

Monsanto Company
Final Report
Product Characterization Center

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MSL No. 20351
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Description: Q45720 bacillus thuringiensis. cryIa(a) (fragment). 6/2001
Accession/ID: Q45720
-----General comments-----
ID Q45720; PRELIMINARY; PRT; 620 AA.
AC Q45720;
DT 01-NOV-1996 (Tremblurel. 01, Created)

SCORES Init1: 2251 Initn: 3103 Opt: 3192 z-score: 3521.0 E(): 3.3e-190
>>TXN5:Q45720
initn: 3103 init1: 2251 opt: 3192 z-score: 3521.0 expect(): 3.3e-190
Smith-Waterman score: 3192; 78.0% identity in 623 aa overlap
(1-621:1-620)

cryIa-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL 60
||||| 10 20 30 40 50
Q45720 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL 60
||||| 10 20 30 40 50

cryIa-105.pe VDIIMGIFGSPQNDALVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREWAD 120
||||| 70 80 90 100 110
Q45720 VDIIMGIFGSPQNDALVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREWAD 120
||||| 70 80 90 100 110

cryIa-105.pe PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVOAANHLHSLVLDVSVFGQ 180
||||| 130 140 150 160 170
Q45720 PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVOAANHLHSLVLDVSVFGQ 180
||||| 130 140 150 160 170

cryIa-105.pe RWGFDAAATNSRYNDLRLIGNYTHAVRWNTGLERVWGPDSRDWRINQFRRELTITV 240
||||| 190 200 210 220 230
Q45720 RWGFDAAATNSRYNDLRLIGNYTHAVRWNTGLERVWGPDSRDWRINQFRRELTITV 240
||||| 190 200 210 220 230

cryIa-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYNPVLENFNGFSRGSNOGIEGSIKPSHLMIDL 300
||||| 250 260 270 280 290
Q45720 LDIVSLFPNYSRTYPIRTVSQLTREIYNPVLENFNGFSRGSNOGIEGSIKPSHLMIDL 300
||||| 250 260 270 280 290

cryIa-105.pe NSTITVDHAGEYVWGHQIMASPVGSGPEFTFPYLGTMGNAAPQQRIVAAQLQGVYR 360
||||| 310 320 330 340 350
Q45720 NSTITVDHAGEYVWGHQIMASPVGSGPEFTFPYLGTMGNAAPQQRIVAAQLQGVYR 360
||||| 310 320 330 340 350

cryIa-105.pe TISSTLYRPP-FNIGINNQSLVLDGTFAYGT-SSNLPAAVYKSGTVDSDLEIPPNNN 410
||||| 370 380 390 400 410
Q45720 TISSTLYRPP-FNIGINNQSLVLDGTFAYGT-SSNLPAAVYKSGTVDSDLEIPPNNN 410
||||| 370 380 390 400 410

cryIa-105.pe NVPPROGSHLSHVMSFRSGFNSVSIIRAPMFTSHSAFNNTIASDSITQIPLVK 470
||||| 420 430 440 450 460
Q45720 NVPPROGSHLSHVMSFRSGFNSVSIIRAPMFTSHSAFNNTIASDSITQIPLVK 470
||||| 420 430 440 450 460

cryIa-105.pe SVPPRAGSHLSHVMTLSQ--AAGAVYTLRAPTFSHQHSRANNTIISQITPLTK 470
||||| 420 430 440 450 460
Q45720 SVPPRAGSHLSHVMTLSQ--AAGAVYTLRAPTFSHQHSRANNTIISQITPLTK 470
||||| 420 430 440 450 460

cryIa-105.pe AHTLOSGLTVVRGPGFTGGDILRRTSGGPFAYTIWNGQLPQRYRIRYASTTNLRIY 530
||||| 480 490 500 510 520
Q45720 AHTLOSGLTVVRGPGFTGGDILRRTSGGPFAYTIWNGQLPQRYRIRYASTTNLRIY 530
||||| 480 490 500 510 520
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Q45720 STNLGSGTGVKPGCGFTGGDILRRTSGQISTLRVNIITAPLSQRYRVRIRYASTTNLQFH 530
480 490 500 510 520

cryIa-105.pe VIVAGERIPAGQFNKMTDGTPLTTFQSFYATINTATFFPMSSQSFVVGADTFSSGNEVY 590
||||| 540 550 560 570 580
Q45720 VIVAGERIPAGQFNKMTDGTPLTTFQSFYATINTATFFPMSSQSFVVGADTFSSGNEVY 590
||||| 540 550 560 570 580

cryIa-105.pe IDRFELIPVTATLEAEYNLERAKAKAVNALFTSTNQLGKINVDYHIDQVSNLVTLSDE 650
||||| 600 610 620 630 640
Q45720 IDRFELIPVTATLEAEYNLERAKAKAVNALFTSTNQLGKINVDYHIDQVSNLVTLSDE 650
||||| 600 610 620 630 640

cryIa-105.pe IDRIEFVPAEVTFFAEVDLERAQ 620
||||| 600 610

Description: Q9am80 bacillus thuringiensis serovar kunthalanags3. insecticidal
crystal protei
Accession/ID: Q9AM80
-----General comments-----
ID Q9AM80; PRELIMINARY; PRT; 1155 AA.
AC Q9AM80;

SCORES Init1: 2134 Initn: 4262 Opt: 3035 z-score: 3343.6 E(): 2.5e-180
>>TXN5:Q9AM80
initn: 4262 init1: 2134 opt: 3035 z-score: 3343.6 expect(): 2.5e-180
Smith-Waterman score: 4176; 61.9% identity in 1168 aa overlap
(1-1148:1-1120)

cryIa-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL 60
||||| 10 20 30 40 50
Q9AM80 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL 60
||||| 10 20 30 40 50

cryIa-105.pe VDIIMGIFGSPQNDALVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREW 110
||||| 70 80 90 100 110
Q9AM80 VDIIMGIFGSPQNDALVQIEQLINQRIEFAFNQAIISRLGLSNLYQIYAESFREW 110
||||| 70 80 90 100 110

cryIa-105.pe EADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVOAANHLHSLVLDVSV 170
||||| 120 130 140 150 160
Q9AM80 EADPTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVVOAANHLHSLVLDVSV 170
||||| 120 130 140 150 160

cryIa-105.pe FGQWGFDAATNSRYNDLRLIGNYTHAVRWNTGLERVWGPDSRDWRINQFRRELT 230
||||| 180 190 200 210 220
Q9AM80 FGQWGFDAATNSRYNDLRLIGNYTHAVRWNTGLERVWGPDSRDWRINQFRRELT 230
||||| 180 190 200 210 220

cryIa-105.pe LTVLDIVSLF----PNVDSYTYPIR--TVSQLTREIYNPVLENFNGFSRGSNOGIEGSI 280
||||| 240 250 260 270 280
Q9AM80 LTVLDIVSLF----PNVDSYTYPIR--TVSQLTREIYNPVLENFNGFSRGSNOGIEGSI 280
||||| 240 250 260 270 280

cryIa-105.pe RSPHLMIDILNITTVTAHGEYVWGHQIMASPVGSGPEFTFPYLGTMGNAAPQQRIV 350
||||| 300 310 320 330 340
Q9AM80 RSPHLMIDILNITTVTAHGEYVWGHQIMASPVGSGPEFTFPYLGTMGNAAPQQRIV 350
||||| 300 310 320 330 340
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[illegible]

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000: 2690 Z-score: 2962.9 expect(): 3.9e-159
0778: 41.1% identity in 1196 aa overlap

MEMPNINECIPYNCISNDEVEVLGGRIETGTP      10      20      30
DPSMTLNSLNTTITOKALSSLSLNNYQDFUSITERE - OPBALASGNTA      40      50
55LSSEF-VPAGH-IGLGVLTGWTGPGSQ - WDAFLVQIEQLINORTEEF      60      70      80      90
ILSLGVPGNASTNFWFKITGLGPHKNLNDEWTEHETLIEQIEQY      100     110     120     130
110 120 130 140 150 160 170 180 190 200 210 220 230
GLSLNLYQIAESFRWEADPTNPAESNRQIFNMNSALTATIRFNO
GLGLGNLTITVOALEDLWLNPPDPTATITRNDRHILDAFEVWSPFRVA
VQAAANLHSLVLRDVSVPQWRGFGDAATINSRYNDLTLLSNYVSAVAVK
VQAAANLHSLLRDSTLYGDKWGFQNNIIEENYNRQKHISEYNSNCVNY

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U04367_1      LEGVAFGNLEVEDGPGVIGEALARKVKQETKRWKLAQMTEETQALYTRAKQALDNLFA
      880      890      900      910      920      930

cry1a-105.pe  NSQDQLQADTNIAAHADKRVHIREAYLPESVIPGVNAAAFEELEGRIFTAFSLYD
      920      930      940      950      960      970

U04367_1      NAQDHLKIDVTFRAEIAAAAKVQSIREVYMSLVVPGVNHPIFTELSGVQRAFLQYD
      940      950      960      970      980      990

cry1a-105.pe  ARNVIRKNGDFNNGLSWNKGVHVDVEEONNORSVLVVPWEAEYSQSVRVCPGRGYILRV
      980      990      1000      1010      1020      1030

U04367_1      VRNVVNGRFGNGLSDMIVTSDVNVQEEGN-NVLVLNNWDAQVRLNVKLYQDRGVYLRV
      1000      1010      1020      1030      1040      1050

cry1a-105.pe  TAYKEGYGSCVTHIEYENNTDELKFSNVEEELYPNNVTVCNDYTVNQEYGGAYTSRN
      1040      1050      1060      1070      1080      1090

U04367_1      TARKIGIGSYITIDEEGHTDLQRTAC--EEDLASN-----AFIS-
      1060      1070      1080      1090

cry1a-105.pe  RGYNEAPSVPADYASVVEEKSVDGGRNCPCEFNRGYRDYTLPLPGVYTKVELEYEPETDK
      1100      1110      1120      1130      1140      1150

U04367_1      -----GVITKELEFPDTEK-----
      1100      1110

cry1a-105.pe  1160      1170
cry1a-105.pe  VWIEIGETEGTFIVDSVELLMEE
      1160      1170
U04367_1      VWIEIGETEGIFLVEISFLMEELC
      1120      1130

cry1a-105.pep
TXN5: C7AB_BACUA

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

SCORES      Init1: 671      Initn: 2624      Opt: 2690      z-score: 2962.9 E(): 3.9e-159
>>TXN5: C7AB_BACUA
      initn: 2624      initl: 671      opt: 2690      z-score: 2962.9      expect(1): 3.9e-159
Smith-Waterman score: 2778;      41.1% identity in 1196 aa overlap
(4-1177:29-1136)

cry1a-105.pe  10      20      30
C7AB_BACUA    MNLNLGSGYEDSRNTLNNLSNVPTQAKVSLKNNMYQDFLSITERE--QPEALASGNTA
      10      20      30      40      50

cry1a-105.pe  40      50      60      70      80      90
IDISLSITQFLSFEF-VPGAGFVIGLVDIIWIGTFGSG--WDAPFLVQIOLINORIEEF
      40      50      60      70      80      90
C7AB_BACUA    INTVSVTGATLSALGVPGASFITFNFLKITGLLWPHNNKINWDEFTVEVTLIEQKIEQY
      60      70      80      90      100      110

cry1a-105.pe  100      110      120      130      140      150
ARNOQAIRLEGLSNLYQIYAESFPEWADPTNPALREEMRIQDNMMSALTTAIPFLFAVQ
      100      110      120      130      140      150
C7AB_BACUA    INTVSVTGATLSALGVPGASFITFNFLKITGLLWPHNNKINWDEFTVEVTLIEQKIEQY
      100      110      120      130      140      150

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C7AA_BACTU -----EF-YGVKGHVHVRGDNKDYDITYDSIDQLPPDGE--PIHEKYTHRLCHATAIFKS
420 430 440 450 460

440 450 460 470 480 490
cyla-105.pe GFSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGGD

C7AA_BACTU
TPDYDNATI---PIFSWTHRSAEYNNRIYPNKITIKIPAVKMYKLLDDPSITVVKGGPGFTGG
470 480 490 500 510 520

Category	Sub-category	Value
A	1	10
	2	20
B	1	30
	2	40
C	1	50
	2	60
D	1	70
	2	80
E	1	90
	2	100

cryla-105.pe ILRRTSGGPFAYTIVNINGOLPORRIRIRYASTTNLRIVYTVAGERIFAGQFNKTMDT-
300 310 320 330 340 350

[illegible]

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560      570      580      590      600      610
cry1a-105.pe --GDLTFQFSYATINTAFTPMNSQSSFTVGADTFSSGNEVYTDRELIPYATLAEAY
C7AA_BACTU  GEGKDLYSGFGVYESTITQFDEHPKPTLHLSDLSNNSSFYVDSFTFIPVDVNVAYSEK

