTSQWPEYLSLFQVNSNYLNGF
      260   270   280   290   300   310
32344731 VALFNDSRRYPRTVSQLTREIVNVLNFDDGSFGMAQRTEQIRQHPLMDLMSI
      260   270   280   290   300

```

```

320      330      340      350
cry2ab2_820.  SGARLSNTFFNVGLPGSTTTTHAARVNVSGGISS---GDIG--ASPFNPNFNCSTF
              :   :   :   :   :   :   :   :   :   :   :   :   :   :
323444731     T-----IYTDVHRGENYWSHQITASPVGSGPEFAFPLFGNAGNAAPPVLVSLTGLGI

```

[illegible]

```

cry2ab_820.  RNISGVLVWNEDLRPLHNEINIASPGTGGARAYTVSVNRRKNNITHVHENGSS
430      440      450      460      470      480
PQNSVSP--PRAGSHLSH---VTVLQAGAYTVTRAPTSQWHRSAEFNIIIPSSQ
32344731    420      430      440      450      460      470

```

```

      490   500   510   520   530   540
cry2ab2_820. --IHLAPDYGTFTSPIHATQVNNQTRTFISEKFGQSGLRFEQNNTARYTLRGNGN
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
TQPLIKSNILSGTSVVVGPGFTGGD--ILRTSPQISLTRLV---NTTAPLSQR-----
      490   490   490   500   510   520

```

cry2ab2_820. SYNLYRVSSIGNSRVTRNGRVYATVNTVNTTNDGVNDGARESDINI GVVVSSNS
 550 560 570 580 590
 32344731 -YRVRYASTNLOFHTSIDGRPNQGNFSATWS- GSNLQSGSFRTVGFITPFPNSNG
 530 540 550 560

cry2ab2_820. DVPDINV-TLMSGTQFLNMIMLVPTNSPLY 610 620 630
 32344731 SSVFTLSAHVFNMSGNEVIDRIEVPVETAEAYDLERAQKAVNELFTSSNQIGLKTDV 580 590 600 610 620 630

cry2ab2_820.pep
SW:61252379

61252379 description="Pesticidal crystal protein cryIAa (Insecticidal delta-endotoxin CryIA(a)) (Crystalline entomocidal protoxin) (133 kDa crystal protein)." library="NA species="Bacillus thuringiensis serovar aizawai" source="Bacillus thuringiensis serovar aizawai" version="NA type="PRT

SCORES InIt1 128 InItn: 168 Opt: 262 z-score: 292.7 E(): 5.2e-08
 >SW: 252375
 InIt1: 168 InItn: 138 opt: 262 Z-score: 292.7 expect(): 5.2e-08
 Smith-Waterman score: 293: 22.0% identity in 600 aa overlap
 (26-634, 27-609)

30 40 50 60 70 80
 cry2ab2-820 FOHSLDIYCKEWETKKNHLSLYLDPPIVGVASFLKKVGSVGRKILSELURNLIFPSG
 61252379 IPNCLSNPEVEVYAGERIENGYTQIDISLSLTQFLSEF--VPGAGFVLGVLDIWIIGIF

[illegible]

```
cry2ab2_820. VFLSTSSVTMTQOOLFNLRFQFNGVYLLPIFAQWHLHLSKFRDINLADEWGJSLIS
150      160      170      180      190      200
LREEMRIQFNDSMSALITAIPIFAVONTGGLLYVVYVNNHLSVDSDYSFGSGRWGEFD
```

```

cry2ab_820. AATLRTYRDYLKNVTRDYSNCINYQSFAK--GLNTLRHML--EFQYFNVFFEN
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
61252379 AATRSNRNDLTRIGNTYDVAVRWYNTGSLERWVGPDSP--DWVRNQRRLTLVLD
|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::

```