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620	630	640	650	660	670
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cr7ia-105.pe
NLERAQKAVNALFTSTNQLGKUNVTYHIDQVSNLTVLSDFCLDEKRELSEKVXKH
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
KLEAKOAVANTIFTEECBN-AVCUNTYDVYNDOVSITUTICSDIYMNVAFFYONTUKUW
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	680	690	700	710	720	730
cr1a-1.05.pe	RLSDERNLLQDNFNFKDINRQPERGWSGTITIGCGDDVFKNVVTLSGTTFDECPPTVLY					
C7AA_BACTU	RLSYERNLLDDTFDSINSSSENGWGSNGIVGNGDFVFKGNLITFISGTTQPTVLY					

cryIa-105.pe QKIDESKLAFYRQLRGYEDSQLEIYSIRYNAKHETVWPGTGLWPLSAQSPIGKC
740 750 760 770 780 790

C7AA BACTU QKIDESKIKEYTPVKIKGFTFESSQOLEAVIVPYNAKUDRTNV--SDNP D--DTLDDNCC
740 750 760 770 780 790

800 810 820 830 840 850
CTyIa-1.05.pe GEPNRC--PHLEMPNDLDCSC-RDEKCAHHSHFSLDIDVGCTLDNELDGWVIFKIK
 | | | | | | | | | | | | | | | | |
C7AA_BACTU GEPNRCAAQYLDENPSPCCSSMQDG--ILSDPSHSFLINDITGSINHNENIGIWVLFKIS

860 870 880 890 900 910
 TQDCHARLGNLFLEERPLVEALARVKAQKKNRDKREKLEWETIVIVYKAESVDALF
 cry1a-1.05.pe
 TLEGVAKFGNLEIVIGDGVIGALARVQPEYQENVTASITETQVATVYDLYQVATVYD
 C7AA BACTU

[illegible]

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cryIa-105_p8    DARNVKNKGDFNGLSCWNTKGVHDVEEQNNORSVLVVPEWEAEVSQEVCPGEGYLLR      980   990   1000   1010   1020   1030  
|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||  
DVRNVVNGEFGFLGLSDWITSVDVKQEENGH-VLVVLNNWDQLVNQVLYLQDRGYILLH      1000
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cryla-105.pe VTAYKEGYGEGCVTIHRIENTNDELKFSNCVEEIIYPNNVTTCNDYTVNQEEYGAYTSR
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CTAA_BACTU VTARKYIGEGKTTTDEEGHTDQLRFTAC--EEIDASN-----AFIS-
1060 1070 1080 1090

cry1a-105.pe NRGWNEAPSVPDWSVVEERSVTDSENPCEFNRGYRDVTPLPVGYVTKLEVPETD
1100 1110 1120 1130 1140 1150
CTAA_BACTU -----GYITKELEFPDTE
1100 1110

cry1a-105.pe KWIIEIGETEGTIVQSVKLLMEE
1160 1170 1180 1190 1200
CTAA_BACTU KWIIEIGETEGTIVQSVKLLMEE
1120 1130 1140 1150

cry1a-105.pe
TXNS:A07236_1
Description: A07236 Bacillus thuringiensis B.thuringiensis (strain PGS1245)
gene. 10/1993

Accession/ID: A07236
LOCUS A07236_1 [A07236]
DEFINITION B.thuringiensis (strain PGS1245) gene.

SCORES Initl: 635 Initn: 2653 Opt: 2684 z-score: 2956.3 E(): 9.2e-159
>>TXNS:A07236_1
Initn: 2653 Initl: 635 Opt: 2684 z-score: 2956.3 expect(): 9.2e-159
Smith-Waterman score: 2772; 41.4% identity in 1197 aa overlap
(4-1177:29-1136)

cry1a-105.pe
A07236_1 MNLNLDGYEDSNRTLNNSLNYPTOKALSPSKMNYQDLSITERE--QPEALASNTA
10 20 30 40 50

cry1a-105.pe IDISLSLTOFLSEF-VPGAGFVLGLVDIIWGIFGDSQ---WDAFLVQIEQLINQRIEEF
40 50 60 70 80 90
A07236_1 INTVSVTGATLSALGVPGASFITNFYKIKIAGLWPGNKIWDFMTEVEALIDQKIEEY
60 70 80 90 100 110

cry1a-105.pe ARNQASRLGSLNLYQIYAESFREWEADPTNPALREEMRIQNDNSLITATLPAVQ
100 110 120 130 140 150
A07236_1 VRNKATAEGLGSLGALDKYOKALADWLQKQDDPEALISVATEPRIIDISFEFSPFVAT
120 130 140 150 160 170

cry1a-105.pe NYQVPLSVYVQAAANLHLSVLRDVSVFGQWGFDAATINSRYNDLRLIGNYTDHVRWY
160 170 180 190 200 210
A07236_1 GVEIFLLTVYQAANLHALLRDSITLYGDKWGFTQNNLEENYNRQKRISEYSDHCTKWY
180 190 200 210 220 230

cry1a-105.pe NTGLERVMGQPSRWIRYNQFRRELTALVDIVSLFNYSRTYPIRTYQSLTRIYNP
220 230 240 250 260 270
A07236_1 NSGLSLNGSTVEQWYNINFRREMILMALDLVAVFPHPPRYSMETSTQUTREIVYDTP
240 250 260 270 280 290

cry1a-105.pe V-IENFDGFRGSAQIEGS--IRSPHLMILINSITIIDARGE-----YKWSGHQI
280 290 300 310 320

A07236_1 VLSISNPIDGSPFSQMENTAIRTPHLVDYLDYLYTSKYAFSHEIQPDLFYWSAHKV
300 310 320 330 340 350

cry1a-105.pe MASVPGSGPEFTFLYITGMNAAPQORIVQAQGVVTLSS-TLYRRPFINNNOOL
330 340 350 360 370 380
A07236_1 SFKKEQSN-LYTTIGYKTSYSSGAVSFH-GNDIYRTILAAFSVVVYITONVGEV
360 370 380 390 400 410

cry1a-105.pe SVLDGTTFAYGTSSNLPASAVYRKSQ-TVDSLEIPQANNVPPRQGSFHSLSVMS-MFRS
390 400 410 420 430
A07236_1 -----EF-YGVKGVHYRGDKYDLYDSIDQLPDGE--PIHEKYTHLCHATAIFKS
420 430 440 450 460

cry1a-105.pe GFSNSSVSIIRAPMSWIRSAEFNIIASDSITQIPLVKAHTLOSQTIVVRGPGFTGGD
440 450 460 470 480 490
A07236_1 TPDYDNATI--PIFSWTHRSAEYNYRIYPNKITIPAVKMYKLDPSFVVKPGFTGGD
470 480 490 500 510 520

cry1a-105.pe ILURTSQGFAYTIVNINCOLDQRYARIYASTTNRIYVTVAGERIFAGQFNKMTD-
500 510 520 530 540 550
A07236_1 LVKRGSTYIGDIKATVNSPLSQKRYRVRYATVNSQGFNVINDKITLQTKFQNTVETI
530 540 550 560 570 580

cry1a-105.pe --GDLPTQFSFATNTAFTFPMSSQSFVTGADTFSSGNEVYIDREFELIPIATLEAEY
560 570 580 590 600 610
A07236_1 GEGDLTYGFGVIEVSTIQPDDEPKITLHLSLNNSSFYVDSIEFIPDVNVYAEKE
590 600 610 620 630 640

cry1a-105.pe NFERAQAVNALFSTNQLGKINTVDYHDQVSNLVYLSDEFCLDEKRELSKVHAK
620 630 640 650 660 670
A07236_1 KLEAOKATLPTERN-ALQKQVTDYKVDQVSLVDCISGDLVFNPKRELOLNVYAK
650 660 670 680 690 700

cry1a-105.pe RUSDRNLIQDSNLS--KXOPERGSGSGITIOGGDDVFKENYVTLSTGDECYPTLY
680 690 700 710 720 730
A07236_1 RLSYGRNLEDPEDSINSFENWYSGNVYTGQDFPKGNILIFSGTNDTOYPTLY
710 720 730 740 750 760

cry1a-105.pe OKIDESKLKATRYOLRGYFESQDLEITGTPAKHETVNFPSGSLMPLSAQSPGKC
740 750 760 770 780 790
A07236_1 OKIDESKLKEYTRYKLAGFISSONLEAVIRYDAKRTLDV--SNLLD--DILPENTC
770 780 790 800 810 820

cry1a-105.pe GENPRCA--PHLEWNPOLDSC--RDGKCAHSHNSLSIDVGCIMNEDLVWVYKX
800 810 820 830 840 850
A07236_1 GENPRCAQQLDENPSCSSQMDG--ILSDSHSFSLNTSTGSHNS--DILPENTC
820 830 840 850 860 870

cry1a-105.pe TQGHARLONLEFEEPLVGEALAEVKAEEKWDEKRELEWETVIVYKSAKAVDAL
860 870 880 890 900 910
A07236_1 TLEGYAKFNGLEVIEDGFPVIGEARVKKQETKWKNAKLAQITETQAIYTRAKQNDNF
880 890 900 910 920 930

cry1a-105.pe VNSQYDQLOADNTNAMIHAADKRVHSIRAYLPFELSVPGVNAAIFEELEGRIFTAFSLY
920 930 940 950 960 970

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A07236_1 ANAQDHLKRDVFAEIAAARKIVQSIIEAAYMSLWVPGVNHPIFTELSGRQVQAFQLY
940 950 960 970 980 990

cry1a-105.pe DARNVIRKGDNNKSCWNVKGVHVDVEONNQRSDVLPWPEAEVQEVVCPGRGILR
1000 1010 1020 1030 1040 1050
A07236_1 DVNVVRNGREGLSDWIVTSDVKVQENG-NVLVLNNWDAQVLQNVKQVQGRGILH
1060 1070 1080 1090 1100 1110
cry1a-105.pe VTAYKEGYGECVTHIEIENNTDELKFSNCVEEIIYNNIVTNCNDVTYQEEYGAYTSR
1120 1130 1140 1150
A07236_1 VTARKIGEGYITIDEGHTDQLRFTAC--EELDASN-----AFIS-
1160 1170 1180 1190 1200 1210
cry1a-105.pe NRGYNEAFSPADYASVYEEKSYTDGRENPCENRGYRDTPLFVGVTKELEYFFPETD
1220 1230 1240 1250 1260 1270
A07236_1 -----GVITKELEFFPDTE
1280 1290 1300 1310 1320 1330
cry1a-105.pe KVMWIEIGESTGTVDSVLLMEE
1340 1350 1360 1370 1380 1390
A07236_1 KVMHIGETGIFLVSIEFLMEELC
1400 1410 1420 1430 1440 1450
cry1a-105.pep
TXN5:AF077326_1
Description: AF077326 Bacillus thuringiensis Bacillus thuringiensis CryIb
delta-endotoxin g
Accession/ID: AF077326
LOCUS AF077326_1 [AF077326]
DEFINITION Bacillus thuringiensis CryIb delta-endotoxin gene, complete cds. . .
SCORES Initl: 1817 Initn: 3239 Opt: 2680 z-score: 2951.4 E(): 1.7e-158
>>TXN5:AF077326_1
initn: 3239 initl: 1817 Opt: 2680 z-score: 2951.4 expect(): 1.7e-158
Smith-Waterman score: 4235, 57.6% identity in 1175 aa overlap
(51-1177:72-1227)
cry1a-105.pe VEVLGGERITGTPTIDISLSLTQFLSEFVPGAGFVLGVDIWIGIFGP---SQWDAFL
30 40 50 60 70
AF077326_1 AEGNNIDPFVSASTVQTGINIAGRILGVLPVFPAGQIASFYSLFVLGWLPRGRDPWEIFL
50 60 70 80 90 100
cry1a-105.pe VQIEQLINQIEFARNQAI SRLEGLSNLYQIYAESFRWEADPTNPALREEMRIQNDM
80 90 100 110 120 130
AF077326_1 ERVQLIRQVQNTENTDATALRQLGNSFRAYQOQSLDMLNENDDARTSRVLYQYIAL
110 120 130 140 150 160
cry1a-105.pe NSALTALPLFAVONYQVELLSVYQANLHLSVLRDVSFVQGRWGFDAATINSRYNDLT
140 150 160 170 180 190
AF077326_1 ELDFLNPFLFAIRNOEVPLWVTAQANLHLLDLGLSLFSEGLTSQEIORYERQV
170 180 190 200 210 220
cry1a-105.pe RLIGNYTDHVRWYNTGLERWGPDSRWIRYNOQFRRLTLVLVDIVSLFPNYSRTYPI
200 210 220 230 240 250
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AF077326_1 EXTREYSDYCARWNTGLANLGRGTNAESWLRYNQFRDLTLGLVLDLVALFSPSYDTRYVPM
230 240 250 260 270 280
cry1a-105.pe RTVSQLTREIYTNFVLEN-----FDGS--FRGSA--QGIEGS--IRSPHLMIDILNSITY
260 270 280 290 300
AF077326_1 NTSAQLTREIYTDIGRTNAPSGFASTNWFNNNAPSALAEAVIRPPHLLDFPEOLTIF
290 300 310 320 330 340
cry1a-105.pe TDAHR--GEY--YWSGHQIMASPGVFGSGPEFFPLPYLGTWGNAPQQRIVLAQL--GQGVYR
310 320 330 340 350 360
AF077326_1 SVLSRWSNTQIMNYWGHRLSRTII--RGSLSSTSTHGNTNTSINP---VTLOFTSRDYYR
350 360 370 380 390
cry1a-105.pe TLS-----STLYRRPFNIGINNOLSVLDGTDFAYGTSSNLPAGAVYRKSGT--VDSLDEIP
370 380 390 400 410
AF077326_1 TESFAGINILLTTPVN-GVPWAFNWRNPLNSLRG--SLLYTIIGYTGVTQLFDSSETLP
400 410 420 430 440 450
cry1a-105.pe PONNVPPROGFSHRLSHVMSFRSGFSNNSVSIIRAPMFESWIHRSAEFNIIASDSITQI
420 430 440 450 460 470
AF077326_1 PETTERPNYESYSHRLSNIRLI-SG-----NTILRAPVYSWTHRSADRNTIISDSTIQI
460 470 480 490 500
cry1a-105.pe PLVKAHTLOSCTVVRSGPGTGTGDIILRTKSGFPATVINGQLPORYRARIRYASTTN
480 490 500 510 520 530
AF077326_1 PLVKSFNLSGISVSGPGTGTGDIIRINWNGSVLMSGNLFNNTSLQRYRVRVRYAASQT
510 520 530 540 550 560
cry1a-105.pe LRIVYTVAGERIFAGQFNKMTGDIPLTFQSFYSYATINTAFTFPMSSQSFVAGADTFSSG
540 550 560 570 580 590
AF077326_1 MWLRVTGGSTTFDQGPSTMANESLTSQSFRAEFPPVGSASGQTA-CISISNNAGR
570 580 590 600 610 620
cry1a-105.pe NEVYIDRFELIPVATLEAEYNLEAQAQVNAFLTSTNOLGKTNVTDYHIDQVSNLVTY
600 610 620 630 640 650
AF077326_1 QTFHFDKIEFIPITATFEAEYDLERAQAVNALFTNPRRLKTVGTDYHIDEVSLVAC
630 640 650 660 670 680
cry1a-105.pe LSDEFCLDEKRELSEKVKHAKLSLDERNLLQDSNFKDINROP-----
660 670 680 690
AF077326_1 LSDEFCLDEKRELLEKVKYAKLSLDERNLLQDPNFTSINKKQPDFISTNEQSNFTSIHQES
690 700 710 720 730 740
cry1a-105.pe EFGWGGSTGITIGDGDVFNENYVTLGTFDECVPTLYQKIDESKLKAFTRVQLRGYIE
700 710 720 730 740 750
AF077326_1 EHGWMGSENITIOEGNDVFNENYVTLGTFDECVPTLYQKIDESKLKAFTRVQLRGYIE
750 760 770 780 790 800
cry1a-105.pe DSQDLLEYSTRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR
760 770 780 790 800 810
AF077326_1 DSQDLLEYSTRYNAKHETVNVPGTGSWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCR
810 820 830 840 850 860
cry1a-105.pe DGEKCAHSHHFLSDLDVCGCTDNLNEDLGWVIFKIKTODGHARLGNLEFLEKPLVGEAL
820 830 840 850 860 870
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CIBE_BACTU      EHGWSGSENIITQEGNDVFKENYVILPGFTFNECYTYLYQKIGAEALKAYTRYQLSGYIE
750      760      770      780      790      800

cry1a-105.pe    DSODLEIYSIRYNKAKHETVNPVPGTSLWPLSAQSGIKGCEPNRCAPHLEWNPDDCSGR
760      770      780      800      810
CIBE_BACTU      DSODLEIYIRINAKHETLDVPGTESWPLSVEPIKGTGCGPNRCAPHLEWNPDDCSGR
810      820      830      840      850      860

cry1a-105.pe    DGEKCAHSHHFSLDIDVGCIDMEDIGVWVIFKIKTODGHARLGNLEFLEEKPLVGEAL
820      830      840      850      860      870
CIBE_BACTU      DGEKCAHSHHFSLDIDVGCIDLHNLGVWVFKIKTQEGHARLGNLEFLEEKPLVGEAL
870      880      890      900      910      920

cry1a-105.pe    ARVKRAEKWRDKREKLEWETNIVYKEAKESVDALFVNSQYDQDQADTNIAHIAADKRV
880      890      900      910      920      930
CIBE_BACTU      SRVKRAEKWRDKREKLETKRYVTEAKEAVDALFVDSQYDRLQADTNIGMHAADKLV
930      940      950      960      970      980

cry1a-105.pe    HSIREAYLPELSVPGVNAAFEELEGRIFTAFSLYDARNVINKGDFNGLSCWNVKGHV
940      950      960      970      980      990
CIBE_BACTU      HRIREAYLSELVPGVNAEIFELEGRIITAIISLYDARNVVKNGDFNGLSCWNVKGHV
990      1000     1010     1020     1030     1040

cry1a-105.pe    DVEEQNNQSVLVVPEWEAEVQVRVCPGRGVILRVAYKEGEGECVTIHEIENNTIDE
1000     1010     1020     1030     1040     1050
CIBE_BACTU      DVO-QSHRHSVLVPEWEAEVQAVRCPGRGVILRVAYKEGEGECVTIHEIENNTIDE
1050     1060     1070     1080     1090     1100

cry1a-105.pe    LKFSNCVEEETPNNTVTCNDITVNOEEYGGAYTSRNGYNEAPVPA-----DYASVYEE
1060     1070     1080     1090     1100     1110
CIBE_BACTU      LKFKNCEEEVPTDTGTCDNYTAHQGT--AACNSRNGAYEDAYEDVDTASVNYKPTVEE
1110     1120     1130     1140     1150     1160

cry1a-105.pe    KSYTDGRRENPCFNRGYDYTPLPVGYVTKLEYFETDKVWIEIGETEGTFIGVDSVEL
1120     1130     1140     1150     1160     1170
CIBE_BACTU      ETYTDVRDNHCEYDRGYVNPVPAGYVTKLEYFETDKVWIEIGETEGTFIGVDSVEL
1170     1180     1190     1200     1210     1220

cry1a-105.pe    LMEE
|||||
CIBE_BACTU      LMEE

cry1a-105.pep
TXN5:L32020_1

Description: L32020 Bacillus thuringiensis Bacillus thuringiensis crystal
protein (cryI ETS)
Accession/ID: L32020
=====General comments=====
LOCUS   L32020_1 [BACCRYIE]
DEFINITION Bacillus thuringiensis crystal protein (cryI ETS) gene, complete
.....