```

260      270      280      290      300      310
cry2ab2_820..VSTWLF--KQSELLVSS-GANLYASSGPGQQTQSTSDQFFLYSFQVNSYKANG
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
VAFSVNDSRRYPRTYSQLTREIVFVLENFDGSPFGMAQRIGENIQROPHLMDILNS
61252379

```


Study No. 06-01-62-01
MSL No. 20307
Page 280 of 361

[illegible]

Monsanto Company
Final Report
Product Characterization Center

Study No. 06-01-62-01
MSL No. 20307
Page 281 of 361

Smith-Waterman score: 2634 24.2% identity in 248 aa overlap
(60-388;72-316)

cry2ab2_820. >>SW:8469138
51090240. LEMCSIKGKSTFAKSTSVQSGELKRAITNLSLSLNPFGPGYPAKLLSIIPFPWP
cry2ab2_820. >>SW:8469138
51090240. TMTQGWAFKVVVEELVDKLTTFARSAKLRGICDVAQLAKDNFNNDYPTSE
cry2ab2_820. >>SW:8469138
51090240. SGSTNLMODILRETEFLNRLTDLKAWA--ELTGMVVEEFNRQVNFNLN-PNRN
cry2ab2_820. >>SW:8469138
51090240. AVPLSITSSVNTMOQLFLNLPQFOMQGYQLLSLFAQAQHLHLSFIRDVINLNDWGI
51090240. PIQORLLSOFTATNTFIVGSMISLFRVGRHEVELLTFTVQANLHLLLDLDAIMFGESWGM
cry2ab2_820. >>SW:8469138
51090240. CPVTGAGYQNDFNRIADYDYSVIYNOGLOKAKTLKANLKDYEKYPWAVYNSVQPE
cry2ab2_820. >>SW:8469138
51090240. FEVVSII--WSLF---KYQSILVSSGANLYASGSPQQTOSFTSQMPFLYSLFQVNSNY
51090240. FAQDMENWNLNRYRDMTLMLDLVALWPTYN-PQGYPIAPKIQLTREIYTELRGNAG
cry2ab2_820. >>SW:8469138
51090240. NTKRPSMDAIDAEILPPPLFTWLESVDHMRWPTSAGYVYVYFONAGIKHRYKYTLDSQT
cry2ab2_820. pep
SW:8469138

8469138 description="PESTICIDIAL CRYSTAL PROTEIN CRYIFA (INSECTICIDAL DELTA-ENDOTOXIN CRYIF(A)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 189 Initn: 189 Opt: 261 Z-score: 291.6 E(): 6e-08
>>SW:8469138
Initn: 189 Initl: 189 opt: 261 Z-score: 291.6 expect(): 6e-08
Smith-Waterman score: 329; 22.5% identity in 627 aa overlap
(32-634;12-603)

cry2ab2_820. QAMDNSVLNSGRITICDAYNVAADHFPFSFOHKSLDTVQKEMTEWKNHSLVLDIPVGV
8469138
MENNIONQCVFYNCLNNPEVEILNEERSTGRPLD-LSLSL
cry2ab2_820. ASFLKXVGLVGRKILSELRLNLIFFPSGSLNLMQDILRETEKFLNQLRLNTDILARNAEL

8469138 TRFLSEFVPGVG--VAFGLFDLWGFITPDSWSLFILOIQELIEQRIETLEENRAITTL
cry2ab2_820. TGLQANVEEFNRQVNF--LNFNRNAVPLSITSSVNTMOQLFLNLPQFOMQGYQLLSLFL
8469138 RGLADSVIELALREWEANEANQALREVRIRFANTDDALITAINNFTLITFEIPLLSV
cry2ab2_820. FAQANLHLSFIRDVILNADWEGISAATLRTVDRVYKNYTRDYNYCINITYQSAF---KG