SCORES   Initl: 1824   Initn: 3419   Opt: 2667   z-score: 2937.1 E(): 1.1e-157
>>TXN5:L32020_1
initn: 3419   initl: 1824   opt: 2667   z-score: 2937.1   expect(): 1.1e-157
```

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Smith-Waterman score: 4431;   59.5% identity in 1174 aa overlap
(51-1177:72-1229)

cry1a-105.pe    VEVLGGRIETGYTIDISLTQFLSEFVPCAGFVLGLVDIIWIGFSPS---QMDAFL
30      40      50      60      70
L32020_1        AEVNNIDPFVSASTVQTGINTAGRIILGLVGFPAQGLASFYSFLVGLMPSGRDPEWIFL
50      60      70      80      90      100

cry1a-105.pe    VQIEQLINQRIEFAFNQAIISRLGELSNQYVQIYAESFFREWEADPTNPALREEMRIQFNDM
80      90      100     110     120     130
L32020_1        EHVQELIRQVQVTEFNTRTAIRALEGLGRGYSYQQALETWLDNRDARSILIERYVAL
110     120     130     140     150     160

cry1a-105.pe    NSALTITAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDVSFVGQWGFDAATINSRYNDLT
140     150     160     170     180     190
L32020_1        ELDTITTAIPLFIRIRNEEYVPLLMVYQAANLHLLLRDASLFGSEWGMASDVNVQYVQEI
170     180     190     200     210     220

cry1a-105.pe    RLIGNYTHAVRWYNTGLERVWGDSDIRINQFRRELTITLVDIVSLFPNYSRTYPI
200     210     220     230     240     250
L32020_1        RYTEEVSNCVQWYNTGLNLRGTNAESLRVYNQFRRLDTLGLVDLVALFPSTYDTRTYPI
230     240     250     260     270     280

cry1a-105.pe    RTVSQLTREIYNPYLEN-----FDGS--FRGSA--OGIEGSI--RSPHLMIDILNSITY
260     270     280     290     300
L32020_1        NTSNAQLTREIYDIPGRINAPSGEASTWNNFNNAPSFSAIEALFRPPLHLDPPQELITY
290     300     310     320     330     340

cry1a-105.pe    TDARHGEY-----YWSGQIMASPVGSGPEFTFLYPLTGMGNAAPQORIVAQLGQGVYRT
310     320     330     340     350     360
L32020_1        SASSRSSTQHMNYWVGHRLNFRPIGOT--ENTSTQGLTNNTSINPVLQFTSRDVRT
350     360     370     380     390     400

cry1a-105.pe    LSST----LYRPFNIGINNQSLVDGTEFAYGTSSNLPASVYRKSQT--VDSLDEIPP
370     380     390     400     410
L32020_1        ESNAGNLIPTFPVN-GVPMARFNFINPQNI-YERGATTYQPYQGVGQLDFDSETELPP
400     410     420     430     440     450

cry1a-105.pe    QNNNVPPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFESWIHRSARENNILASDSITQIP
420     430     440     450     460     470
L32020_1        ETTERPNYESYSHRLSHLIGLI---IGNT---LRAPVYSWTHRSADRETNTIGENRITQIP
440     450     460     470     480     490     500

cry1a-105.pe    LVKAHTLQSGTTVWRPGFTGGDILARTSGGPFAYTIIVNQGQLPQRYRARIYASTTNL
480     490     500     510     520     530
L32020_1        LVKALMLHSGVTWVGPGFTGGDILARTTGTGDIRLNLNINPLSORVYRARIYASTTDL
510     520     530     540     550     560

cry1a-105.pe    RIVYTVAGERIFAGQFNKMTWDTGDLTFQSFYSYATINTAFTFPMSSQSFVGVADTFSSGN
540     550     560     570     580     590
L32020_1        QFFIRRTVTVNIGNFNRKSNLEYSRFTGFTSPFFNLNAQSTFTFLGAQSFNS-Q
570     580     590     600     610     620

cry1a-105.pe    EVVIDREFELIPVTALAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDOVSNLVTYL
600     610     620     630     640     650
L32020_1        EVVIDREFELIPVTALAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDOVSNLVTYL
610     620     630     640     650     660
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CRY1A-105.pe EVYIDRAVEFVPAEVEATEAYDLERAQKAVNALFTSTNPRRLKTDVTDYHIDQVNMVACL
L32020_1 630 640 650 660 670 680 690
CRY1A-105.pe SDECLDEVEVEVYKAKGKDEKLNLOD-----SNFKDINROPE
L32020_1 660 670 680 690 700 710 720 730 740 750
CRY1A-105.pe RGMGSGTITIOGQDNVFNENVTLSDEDEYPTVYDOKDESKLAFRYQLRGYIED
L32020_1 700 710 720 730 740 750 760 770 780 790 800
CRY1A-105.pe SODLEIYSIRYNAKHETVNVFGTSLWPLSQSKCKGCEPTCAPHLEWNPDLNDCSD
L32020_1 760 770 780 790 800 810 820 830 840 850 860
CRY1A-105.pe GEKCAHSHHFSJIDVGCITDLNEDLGWVIFKIKTQDGHARLNEPDEKPLNCEAT
L32020_1 820 830 840 850 860 870 880 890 900 910 920
CRY1A-105.pe RYKRAEKKWRDKRELEWETINIVYKEAKESVDALFVNSQYDQLOQADTNIAHAAKRVH
L32020_1 880 890 900 910 920 930 940 950 960 970 980
CRY1A-105.pe SIREAYLPESVIPGVNNAIFEELEGRIPTAFSLYDARNVKNQDNNGLSCWNVKGVHD
L32020_1 940 950 960 970 980 990 1000 1010 1020 1030 1040
CRY1A-105.pe VEEQNNORSVLVPEWEAEVSEVRCVGRGYILRVYAYKEGEGCVTIHEIENNTDEL
L32020_1 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100
CRY1A-105.pe KFSNCEVEEIPNNVTICNDYTNQOEYGGAYTSRNGYNEAPSPA---DYASVTEEK
L32020_1 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160
CRY1A-105.pe SYTDGERNPCEFRNGYEDYTPLPVGYVTKELEFPETDKVWIEIGETGTFIVDSVELL
L32020_1 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220
CRY1A-105.pe LMEE
L32020_1 LMEE
CRY1A-105.pe
TXNS:CIBB_BACTU

Description: Q45739 bacillus thuringiensis. pesticidal crystal protein cryIbb
(insecticidal)
Accession/ID: Q45739
ID CIBB_BACTU
AC Q45739;
General comments: PRT; 1229 AA.
STANDARD:
SMITH-WATERMAN SCORE: 4431; 59.5% identity in 1174 aa overlap
(51-1177:72-1229)
CRY1A-105.pe VEVLGGERIEGTVPIDISLSLTQFLSEFVPGAGFVLGLDIWIGIFGPS---QWDAFL
CIBB_BACTU 30 40 50 60 70 80 90 100
CRY1A-105.pe VOIEQLINQRIEFARNOAISLEGLNLYOIAESFREWEADPTNPALREEMRIQFNDM
CIBB_BACTU 80 90 100 110 120 130 140 150 160
CRY1A-105.pe NSALTTAIPFAVONYQVPLLSVYVORANLHLSVLRDVSFVGORWGFDAATINSRYNDLT
CIBB_BACTU 140 150 160 170 180 190 200 210 220
CRY1A-105.pe RLIGNYTDHARNNTGLERWVGSDRDMRYNQFRRELTTLVLDIVLSLFENYDSRTYPI
CIBB_BACTU 200 210 220 230 240 250 260 270 280
CRY1A-105.pe RTVSLTTSITVTVN-----FDGS--FRGSA---OGIEGSI-RSPHLMIDILNSITII
CIBB_BACTU 260 270 280 290 300 310 320 330 340
CRY1A-105.pe TDARHGEY-----VWSGCHQMASSVGFSGEPTPLLYGTNMAZACQORIVAQLGQGVYRT
CIBB_BACTU 310 320 330 340 350 360 370 380 390 400
CRY1A-105.pe LGST----LYRRPPIGNNQQLSLDGTETAYGTSNPSAVYRSGT-VDSLSTIPS
CIBB_BACTU 370 380 390 400 410 420 430 440 450 460 470 480 490 500
CRY1A-105.pe QNNVPPVPGFSGHLSHVSFNRSGFNSVSLIAPMFSMIHSAFNNIASCETQI
CIBB_BACTU 420 430 440 450 460 470 480 490 500 510 520 530 540 550
CRY1A-105.pe LVKAHTLOSCTTVRGPGTGGDILARTSGGPFATVINGOLPORVARIYASTTNL
CIBB_BACTU 480 490 500 510 520 530 540 550

CIBB_BACTU LVKALNLSGVTWVGPGTGGDILRLRTNTGTGDIRLNNINVLSQLRYRVRIRYASTTDL
510 520 530 540 550 560
cry1a-105.pe RIYVYAGERIFAGQFNKMTDGLTFQSFYATINTAFTFPMQSFVTVGADTFSSON
540 550 560 570 580 590
CIBB_BACTU OFFTRINGTIVNIGFNTMRGNLEYSFRTAGFTFPMFLNAQSTFTLGAQSFN-Q
570 580 590 600 610 620
cry1a-105.pe EVIDRFEIPVATLEAEYNLERAQAVNALFTSTNOLGLKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
CIBB_BACTU EVIDRVEFVPAEVTFEAEYDLERAQAVNALFTSTNPRRLKTDYDHYDQVSNVACL
630 640 650 660 670 680
cry1a-105.pe SDFCLDEKREUSEKVXKAKLSLDERNLQD-----SNFKDINRQPE
660 670 680
CIBB_BACTU SDFCLDEKREIFVKYAKLSLDERNLQDPNFTFISQLSFASIDGQNFPSINELSE
690 700 710 720 730 740
cry1a-105.pe RGMGSGTITIGCGDDVFKENYVTLSTGTFDECYPTVLYOKIDESKLAFTRYOLRGYIED
700 710 720 730 740 750
CIBB_BACTU HGWGSANVTIQEGNDVFKENYVTLPTGTFNECYPNLYOKIGESLKAFTRYOLRGYIED
750 760 770 780 790 800
cry1a-105.pe SQDLEIYSIRYNAKHETVNFCTGSLWPLSAQSPIGKCGEPCNRCAPHLEWNPDLDCSRD
760 770 780 790 800 810
CIBB_BACTU SQDLEIYIRYNAKHETLDVPGTDSLWPLSVESPIGRCGEPCNRCAPHLEWNPDLDCSRD
810 820 830 840 850 860
cry1a-105.pe GEKCAHSHHFDLIDVCGTDLNEDLGWVFKIKTQDCHARGLNLFEELKEPLUGEALA
820 830 840 850 860 870
CIBB_BACTU GERCAHSHHFDLIDVCGTDLNEDLGWVWVFKIKTQDCHARGLNLFEELKEPLIGEALS
870 880 890 900 910 920
cry1a-105.pe RVKRAEKKWRDKREKLEWETNIVYVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVH
880 890 900 910 920 930
CIBB_BACTU RVKRAEKKWRDKREKLEWETNIVYVYKEAKESVDALFVNSQYDQLQADTNIAHIAADKRVH
930 940 950 960 970 980
cry1a-105.pe SIREAYLPELSVIPGNNAIFEELEGRIFTAFSLYDARNVTKNGDFNNGSCNVKNGHVD
940 950 960 970 980 990
CIBB_BACTU RIREAYLSELVIPGNNAIFEELEGHIIITAMSLYDARNVTKNGDFNNGSCNVKNGHVD
990 1000 1010 1020 1030 1040
cry1a-105.pe VEQNNORSLVLPWEAEVSOEVRVCPGRGYLAVTAYKEGEGCVTHIELENNTEL
1000 1010 1020 1030 1040 1050
CIBB_BACTU VQ-QSHRSDLVLPWEAEVSOEVRVCPGRGYLAVTAYKEGEGCVTHIELENNTEL
1050 1060 1070 1080 1090 1100
cry1a-105.pe KFSNCEEEELVNTVTCNDYVNOEYGGAYTSNRNGNEAPSPA---DYASVREK
1060 1070 1080 1090 1100 1110
CIBB_BACTU KFSNCEEEELVNTVTCNDYVNOEYGGAYTSNRNGNEAPSPA---DYASVREK
1110 1120 1130 1140 1150 1160
cry1a-105.pe SYTDGRENPCFNRGDRYDTPLEVGVTKELEYFETDKVMIEIGETGTFIVDSVELL
1120 1130 1140 1150 1160 1170

CIBB_BACTU TYTDRNRDNCHEYRGYVNPVPAGVTVTKLEYFETDVTVMIEIGETGTFIVDSVELL
1170 1180 1190 1200 1210 1220
cry1a-105.pe LMEE
CIBB_BACTU LMEE
cry1a-105.pep
TXN5:X06711_1
Description: X06711 Bacillus thuringiensis B. thuringiensis cryA4 gene for
delta-endotoxin; d
Accession/ID: X06711
=====General comments=====

LOCUS X06711.1 [BTCRYA4]
DEFINITION B. thuringiensis cryA4 gene for delta-endotoxin; . . .
SCORES Initl: 1835 Initn: 3007 Opt: 2661 Z-score: 2930.4 E(): 2.5e-157
>TXN5:X06711_1
Initn: 3007 Initl: 1835 Opt: 2661 Z-score: 2930.4 expect(): 2.5e-157
Smith-Waterman score: 4340; 59.0% identity in 1177 aa overlap
(51-1177:67-1228)

cry1a-105.pe VEVLGGERIETGYTPIDISLSLTQFLSEFVPCAG---FVLGLVDIIMGIFGPSOWDAF
30 40 50 60 70
X06711_1 AEGNNIDPFVSASTVQTGTINAGILGLGVFPAGQLASFSYFLVGLWLP-RGRDQWEIF
40 50 60 70 80 90
cry1a-105.pe LVQLEQLINQRIEEFARNQAIISRLGLSNIYQIYAESFREWADPTNPALREEMRIQFND
80 90 100 110 120 130
X06711_1 LEHQLEQLINQRIEEFARNQAIISRLGLSNIYQIYAESFREWADPTNPALREEMRIQFND
100 110 120 130 140 150
cry1a-105.pe MNSALTTPLEFAVONQVPLISVYVQANLHLSVLSDVSVFGQWGFDAATINSYNDL
140 150 160 170 180 190
X06711_1 LEIDFLNAPLEFAVONQVPLISVYVQANLHLSVLSDVSVFGQWGFDAATINSYNDL
160 170 180 190 200 210
cry1a-105.pe TRILGNVTHAVRWNTGLERVMGPDSDRWIRYNQFRELTLTVLSDIVSLFNPYDSRTYP
200 210 220 230 240 250
X06711_1 VERTRDYSYCVQEWNTGLSLRGNTNAASVWRINQFREDLTLGVLDLVALFSPSYDRTYP
220 230 240 250 260 270
cry1a-105.pe IRTVSQLTRITNTINPVLE-----NFDGSRGSAQIGES-IRSPHLMILNLSITYT
260 270 280 290 300
X06711_1 INTSAQLTRITNTINPVLE-----NFDGSRGSAQIGES-IRSPHLMILNLSITYT
280 290 300 310 320 330
cry1a-105.pe DAHRE-----YVWGHQIMASPVGSGPEFTFPLVGTGMGNAAPQQRIVLAQLGQGVRTL
310 320 330 340 350 360
X06711_1 ASSWNSRTHMYTWGHIIQSRPIG--GGLNTSTGATNTSINPVTLPFPAS--RDVYRTE
340 350 360 370 380 390
cry1a-105.pe SST-----LYRRPNIGINNQQLSVLDGTFEAYGTSSNLPASVYRKSGT--VDSLEIIP
370 380 390 400 410

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AAK51084 LELEDFNAMPDRATINQVEVPLLMVYAQAANLHLLLRDASLFGSEFGLTQEIQRYYERQ
160 170 180 190 200 210
cry1a-105.pe TRACNTYTHAATNTGLERWGPQSDWIRYNQFRRELTITVLIDVSLFPVNDRTYTP
200 210 220 230 240 250
AAK51084 VERNDTSYCVEMVTEJNLGRGNAISNRINQPRDLILGLVDLVALFPYDRTYTP
220 230 240 250 260 270
cry1a-105.pe IRTVSQLTREIYTNWLE-----RSGSTRGSGGIES-IRSPHLMIDILNSITIVT
260 270 280 290 300
AAK51084 INTSAQLTREYVDAIGATGNNMAMNWNANAPSTSAIEAAATPSPHLLDFLEQLTIFS
280 290 300 310 320 330
cry1a-105.pe YWSGHQIMASPVGSGPEFTPLVGTGMAATQORIVAQSGQVRLT
310 320 330 340 350 360
AAK51084 ASSRWSNTRHMYRGTHTIOSRPIG--GGLNTSTRGNTNISINPVTLPFAS--RDVWTE
340 350 360 370 380 390
cry1a-105.pe SST-----LYRPFENIGINQOLSVLDTGEFAVGTSSNLPQAVTAKST--VDSDEP
370 380 390 400 410
AAK51084 SYAGVLLWGIYLEPIH-GVPTVRFNFTNPQNISDRGTANY-SOPYESPGQLKXSETELD
400 410 420 430 440
cry1a-105.pe PONNVPPROQFQSHRLSHVSMFRSGFNSSYSIIRAPMFSWIRHAEFNIIADSITQI
420 430 440 450 460 470
AAK51084 PETTERPNYESYSHLSHGIIQL-----SRVNV---PVYSWIRHAEFNIIADSITQI
450 460 470 480 490 500
cry1a-105.pe PLVKAHTLOSITVVRGPGFTGDIILRTSGPPAYTININGQLPQVRIARIVASTTN
480 490 500 510 520 530
AAK51084 PMVKASELPQGITVVRGPGFTGDIILRTSGPPAYTININGQLPQVRIARIVASTTN
510 520 530 540 550 560
cry1a-105.pe LRIYTVAGERIFAGQFNKMTDGPPLTFQSFVATINTAFTPMQSQSFVTGADTFSSG
540 550 560 570 580 590
AAK51084 FDFVSRGTTVNNFRFLRTMSGDELKYGNFVRAFTTFTTQDIIRTSIQLSGN
570 580 590 600 610 620
cry1a-105.pe NEYIDRFELIPVTATLEAEYNLERAQKAVNALFTSNQGLKNTVTDVHIDQVSNLVTY
600 610 620 630 640 650
AAK51084 GEVYIDKIEIIPVTATFEAEYDLERAQKAVNALFTSNPRRLKTDVTDVHIDQVSNLVAC
630 640 650 660 670 680
cry1a-105.pe LSEDFCLDEKELSEKVKHAKRLSDERNLLQDSNFKDINQRP-----
660 670 680 690 700 710
AAK51084 LSEDFCLDEKELSEKVKHAKRLSDERNLLQDSNFKDINQRP-----
690 700 710 720 730 740
cry1a-105.pe ERGMGSGTGTITQGGDDVFNKENVTLSTGTFDECYTYLYQKIDESLKAFTYQLRGYIE
700 710 720 730 740 750
AAK51084 EHWGWSENITIQEGNDVFNKENVTLSTGTFDECYTYLYQKIDESLKAFTYQLRGYIE
750 760 770 780 790 800
cry1a-105.pe DSQDLSEIYSIRYNAKHETVNPVGTGLMPLSAQSPDGKCGEPNRCAPHLEWFPDLDSCSR
760 770 780 790 800 810

AAK51084 DSQDLSEIYSIRYNAKHETVNPVGTGLMPLSAQSPDGKCGEPNRCAPHLEWFPDLDSCSR
810 820 830 840 850 860
cry1a-105.pe DGEKCAHSHHFLDIDVCGTDLMEDLGVWVFKIKITQDGHARLGNLEFLEKPLVGEAL
820 830 840 850 860 870
AAK51084 DGEKCAHSHHFLDIDVCGTDLMEDLGVWVFKIKITQDGHARLGNLEFLEKPLVGEAL
870 880 890 900 910 920
cry1a-105.pe ARVKRAEKKWRDKREKLEWETINIVYKAESVDALFVNSOYDQADNTIAMIHAAKRV
880 890 900 910 920 930
AAK51084 SEVKRAEKKWRDKREKLEWETINIVYKAESVDALFVNSOYDQADNTIAMIHAAKRV
930 940 950 960 970 980
cry1a-105.pe HSIREAVLPELSVIPGVNAAFEELEGRIFTAFSLYDARNVKNKGFNNGLSWNVKGVH
940 950 960 970 980 990
AAK51084 HRIREAVLSELPIVPGVNAAFEELEGRIFTAFSLYDARNVKNKGFNNGLSWNVKGVH
990 1000 1010 1020 1030 1040
cry1a-105.pe DVEEQNNQSRVLPVPEWEAEVSEQVVRVCPGGYILLRVATYKEGEGCVTIHEIENNTDE
1000 1010 1020 1030 1040 1050
AAK51084 DVO-QSHRSRLVLPWEAEVSEQVVRVCPGGYILLRVATYKEGEGCVTIHEIENNTDE
1050 1060 1070 1080 1090 1100
cry1a-105.pe LKPSNCEVEEIIYFNNTVTCNDVTNOEYG--GAYTSRNGVNEAPSVPA---DVASVY
1060 1070 1080 1090 1100 1110
AAK51084 LKPSNCEVEEIIYFNNTVTCNDVTNOEYG--GAYTSRNGVNEAPSVPA---DVASVY
1110 1120 1130 1140 1150 1160
cry1a-105.pe EEKSYTDGRRNNTPEFRNGVRDYVTPLPVGYVTKLEYFPETDKVMEIGETEGTIFVDSV
1120 1130 1140 1150 1160 1170
AAK51084 EEKSYTDGRRNNTPEFRNGVRDYVTPLPVGYVTKLEYFPETDKVMEIGETEGTIFVDSV
1170 1180 1190 1200 1210 1220
cry1a-105.pe ELLMEE
1180 1190 1200 1210 1220
AAK51084 ELLMEE
1220 1230 1240 1250 1260 1270
cry1a-105.pe ELLMEE
1270 1280 1290 1300 1310 1320
AAK51084 ELLMEE
1320 1330 1340 1350 1360 1370
cry1a-105.pe TXN5:CIBA_BACTK
1370 1380 1390 1400 1410 1420
Description: P05517 bacillus thuringiensis (subsp. kurstaki) and bacillus
thuringiensis (sub
Accession/ID: P05517
ID CIBA_BACTK STANDARD; PRT: 1228 AA.
AC P05517; Q45731; .
=====General comments=====

SCORES Initl: 1835 Inith: 3007 Opt: 2661 z-score: 2930.4
>>TXN5:CIBA_BACTK
Initl: 3007 Inith: 1835 Opt: 2661 z-score: 2930.4 expect(): 2.5e-157
Smith-Waterman score: 4340; 59.0% identity in 1177 aa overlap
(51-1177:67-1228)

cry1a-105.pe VEVLGSERIETGCTPIDISLSLTQFLLSFVPGAG---FVLGLVDIIVGIFGSPQDFAF
30 40 50 60 70

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CIBA_BACTK AEGNNIDPFVSASTVQTGINIAGRILGVLPFAGQLASFSYFLVGLWP-RGRDQWEIF
40 50 60 70 80 90
cry1a-105.pe LVQEQILNORIEEFARNQAISRLEGSLNLYQIYASFFREAFDTNPALREEMRIQFND
80 90 100 110 120 130
CIBA_BACTK LEHVEQLNQINQINENARNTALARQLGDSFRAYQOSLEDNLENRDDARTRSVLYTQYIA
100 110 120 130 140 150
cry1a-105.pe MNSALTATPLFAVQNYQVPLLSVVQAAHLHLVLRDVSFVGORWGFDAATINSRYNDL
140 150 160 170 180 190
CIBA_BACTK LELDFLNAELFAIRNQEVPLLMVYQAANHLHLLRDASLFGSEFGLTSQELQRYIERQ
160 170 180 190 200 210
cry1a-105.pe TELIGNYTHAVENYNTGLERWGPDSRDWIRYNQFRRELTITLVLDIVSLFPNYDSRTYP
200 210 220 230 240 250
CIBA_BACTK VERTROYSDYCVENYNTGLNSLGRGTNAASWVRYNQFRDLTIGVLDLVALFPYDYRTYP
220 230 240 250 260 270
cry1a-105.pe IRTYSOLTRIEYNPVLE-----NFDGFRGSAQIEGS-IRSHPLMDILNSITVT
260 270 280 290 300
CIBA_BACTK INTSAQITREVIYDAIGATGVNMAWMYNNAPSFSAIEAARSHRSHLLDFLEQITFS
280 290 300 310 320 330
cry1a-105.pe DAHGE-----YWSGHQIMASPVGFGPEFTPLPYGTMGNAPOQRIVAQLQGQYRTL
310 320 330 340 350 360
CIBA_BACTK ASSWSNTRHMTWGRHTIQSRFIG--GGLNSTHCAWTNSINPVLRFAS--RDVYRE
340 350 360 370 380 390
cry1a-105.pe SST-----LYRPFNIGINNQQLSVLDGTEFAYGTSSNLPASVYRSGT--VDSLEDETP
370 380 390 400 410
CIBA_BACTK SYAGVLWGIYLEPIH-GVPTVRFNFTNPQINSDRGATNY-SQPYSPGLQKLDSETELP
400 410 420 430 440
cry1a-105.pe PONNVPPRGFSHRLSHVMSFRSGFSNVSIIIRAPMSWTHRSFAFNIIASDSITOI
420 430 440 450 460 470
CIBA_BACTK PETERPWYESYSHRLSHIGIILQ-----SRVNV---PVYSWTHRSADRTNIGFNRIOT
450 460 470 480 490 500
cry1a-105.pe PLVKAHTLOSITTVRGFGFTGGDILRRTSGGPFAYTIVNIGQLPKRYRARIRVASTTN
480 490 500 510 520 530
CIBA_BACTK PMVKASELPQGITTVRGFGFTGGDILRRTNTGFGFIRVTVNGPLTORIYRIGFRVASTVD
510 520 530 540 550 560
cry1a-105.pe LRIYTVAGERIPACQFNKMTDGLTTFQSPSIATINTATTFPMSSSTTVGADTFSSG
540 550 560 570 580 590
CIBA_BACTK FDFVSRGGTGVNFRFLRTMNSGDELKYGNFVRRAFTPTFTQIQDIIRTSIQGLSGN
570 580 590 600 610 620
cry1a-105.pe NEVYIDRFELIPVATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDVSNLVTY
600 610 620 630 640 650
CIBA_BACTK GEVYIDKIEIIPVATLEAEYDLERAQAVNALFTNTNPRKIDVTDYHIDVSNLVC
630 640 650 660 670 680
cry1a-105.pe LSDDFCLJDEKRELSEKVKHAKRLSDERNLLQDSNFKDINROP-----
660 670 680 690
|||||

CIBA_BACTK LSDFECLJDEKRELSEKVKYAKELSDERNLLQDNFTSINKQPDFISTNEQSNFTSIHEQS
690 700 710 720 730 740
cry1a-105.pe ERMGSGTGITIGGDDVFKENYVTLSTGTFDECYPTLYLKIDESKLKAFTRYQLRGYIE
700 710 720 730 740 750
CIBA_BACTK EHGWMGSENIITQEGNDVFKENYVTLPGTNECYPTLYLKIDESKLKAFTRYQLRGYIE
750 760 770 780 790 800
cry1a-105.pe DSQLEIYTRYNAKHETVNVPGTGSWPLFSAOSPIKCGEPNRCAPHLEWNPDLDCSR
760 770 780 790 800 810
CIBA_BACTK DSQLEIYTRYNAKHETVNVPGTGSWPLFSAOSPIKCGEPNRCAPHLEWNPDLDCSR
810 820 830 840 850 860
cry1a-105.pe DGEKCAHSHHFLSDIDVCGTDLNEGLVWVFIKIQDGHARLGNLEFLEEKPLVGEAL
820 830 840 850 860 870
CIBA_BACTK DGEKCAHSHHFLSDIDVCGTDLNEGLVWVFIKIQDGHARLGNLEFLEEKPLVGEAL
870 880 890 900 910 920
cry1a-105.pe ARVKRAEKWRDKREKLEWETNIVYKAESVDALFVNSQYDQLQADNTNAMIHAADKRV
880 890 900 910 920 930
CIBA_BACTK SRVKRAEKWRDKREKLEWETNIVYKAESVDALFVNSQYDQLQADNTNAMIHAADKRV
930 940 950 960 970 980
cry1a-105.pe HSIREAVLPESLVIPGVNAAIFEELEGRIETAESLYDARNVKKNGDNGLSCWVUKGHV
940 950 960 970 980 990
CIBA_BACTK HRIREAVLPESLVIPGVNAAIFEELEGRIETAESLYDARNVKKNGDNGLSCWVUKGHV
990 1000 1010 1020 1030 1040
cry1a-105.pe DVEEQNNQSVLVPEWAEVSQEVVPCGRGYILRVATYKEGYEGECVTIHEINNTDE
1000 1010 1020 1030 1040 1050
CIBA_BACTK DVQ-QSHRSDLVIPEWAEVSQEVVPCGRGYILRVATYKEGYEGECVTIHEINNTDE
1050 1060 1070 1080 1090 1100
cry1a-105.pe LKFSNCVVEEIIYFNNTVTCNDYTNQEEYG--GAYTSRNRGYNAPSVA----DYASVY
1060 1070 1080 1090 1100 1110
CIBA_BACTK LKFSNCVVEEIIYFNNTVTCNDYTNQEEYG--GAYTSRNRGYNAPSVA----DYASVY
1110 1120 1130 1140 1150 1160
cry1a-105.pe EEEKYTDGRENPCFENRGYRDYPLVGVVTKLEYFPEDDKWVIEIGETGTFIDSV
1120 1130 1140 1150 1160 1170
CIBA_BACTK EEEKYTDGRENPCFENRGYRDYPLVGVVTKLEYFPEDDKWVIEIGETGTFIDSV
1170 1180 1190 1200 1210 1220
cry1a-105.pe ELLMEE
cry1a-105.pe ELLMEE
cry1a-105.pe ELLMEE
cry1a-105.pe ELLMEE
TXN5:CIBD_BACTZ
Description: Q9Za25 bacillus thuringiensis (subsp. wuhanensis). pesticidal
crystal protein c
Accession/ID: Q9Za25
====General comments=====
ID CIBD_BACTZ STANDARD; PRT; 1231 AA.

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C1BC_BACTM  YVNYPPVAGVYTKLEYFPETDVTWIEIGETGKFIYDVSVELLMEE 1190 1200 1210 1220 1230
cryla-105.pep
TXNS:C1BC_BACTM

Description: Q45774 bacillus thuringiensis (subsp. morrisoni). pesticidal
crystal protein cr
Accession/ID: Q45774
=====General Comments=====
ID C1BC_BACTM STANDARD; PRT; 1233 AA.
AC Q45774; .

SCORES Initl: 1760 Initn: 3383 Opt: 2550 z-score: 2807.9 E(): 1.7e-150
>TXNS:C1BC_BACTM
Initn: 3383 initl: 1760 opt: 2550 z-score: 2807.9 expect(): 1.7e-150
Smith-Waterman score: 4314; 58.7% identity in 1176 aa overlap
(51-1177:72-1233)

cryla-105.pe 30 40 50 60 70
VEVLGGERIEGTPTDLSLTQFLSEFVPGAGFVLGVDLIINGIFGPS---QWDAPFL
C1BC_BACTM AEVNIDFVSASTVQTGINAGRIILGVLPFAGQASFYSLFVGEIWPGRDPWFEL
50 60 70 80 90 100
110 120 130 140 150 160
cryla-105.pe 80 90 100 110 120 130
VQIEQLINQRIEFARNQAIISLEGLSNLYQIYAESFRFEWAEDPTNPALREEMRIQFNDM
C1BC_BACTM EHVEQLIRQVQNTENTAIARLEGLGEGYASVQDALETWLDNRDARSIIILERYVAL
110 120 130 140 150 160
140 150 160 170 180 190
cryla-105.pe NSALTAIPFAYQNVQVPLLSVYQAAANLHLSVDSVFGQRFDAATINSRYNDLT
C1BC_BACTM ELDIITAIPIFRIRNEEVPLLVYQAAANLHLLLDASLFGSENGMASSDVNQYQEQI
170 180 190 200 210 220
200 210 220 230 240 250
cryla-105.pe RLIGNYTDHVRVYNTGLERVMGPDSDRMVYNGFRRELTLTLDIVISLFNVDSTRTPI
C1BC_BACTM RYTEYSNHCVOQWYNTGLNLRGTWASNLRYNQFRDRUTLGLVDLVALFPYSDTRTYPI
230 240 250 260 270 280
260 270 280 290 300 310
cryla-105.pe RTVSQLTREIYTPVLEN-----FDGS--FRGSA--QIGESI-RSPLHMDIINSITII
C1BC_BACTM NTSAGLTREIYTPDIGRTNAPSGFASFTWFFNNAPSFSALEAAIFRPPLDLPPEOLTY
290 300 310 320 330 340
310 320 330 340 350 360
cryla-105.pe IDAHR-----GEYNSGHQIMASPVGSGFEFTFLYGTNGNAAQQRIVAQLGQGYRT
C1BC_BACTM SASGRWSSTQHMNYVGHRLNRPFGGT--LNTSTQGLTNNTSINPVTLOFTSRDYRT
350 360 370 380 390
370 380 390 400 410
cryla-105.pe LSST-----LYRRPFGNIGNNQSLVDGTETPAYGTSNLPFSAYRKSG--TVDSLEIHP
C1BC_BACTM ESNAGTILFTIPVNV-GVPWAFNFIPQNI-VERGATTSYQPYGVGIGIQLFSETELPP
400 410 420 430 440 450
420 430 440 450 460 470
cryla-105.pe QNNYVPRQGFHRLSHVGMFRSGFSNSVSIIRAPMFWIHRSAEFNNIADSDITQIP
460 470
```

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C1BC_BACTM  ETTERPNVYESHRLSHIGLI---IGNT-----LRAPVYSWTHRSADRTNTIGPNRIQTQIP 460 470 480 490 500
cryla-105.pe 480 490 500 510 520 530
LVKAHTLOSQTIVVRGPGTGGDILRRTSGGPFAYFTVINGQLPQRYRARIRYASTNNL
C1BC_BACTM LVKALNLSHSGVTGVGGDILRRTNTGTCTGDIRLAINIVPLSRQYRVRIRYASTTDL
510 520 530 540 550 560
540 550 560 570 580 590
cryla-105.pe RIYVTVAGERIFAGQFNKMDYGDPLTFQSPFSYATINTAFTPMQSSFTVGAOTFSSGN
C1BC_BACTM QFTTRINGTIVNIGNFRTNMNRGDNLEYSRPTAGSFPTFNFLNAQSTFTILGAQSPFN-Q
570 580 590 600 610 620
600 610 620 630 640 650
cryla-105.pe EYVIDRFELIPVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTDYHIDOVSNLVTYL
C1BC_BACTM EYVIDRFVPAEVTPEAEYDLERAQKAVNALFTSTNPRELKTVDYHIDOVSNMVACI
630 640 650 660 670 680
660 670 680 690 700 710
cryla-105.pe SDEFCLEKRELSEKVKHAKRLSDERNLLQD-----SNFKDINRQPE
C1BC_BACTM SDEFCLEKRELFEKVKYAKRLSDERNLLQDPNFTFISQGLSPASIDQGSNFPFSINELSE
690 700 710 720 730 740
700 710 720 730 740 750
cryla-105.pe RCMWGSTGINTIOGGDDVFENYVTLSTGTEDECYTYLYOKIDESKKAFTYQYLRGYIED
C1BC_BACTM HGMWGANVITIQGNDVFNENYVTLSTGTEDECYTYLYOKIDESKKAFTYQYLRGYIEN
750 760 770 780 790 800
760 770 780 790 800 810
cryla-105.pe SODLEIYSIRYNAKHETVNPVGTSLWPLSAQSPGKCGEPCNRCAPHLEWNPDLDCSCR
C1BC_BACTM SODLEIYLIRYNAKHEAINVPGTESISAEISTGKTEPCNRCAPHYENWNPDLDCSCR
810 820 830 840 850 860
820 830 840 850 860 870
cryla-105.pe GEKCAHSHHPSLIDIVGCTDLDNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALA
C1BC_BACTM GEKCAHSHHSTLIDIVGCTDLDNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALR
870 880 890 900 910 920
880 890 900 910 920 930
cryla-105.pe RVKRAEKKWRDKREKLEMTNIVYKAEKESVDALFVNSOYDQLOADTNIAHAAKRVH
C1BC_BACTM RVKRTKRWDRDKREKLEMTNIVYKAEKESVDALFVNSOYDQLOADTNIAHAAKRVH
930 940 950 960 970 980
940 950 960 970 980 990
cryla-105.pe SIREAYLPELSVIPGVNAAFIEFELEGRIPTAFSLYDARNVINKGDFNNGLSCMNVKGVHD
C1BC_BACTM SIREAYLSELPVIRGVNADIFEELEGHILTAFLSYDARNVINKGDFNNGLTCMNVKGVHD
990 1000 1010 1020 1030 1040
1000 1010 1020 1030 1040 1050
cryla-105.pe VEEQNQRSVLVVPWEAEVSVGVCPGRGILRVYTAKEGYGEGCVTHIEINNTDEL
C1BC_BACTM VQ-QSHRRFLDVLVVPWEAEVSVGVCPGRGILRVYTAKEGYGEGCVTHIEINNTDEL
1050 1060 1070 1080 1090 1100
1060 1070 1080 1090 1100 1110
cryla-105.pe KFSNCVVEEYTPNNTVTCNDYVWQ--EEYGGAYTSRNRGYNAPSVFA---DYASVYE
1100 1110
```

CIBC_BACTM NFKNRVEEIIYPTCTCKKYTENQGTTCNCGSNNEGYDWAYEINKSLESRYTYE
1110 11120 11130 11140 11150 11160

cryla-105.pe EKSTGDRKSNPEKNGYRDNPPLNGVYKKELEYEPEDKWKWIEIGTEGTFIVDSVE
1120 1130 1140 1150 1160 1170
CIBC_BACTM EETVYRSEHCEYEGYINVSVPKSNVYKKELEYEPEDTWTWIEIGTEGTFIVDSVE
1170 1180 1190 1200 1210 1220

cryla-105.pe LLLMEE
|||||
CIBC_BACTM LLLMEE
1230

cryla-105.pep
TXNS:Z46442_1

Description: Z46442 Bacillus thuringiensis B.thuringiensis cryIb gene for
delta-endotoxin. 1
Accession/ID: Z46442
LOCUS Z46442.1 [BTHCRYIBC]
DEFINITION B.thuringiensis cryIbC gene for delta-endotoxin.

SCORES Initl: 1760 Initn: 3383 Opt: 2550 z-score: 2807.9 E(1): 1.7e-150
>>TXNS:Z46442_1
initn: 3383 initl: 1760 opt: 2550 z-score: 2807.9 expect(1): 1.7e-150
Smith-Waterman score: 4314; 58.7% identity in 1176 aa overlap
(51-1177:72-1233)

cryla-105.pe VEVLGGERIETGVTIDISLSLTQFLSEFVPGAGVLGLVDIIIGFGPS---QWDAPL
30 40 50 60 70
Z46442_1 AEVNNIDPFVSASTVQTGINTAGILGVLPFPGQALSFYSFLVGLWFSRGRDWEIFL
50 60 70 80 90 100

cryla-105.pe VQIEQLINQRIEFARNQAIKSLRLEGLSNLYQIYAESFREWADPTNPALREEMRIQFNDM
80 90 100 110 120 130
Z46442_1 EHVQLIRQOQVIENTNTAIAKLEGLGRYSYQQALETWLDNRDARSIIILERYAL
110 120 130 140 150 160

cryla-105.pe NSALTATPAPVQNVQPLISVVOAANHLVLSVRDVSFGQMGFADATINSRYNDLT
140 150 160 170 180 190
Z46442_1 ELDTTAPLPIFRIRNEEVPLMVAQAANHLLELLDASLFGSENGWASSDVNQYQEQI
170 180 190 200 210 220

cryla-105.pe RLIGNYTHAVRYNTGLERVWGDPDSRWIRYNOFRRELTITVLVDIVSLFPNDYSRTYPI
200 210 220 230 240 250
Z46442_1 RYTEEYSHCVQVYNTGLNLRGTNAESWLRYNQFRDITLGLVDLVALFPYDTRTYPI
230 240 250 260 270 280

cryla-105.pe RTVSQLTREIYTPVLEN-----FDGS--FRGSA---QIGESI--RSPHLMIDILNSITY
260 270 280 290 300 310
Z46442_1 NTSAGLTREIYTPDPIGRTNAPSGFASTWFWNNAPFSFAIEAAIFRPPLDLPQOLTYI
290 300 310 320 330 340

cryla-105.pe TDARR-----GEYVWSGHQIMASPVGSGPEFTFLYGTMGNAAPQQRVAQLGQGVRT
310 320 330 340 350 360

Z46442_1 SASSRWSSTOHMYWVGHRLNFRPIGTT---LNTSTOGLTNTNTSINPVTLOFTSRDVRT
350 360 370 380 390

cryla-105.pe LSTST---LYRRPNIGINNQQUSVLDGTEFAYGTSNLSNLSAVYRMSG---TVDSILDEIPP
370 380 390 400 410
Z46442_1 ESNAGTNILFTTPYN-GVPWARENFINPQNI-YERGATTYSQPYQGVGLQJDFDSEITLPP
400 410 420 430 440 450

cryla-105.pe ONNVPPRGSHSLSHSVMSFRSFSNVSIIIRAPMFSWIRHSAAEFNNIIASDSITQIP
420 430 440 450 460 470
Z46442_1 ETTERPNYESVSHRSLHIGLI---IGNT---LRAPVYSWTHESADRTNTIGPNRITQIP
460 470 480 490 500

cryla-105.pe LVKAHTLQSGTIVVRGFGFTGGDILRRTSGGPFAYTIIVNGQLPORVYRARIYASTTNL
480 490 500 510 520 530
Z46442_1 LVKALNLHSGVTWVGPGFTGGDILRRTNTGTGDIRLININVLPSQVRYRIRYASTITDL
510 520 530 540 550 560

cryla-105.pe RIYTVAGERIPAGQFNKTMDTGDLPTFOSFSYATINTAFTFPMSSOSTFVGADTFSSGN
540 550 560 570 580 590
Z46442_1 OFFTRINGTIVNIGNFSRTMRGNDNLEYRSFRTAGFTTPFNLNAQSTFTILGAQFSN-Q
570 580 590 600 610 620

cryla-105.pe EVYIDRFELIPVTALEAYENLRAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYL
600 610 620 630 640 650
Z46442_1 EVYIDRVEVPAEVEFEAEVLELRAQKAVNALFTSTNPRRLKTDVTDYHIDQVSNVACL
630 640 650 660 670 680

cryla-105.pe SDEFCLEDRRLSSKVKHAKSLDERNLQD-----SNFKDINRQPE
660 670 680
Z46442_1 SDECDDESEELFERKTKAKSLDERNLQDYNFTFISQGLSFASIDGOSNFPFSINELSE
690 700 710 720 730 740

cryla-105.pe RGMKSTTGTIGSDGDEKRYNYVTLSCTDECYPTLYOKIDESKKAFTRYOLRGYIED
700 710 720 730 740 750
Z46442_1 HGWWGSANVTIQDENDVFEKAYLPQGFNCTPPLVYOKIGESLAKAYTRYOLRGYIEN
750 760 770 780 790 800

cryla-105.pe SQDLEIYIRYNAKHETVNGCTSLMPLAQTGKQGEFNRCAPHEWNPDLDCSRD
760 770 780 790 800 810
Z46442_1 SQDLEIYIRYNAKHETVNGCTSLMPLAQTGKQGEFNRCAPHEWNPDLDCSRD
810 820 830 840 850 860

cryla-105.pe GEKCAHSHHFSLDIDVGTCTDNLNEDLGVWIFKIKQDCHRELGNFELEKPLVNEAL
820 830 840 850 860 870
Z46442_1 GEKCAHSHHSTLDIDVGTCTDNLNEDLGVWIFKIKQDCHRELGNFELEKPLVNEAL
870 880 890 900 910 920

cryla-105.pe RVKKAEEKWQKREKLEMETNIVYKEAKESVDALFVNSOYDQLOADTNIAHAPKRVH
880 890 900 910 920 930
Z46442_1 RVKTEKKWQKREKLEMETNIVYKEAKESVDALFVNSOYDQLOADTNIAHAPKRVH
930 940 950 960 970 980

cryla-105.pe STREAYLPELSVPGVNAAFEELEGRIFTAFSLYDARNVKNKGDFNNGSCMNVKGVHD
940 950 960 970 980 990

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[illegible]

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C9EA_BACTA  SCSSGNNCEQKQVNDVOLDADHPKDCCEAAQTHFEFSYIHTGDLNLSVDQGIWVVLQVR
860 870 880 890 900 910
cry1a-105.pe  TQSHARLNLNLEKPLVGEALAKRAEKWDKREKLEMETNIVYKEAGSEDALE
860 870 880 890 900 910
C9EA_BACTA  TTQGHATLNLLELVGEPJSCESLEREDNKAWEVGRKRAETDRIQDAKQAINLHF
900 910 920 930 940 950
cry1a-105.pe  VNSQYDQLQADNTIHTADKRVHSCNAYVPELSVPRGYNAAIFEELEGRIFTAFSLY
920 930 940 950 960 970
C9EA_BACTA  VDQDQGLPEVGMADIIDAQNLNLSISDVAGDAVQIPGINSMTNLSNRLQOASLY
960 970 980 990 1000 1010
cry1a-105.pe  DARNVKNGDFNGLSCNWKGVHDVEEQNORSVLVPEVQVSVQVVCGRGHLR
980 990 1000 1010 1020 1030
C9EA_BACTA  TSRNVVNGDFNSGLDSWNAITDVAQDGNMH-FHLSKNDQVSOQFVDPNCKYLR
1020 1030 1040 1050 1060 1070
cry1a-105.pe  VTAKYGEYGGCVTHETENNTDELKFSNCVEEYIPNNVTICNDVYNVEEYGGVTPR
1040 1050 1060 1070 1080 1090
C9EA_BACTA  VTAKVNGGVYTIQDGAHRETLTNAC-----DYDVN-----SHVND
1070 1080 1090 1100 1110 1120
cry1a-105.pe  NRGYNEAPSVADYASVVEEKSYYDGRRENPCFNGVADYTPFVGVTKELEYFETD
1100 1110 1120 1130 1140 1150
C9EA_BACTA  N-----SYTKELVFYFKTE
1120 1130 1140 1150
cry1a-105.pe  KVMIEIGETGTVDSVLLIMEE
1160 1170
C9EA_BACTA  HMWVESETGTFYIDSIEFTQE
1130 1140 1150
cry1a-105.pep
TXN5:X96682_1
aizawai 7.29 5/1
Description: X96682 Bacillus thuringiensis B.thuringiensis CryIC gene, ssp.
aizawai 7.29 5/1
Accession/ID: X96682
=====General comments=====
LOCUS X96682_1 [BTA729]
DEFINITION B.thuringiensis CryIC gene, ssp. aizawai 7.29 . . .
SCORES Initl: 1104 Initn: 2337 Opt: 1851 z-score: 2039.7 E(): 1.1e-107
>>TXN5:X96682_1
initn: 2337 Initl: 1104 Opt: 1851 z-score: 2039.7 expect(): 1.1e-107
Smith-Waterman score: 2658; 55.8% identity in 773 aa overlap
(1-748:1-756)
cry1a-105.pe  MDNNPNIINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
X96682_1  MEEN-NQNCQIPYNCLSNPEVEVLGGERISTGNSSIDISLSLVQFLSNFVPGGGLVLGL
10 20 30 40 50
cry1a-105.pe  VDIWIGFGPSQWDALFVQIEQLINQRIEERFARNQASRLSEGLSNLYIAYESFREAWD
70 80 90 100 110 120
```