8469138 YVQANLHLSLRLDAVSGQGLDIATVNNHYNRLINLHRYTKHCLDTYNOGLENRG
cry2ab2_820. LNTLRLHML--ERTYMFNLNVFYSVMSLEKYSQSLVSSGANLYASGSPQQTOSFTSOD
8469138 TNRQWAFNPQPRDUTLVLDIVALPNDYVTPYIQTSSQL---TREIYTSVI-ED
cry2ab2_820. WPFYLSLFQVNSYVILNGFSGARLSNTFPNIVGLPGSTTTTHALLAARVNYSGG--ISSGD
8469138 SP-----VSAN-IPNGFNRAEFPFPHLMDFMNSLFTVTAETVRSQTVMGHGLVSSRN
cry2ab2_820. ETTTCHRSGLFARGNSVFPDYFIRNISGVPLVVRNEDLRPL-HYNEIRNIASPSGTP
8469138 QUTGNHRTAFRRSGTIRGSDRLPPQDNSGAPW----NDYSHVLNHTVFWPGEISGSD
cry2ab2_820. GGARAQVSVHNRKNMFAVHENGSMHLAANDYTGTFTSPIHATQVNNQTRTFISEKFG
8469138 SW-RAPMFSWHLRS---ATLNTN---IDPEKITLPLVKAHTIQ--SGTIVVRGEGT
cry2ab2_820. NOGDSLRFEQNTTARTYLRGNN--SYNLKLSGSGNSTRKING-RVYATNNT
8469138 G-GDILRRTSGGPFATYIVNINGQLPQRYARIRYATTPSYVYVAGENFAGQFNKT
cry2ab2_820. TINNGVNDGARGSDINIGNVAVSSNSDVLDDNLNSCTOFDLNIMVLPNTNLSLY
8469138 MDTGDLPLTFQSFYSYATINATFTFPMSSQSFTVGAD-TFSSGAEVADRFEFETFEA
8469138 EYDLERAQKAVNALFTSINOIGIKTDVTDYHDQVSNLVDCISDEFCLDERKRSKVRK
cry2ab2_820. pep
NRAA:8469138

Study No. 06-01-62-01
MSL No. 20307
Page 282 of 361

STV2ab2	820	440	450	460	470	480
	NOGDSI:PEPPNNNTTAVTI:PCNEN--SVNI:VI:BUSS:GNETTITING--PIVATATNT					
		530	540	550	560	570

84609138 G-GDLRLKRTSGGPFATYINNGOLPORVRAIRVASTTNIRIVTVVAGERIVVAFQFNK
490 500 510 520 530 540 550
cry2ab2_820. TTNNDGVDNGARFSDINIGNVVASSNDVPLDINVTLNSCTQDLNMLVPTNISPLY
580 590 600 610 620 630

8469138
EYDLERAQKAVNALFTSINQIGIKYTDVYHIDQSNLVCLSEDFCLDEKRELSEKVKH
610 620 630 640 650 660

cry2ab2.820.pep
NR04:21239436
21239436 source="GENBANK PROT" crysra] protein Crv1ab13 [Bacillus thuringiensis]

SCORES Init1: 128 Initn: 168 Opt: 261 z-score: 291.6 E(): 6e-08
 >>NRAA:21239436 (1180 aa)

Smith-Waterman score: 292; 22.2% identity in 600 aa overlap
(60-634:41-609)

cty2ab2_820. STNLMQDILRETEKFLNORLNTDTLAFVNAELTGI---QANTPEEFNQVDNPLNPNRA
21239436 90 100 110 120 130 140
IPYNCLSNPEVEVLGGERTGYTPDIDLSLSTQFLSEF--VFGAGFVLGLVDIINGIT

crv2ab2_820. VPLSITSSVNTWQQLF.NRLPQFMQGYQLLLPLPFAQANLHLSFTFROVILNADENGIS

cty2ab2_820. AAILRTYRDYLNKYTRDYSNVCINTQSAFK---GLNTRLHDM---EPRTYNFINVPEY

cry2ab2_820. VSIWSLF--KYQSLVSS-CANLYASGGPQQTQSTFSQDWFLYSLFQVNSNVLNGF

	250	260	270	280	290	300
CIV2ab2	320	330	340	350	360	
	SGARLNTFNIVGLPGSTTHAIJAARVNVSGGTS---	GDIG--ASPENONENCSTF				