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X96682_1  IDFWGIVGPSQWDALFVQIEQLINERIAEFARNAATANLEGLNFFNIYVEAFKWEED
60 70 80 90 100 110
cry1a-105.pe  FTPALREMRIOFNWNSALTTAIPFAVQYQVPLLSVYQAAHLNLSVLVDVSFQO
130 140 150 160 170 180
X96682_1  PNNPATRTVIDRFDLGLERDIPFRISGFEVPLLSVYQAAHLNLAIRDVSIFGE
120 130 140 150 160 170
cry1a-105.pe  RWGFDATINSEVNDLLELIGNYTDHAVWYNTGLERVGPDSDRDWIRYNQFRRLTLTV
190 200 210 220 230 240
X96682_1  RWGLTTINWENYNLRIHIDEVADHCANTYRGNLNLPKSTYQDWTYNLRLRLTLTV
180 190 200 210 220 230
cry1a-105.pe  LDIVSLFPNYDSRTPIRTVSQLTREIYNPNVLENFDFGSRGSAQ-----GIEGS-IRSP
250 260 270 280 290
X96682_1  LDIAAFPNYDNRYPIDQVQLTRREVYTDPLI-NFNPLQSLVAQLFTFNMESSAIRNP
240 250 260 270 280 290
cry1a-105.pe  HLMILNLSITTIYDHR-GE-YWVGHCQIMASVPGFSGPEETFFLYCTMGNAPQRIVA
300 310 320 330 340 350
X96682_1  HLFILNLTITFTDFWFSVGRNFWGHRVHVISSLIG--GNITSIYIGREANQEPFRSFT-
300 310 320 330 340 350
cry1a-105.pe  OLGGGVRTLS--TLVRRPNIGINNQOLSVDLDCTEFAYGTSNLPSSAVYKSGTVD
360 370 380 390 400
X96682_1  FNRVFTLSNPTLELLQOPAPPEN--LRGVEGVFS--TPTN--SFTYGRGTVD
360 370 380 390 400
cry1a-105.pe  DLEIDPQNNNTPRQFSHRLSHVSMF-RSGFNSSVSIIIRAPMFSWIHSAFNNIIAS
410 420 430 440 450 460
X96682_1  LTESDEFEVPPRENSHRLCHATFVQSGTPTLTIGVW---FSWTHRSALTITIDP
410 420 430 440 450 460
cry1a-105.pe  DSITIDPDKAHTDSEFTWVRGPGSGTGLLRTSGGPFAYTIWINGOLPORYRIR
470 480 490 500 510 520
X96682_1  ERINQIPLVGFRNGGIVSVGGFTGGDNRNFTGDFVSLQVNSPITQRYRLFR
470 480 490 500 510 520
cry1a-105.pe  YASTTNLRIVV-TVAGERIAGQ-----NFMVDTGDELTKQSTSVATINTAFTPMSC
530 540 550 560 570 580
X96682_1  YASSRDARVILTGAASTGVGGQVSNNNLQKTMEGENLTSTRTETDTSNPFSAFNP
530 540 550 560 570 580
cry1a-105.pe  SSFTV-----GADTSSNGNEVIIDFELIPVIRAEKYNLERAKKAVMALETSSVQD
590 600 610 620 630 640
X96682_1  DIIGISEQLPFGAGSSSG-ELYIDKIEILLADATFEASLERCKKAVKAFVSNQIG
590 600 610 620 630 640
cry1a-105.pe  LKNTVYDHIDQSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLQSNINDNR
640 650 660 670 680 690
X96682_1  LKTDVTDHIDQSNLVYLSDEFCLDEKRELSKVKHAKRLSDERNLQSNINDNR
640 650 660 670 680 690 700
cry1a-105.pe  PERGWSGTGITIQGGDVFKNYVLTSGTDECYPTYLYQKIDESKLKAFTRYQLRGYI
700 710 720 730 740 750
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[illegible]

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cryla-105.pe	180	190	200	210	220	230	240	250	260	270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790
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[illegible]

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Q45745 GPGVGIITGFLSTLFGFLWPSNDQAVWEAFIEQWEELEIQRISDQVWRALDLDLTGIONY
70 80 90 100 110 120
cry1a-105.pe YQIYAESPREWEADPTNPALREMIQ--FNDMSALTALPFAV-----QNYQVPLSVY
110 120 130 140 150 160
Q45745 YNOYLIALKEWEERPNG--VRANVLORFEILHALFYSSWPSFGSGPSQSFQOQLLVY
130 140 150 160 170
cry1a-105.pe VOANHLVLSDVSVFGORWGFDAATI--NSRYNDLRLIGNYTHAVRWYNTGLEVMG
170 180 190 200 210 220
Q45745 AQANHLHLLADAEKYGARWGLRESQIGNLYFNELOTRDTYTHCVNAYNGLAGLRG
180 190 200 210 220 230
cry1a-105.pe PDSRDWIRYQFRRELTLVLDIVSLFPNYSRTYPIRTVSQJTRIEYTNV-LENFDGS
230 240 250 260 270 280 290
Q45745 TSAESWLKYHOFREATLMAMDLIALFPYNTRRYPYAVNPOLTRREVYTDPLGVPSSESS
240 250 260 270 280 290
cry1a-105.pe F-----RGSa---QIEGSI-RSPHMDILNSITIYTDa---HRGEY---WSGH
280 290 300 310
Q45745 LPEELRURWQETSAMTFNSLENAIISPHLFDITNNLMYITGSFVSHLTNOLIEGMIGH
300 310 320 330 340
cry1a-105.pe QMASPVFGSGPEFTPLXYGTMGNAPOQIVAQOGCVYRTLSSTLVRFPNIGINNOQ
320 330 340 350 360 370
Q45745 SVTSSILA-SGP--TTVLRENYGSTISIVNYFSFNDRDVQINT----RSHTGLGFONAP
360 370 380 390 400 410
cry1a-105.pe LSVLDGTFE-AYGTSSNLPSAVYRSGTVGVSLEIIPQNNVPPRGFSHRLSHV-SMFR
380 390 400 410 420 430
Q45745 LFGITRAQFYPGGYSTVQTNALTCQNYNSIDELPDNEPISRSYSHRLSHITSLYH
420 430 440 450 460 470
cry1a-105.pe SCFSNYSYIIRA--PMFSWIHSAEFNNIIASDSITQIPLVKAHTLQSGTIVVRGSGFT
440 450 460 470 480 490
Q45745 RVLTIDGINISYGNLPTYWTHRDVLDITADRIITQLPLVKSFEIPAGTIVVRGSGFT
480 490 500 510 520 530
cry1a-105.pe GGDILRRTSGGFPAYTIVNIGOLPQYRARIYASTTNLRIVTVAGERIFAGQFNKTM
500 510 520 530 540 550
Q45745 GGDILRRTVGVTGTRIVRTAPLQRYRIRFRFASTTNLFIGIRVGDRQVNYDFGRIM
540 550 560 570 580 590
cry1a-105.pe DTGDELTTQSFYSATINTAFTPMQSGSFTVCADTFSSGNEVYIDRFELIPVATLRAEY
560 570 580 590 600 610
Q45745 NRGDELRYESFATREFTIDFNFRQFQELISVFANAFSAGQEVYFDRIETIIPVNPAREAKE
600 610 620 630 640 650
cry1a-105.pe NLERAKAVNALFTSTNQLGKTNVTDHIDQVSNLVTYLSDFCLDKRELSKVKHAK
620 630 640 650 660 670
Q45745 DLEAKKAVASLFTTRTD-GLQVNVKDYQVQAAANLVSCLSDEQYGYDKMKLELVAARAK
660 670 680 690 700 710
cry1a-105.pe RLSDERNLLQDSNFKDINRQPERGWSGTIGTIOGGDDVFKENYVTLSTGTFDECPTYLY
680 690 700 710 720 730

Q45745 RLSRERNLLQDPDNTINSTEENGWKAASNGVTISEGGFFYKGRALQLASA-RENYPTYIY
720 730 740 750 760
cry1a-105.pe QKIDSKLKAATRYQLRGVIESQOLEIYSIRYNAKHETVNVPGT--GSLMPLSAQSPIG
740 750 760 770 780 790
Q45745 QKVDASELKPYTRYRSDFGVFSQOLEIDLIHHKHVFLKKNVPDNLVSDTYDPDSCSGIN
770 780 790 800 810 820
cry1a-105.pe KCGENRCAPHLE--WNPDLDCSRDGEKCAHSHHSLDIDVGCTDLNEDLGVWVIFKI
800 810 820 830 840 850
Q45745 RCQEQOMVNAQLETEHHPNDC-CE-----AAQTHEFSSVIDTGLNNGSVQOGIWAIFKV
830 840 850 860 870 880
cry1a-105.pe KTDQGHARGLNLEELKPKLVGEALRYKRAEKWKDRKLEMETNIVYKEAKESVDAL
860 870 880 890 900 910
Q45745 RTTDGVAITGLNLELVGVLPSGESLERQDRONTKWSAELGRKRAETDRVYQDAKQSIHL
890 900 910 920 930 940
cry1a-105.pe FVNSQVQLOQADTNIAIMIHAADKRVHSIREAYLPELSVIFGVNAAIFBELSGRIFTAFSL
920 930 940 950 960 970
Q45745 FVDYQDQQLNPEIGMADIMDAQNLVASISDVYSDAVIQIPGINYEIYTELSNRLQQAAYL
950 960 970 980 990 1000
cry1a-105.pe YDARVIVKNGDFNGLSKMNVKGVHDVEEQNQRSLVLPWEAEVSOQVRCVPGRGVIL
980 990 1000 1010 1020 1030
Q45745 YTSRAVQNGDFNGLSDSNWATAGASVQDGNTH-FLVLSHMDAQVSOQFRVQPNCKXVL
1010 1020 1030 1040 1050 1060
cry1a-105.pe RVTAKEGSGGCVTTHIEENNDELKFSNCVVEEIIYPNNVTTCNDYTNQOEYGGAYTS
1040 1050 1060 1070 1080 1090
Q45745 RVTAKEGSGGCVTIRDGAHTETILTINAC-----DYDIN-----GTVVT
1070 1080 1090 1100
cry1a-105.pe RNNGYNEAPSPADYASVYEKSYTDGRENPCFNCGYRDYTPLPVGYVKELEYFET
1100 1110 1120 1130 1140 1150
Q45745 DNT-----YLTKEVIFYSHT
1110
cry1a-105.pe DKVWIEIGETGTFIVDSVELLIMEE
1160 1170
Q45745 EHMWVEVNETEGAFHIDSIEFVETEK
1120 1130 1140
cry1a-105.pe TXNS:Q9FDCO
TXNS:Q9FDCO
Description: Q9fDCO bacillus thuringiensis (subsp. finitimus). parasporal
inclusion protein c
Accession/ID: Q9FDCO
ID Q9FDCO PRELIMINARY; PRT; 1128 AA.
AC Q9FDCO;
=====General comments=====

SCORES Init1: 519 Initn: 1660 Opt: 1741 z-score: 1915.6 E(): 8.6e-101
>TXNS:Q9FDCO (1128 aa)
initn: 1660 init1: 519 opt: 1741 z-score: 1915.6 expect(): 8.6e-101

Smith-Waterman score, 1924. 34.9% identity in 1207 aa overlap
(18-117-23-1128)

cryla-105.pe MDNNHPEPYNCLSPNPNVLGGERIEGYTPIDISLSLTOFLSEFV-PGA
Q9FDC0 MDKHKIKKQSTEVSEIFNPEVDSNDNAVSAGIVV-VGILITAF--ASFVNPV
cryla-105.pe GFV-LG-LVDIIMG--IFGRSO-WDAFNDIOLINQNEERARNOAISRLGLSNLYQI
Q9FDC0 VLISGTLAPVLPDPEEDPKLMSQFMKHEDLNNTISTAKWENLAHLNGFKDLVLY
cryla-105.pe YAESTRWEADPTPALREMRIOQNDMSATTAFLFAVAVTPVPLSTVQAAHL
Q9FDC0 YRAFDNWKPNFSANTARL-VSORFENAHFNFSVNNQDQPTDYDTLLSCYTEAANDHL
cryla-105.pe SVLRDVSFGORMGFDA-----TINSRYNDLRLGNVTDHAFVNNGLERAVGPPS
Q9FDC0 NLHGQGVFAQWNADQPHSPMLKSSGTYIDELLVYIEKINCYCTYHKCANDESEK
cryla-105.pe RDWIRYQFRRELTLYLDIVSLFNYSRTYPIRTVSQITREIYT--NPVLENFDSFR
Q9FDC0 ITWDAYTRYREMTLIVLDLVATFPFYDIRRFPGRGVELELTREVYTSLDPPGLNAGPIPE
cryla-105.pe GSAQGIKESI-RSPHMDILNSITIYDA-HRGEVYWSGQIMASVPVSGSGPEFTFLYG
Q9FDC0 IDPSYLEDHLTRPGLFTWLSDELITESTVAEGDL-SG--IRESKY-VTGNQF-FWKVN
cryla-105.pe TMGNAAPQORIVAGLGQGVYRTLSLTYRRPFI--GINNQQLSVLDGTEFAYGTSSNLP
Q9FDC0 IYGNTRLSKQILITLLPGEFITHLSI--NRGFOTIAGIN-KLYSLIQKIVFTFEKNDNE-
cryla-105.pe SAVYKSGTVDSLEIIPQNNVPPRQG-----FSRLSHVSNF--RGFSNSVSIIIR
Q9FDC0 ---YQKNFVNNQNE-POETTYNPYDGGNSQKFKNLSHFPLIIHQVEFAEYFHSIF-
cryla-105.pe APWFSEIHRSAFENIIASDSITQIPLVAAHTQSGTVVRGPGFTGGDILARTSGGPFA
Q9FDC0 --ALGHTNSVNSQNLISESVSTQIPLVAYEVTTNS-VIRGPGFTGGDILIELRKCSIK
cryla-105.pe YTVINNGQLPORVARIYASTINRIYTV-----AG---ERIFAGQKMTMDGDLT
Q9FDC0 CKASSL-----KKYALSIFYAANNAIVSIDVGDGAGVLQPTFSRKGNNNFTIQD-LN
cryla-105.pe PQFSYATINTAFTFPMQSSFT--VCADTFSSGNEVYIDRFELIPVATLAEVNLERA
Q9FDC0

Q9FDC0 YKDFQYHTLLVDIELPESEHIIHKREDDEYEGVILLIDKLEFKPIDENTYNNMEXA
cryla-105.pe OKAVNAFTSTNOLGKTNVTDYHIDQVSNLVTYLSDEFCLDEKSEKVKHAKRLSDE
Q9FDC0 KKAUNVFINATN-ALKMVDVTDYHIDQVANLVEICISDILYAKEKIKLHAIKFAKQLSOA
cryla-105.pe RNLLQDSNFKDINRQPERGMSGSTGITTQGGDDVFNENVTLSGTFDECYTYLYQKIDE
Q9FDC0 RNLLSDPNFNLN--AENSGWTANTGVTIIEGDPYKGRALQISAARDENFFTYLYQKIDE
cryla-105.pe SKLKAFTEYQVLRGVIEDSODLEIYSIRYNAKHETVNPVGTGSLWPLSAQSPIGKC-----
Q9FDC0 SLKPYTYQRGVEGSGDLELDIVRGATDIVMNVPG--DLEILYSAPINCEEIEIET
cryla-105.pe -----GEPNRCAPHEWNPDLDCRDEGKCAHSHHFSLDIDVCGTDLNEDLGWVWIF
Q9FDC0 RLDTTCGALDRCKQSNVNSAADVR---PDQVNGDPHAFSHFIDTGTDTNNRNLGIWIF
cryla-105.pe KKTQDGARIGNLEFLEEXPUGENARVYAEKKW-RDKREKLEWETNIVYKEAESV
Q9FDC0 KTAEDGATFNGLELIEFGSGEALQVQKQKMGKNITOKRE-EAALKYAAAKQTI
cryla-105.pe DALFVNSQVDLQSTNIAHAAKRVHSIREAYLPPELSVIFGVNNAIFEELEGRIFTA
Q9FDC0 NQLESDNLRDREFSNLSADKLVKIRDVYSEVLSVIFGLVYDLFMELENRIQNA
cryla-105.pe FSLYDARNVIRKGDFFNGSCWNVKQVNDNEQNNQSVLVPEWEAEVSQEVVCPGRG
Q9FDC0 IDLYDARNTVNGFRNGEAMSSNTEVR-QTSQTSVLVLSWNAQVAQSLNVKPDHG
cryla-105.pe YILRVTAKEGVEGCVTITRLEMTDELSESVEEIEYNTNCTNDYTVNQVEYGA
Q9FDC0 YILRVTAKEGVEGCVTITRLEMTDELSESVEEIEYNTNCTNDYTVNQVEYGA
cryla-105.pe YTSRNGYNEAPSVPAIYASVYEEKSYKSTGDRNPFSENGYRDYTLFVGVYTKSEYF
Q9FDC0 TTSSN-----ELAA-----1090
cryla-105.pe PETDKVWIEIGTEGTFFIVDSVELLME
Q9FDC0 PDTQIRIEIGTEGTFFIVDSVELLME
cryla-105.pe
TXNS:C1IB_BACTE

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CLIB_BACTE
ITQIPLVKAFNLSSGAAVVRGPGTGGDILRRTNTGTFGDIRVNIINPFAQRYRVRIRYA
510 520 530 540 550 560

[illegible][illegible]

```

cry1a-105.pe 660 670 680 690 700 710
LVTVLSDFCDKREKLEGEKVHAKRLSDERNLQDSNFKQINRQPERGGSGTITGG
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
CL1B_BACTE 660 670 680 690 700 710
LVESLSDFYLDKRELFKFEIVKAKQIHIERNM

```

	720	730	740	750	760	770
cry1a-105.pe	GDVFKENVYTL	SGFDCEYTYL	YQKIDSKL	KAFYQLRGV	IEDSQDLEI	YSIRYNA
cry1a-105.pap						

cryla-105.pap
TXN5:C9DA_BACTP
Description: O06014 bacillus thuringiensis (subsp. japonensis) . pesticid
crystal protein c

```

SCORES      Init1: 756      Initn: 2154      Opt: 1715      z-score: 1886.7 E(): 3.5e-99
>>TXNS:C9DA BACTP
      Initn: 2154      Initl: 756      Opt: 1715      z-score: 1886.7      expect(): 3.5e-99
Smith-Waterman score: 2285;      36.0% identity in 1197 aa overlap
(16-1177:57-1169)

```

cr1a-105.pe MDNNPNINCEPNCPSNEPEVLGSERTGTVPIDISLSTOF 10 20 30 40

C9D₄ BACTP YPLTDDPNAGLQNNKYKLYOTGYGDDTDLPLNPILSVSGKDVTQGINIVGLSLFFGFG 30 40 50 60 70 80

```

cryla-105.pe      -LLSEVPFGAGFVLGVDLIINGIFGPSQWDAFLVTEQLINRIETFEARQAISREGLGS
                  : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
C9DA_BACTP       PFSSQWTVVTYLL---NSLAPDDDNSVMDAFNRYVEELIDQKTSKAVKGRAALDITGLQ
                  90   100   110   120   130   140

```

[illegible]

	170	180	190	200	210	220
cryIa-105.pe	YVQAANLHLSDVDSVFQRMGDAATINSRYNDLTRIGNYTDHRAWNTGLERVMG					
	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :					
C9D _a _BACTP	YAQAANLHLLLNDADIVYGARGNLNOTOIDPFHSROOSTQTQTYTHNCVTAINDGLAELRG					
	: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :					

©07

[illegible][illegible]

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cryla-105.pep
TXN5:Y08920_1

Description: Y08920 Bacillus thuringiensis B.thuringiensis cryV gene; 159.
10/1996

Accession/ID: Y08920
=====General comments=====
LOCUS Y08920_1 [BICRV159]
DEFINITION B.thuringiensis cryV gene; . . .

SCORES Initl: 889 Initn: 1600 Opt: 1709 z-score: 1883.3 E(): 5.4e-99
>>TXN5:Y08920_1
Initn: 1600 Initl: 889 Opt: 1709 z-score: 1883.3 expect(): 5.4e-99
Smith-Waterman score: 1725; 42.7% identity in 705 aa overlap
(4-683:36-719)

cryla-105.pe
Y08920_1
QDKHQFSFNAKVDKISTDLKNETDIELQNIHEDCLMKSEYENVEPFV-SASTIQG-
10 20 30 40 50 60
MDNPNINECIPIYRCLSNPEVEVLGERIETGY
40 50 60 70 80 90
TPIDISLSITQFILSEVRGAGFVLGLVDIINGIFGP---SQWDAFLVQIEQLINQRIEE
100 110 120 130 140 150
FARNOAISRLGLESLNLYQIVAESFREWEADPTNPALREEMRIQFNDNSALITAIPIFAV
160 170 180 190 200 210
QNYQVPLLSVTVQAANLHLSVLSDVSGVQRMGDAATINSRYNDLTRILGNYTDHVAVRW
220 230 240 250 260 270
YNTGLRWGDDSDMIRNQPRRELTLTLDIVSLFYNDSRTYPIRTVSQLTREIYN
280 290 300 310
QVTEGSLRSPHLDIINSLTIYTDHGRGYWSGH
320 330 340 350
AIGTVHPISFTSTTNNNAESFAIEAAVNRPHLLDFLEQVTIYSLLSR---WSNT
360 370 380 390 400 410
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
420 430 440 450 460 470
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
480 490 500 510 520
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
530 540 550 560 570 580
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
590 600 610 620 630 640
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
650 660 670 680 690 700
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
710 720 730 740 750 760
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
770 780 790 800 810 820
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
830 840 850 860 870 880
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
890 900 910 920 930 940
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
950 960 970 980 990 1000
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1010 1020 1030 1040 1050 1060
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1070 1080 1090 1100 1110 1120
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1130 1140 1150 1160 1170 1180
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1190 1200 1210 1220 1230 1240
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1250 1260 1270 1280 1290 1300
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1310 1320 1330 1340 1350 1360
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1370 1380 1390 1400 1410 1420
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1430 1440 1450 1460 1470 1480
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1490 1500 1510 1520 1530 1540
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1550 1560 1570 1580 1590 1600
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1610 1620 1630 1640 1650 1660
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1670 1680 1690 1700 1710 1720
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1730 1740 1750 1760 1770 1780
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1790 1800 1810 1820 1830 1840
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1850 1860 1870 1880 1890 1900
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
1910 1920 1930 1940 1950 1960
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
1970 1980 1990 2000 2010 2020
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2030 2040 2050 2060 2070 2080
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2090 2100 2110 2120 2130 2140
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2150 2160 2170 2180 2190 2200
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2210 2220 2230 2240 2250 2260
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2270 2280 2290 2300 2310 2320
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2330 2340 2350 2360 2370 2380
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2390 2400 2410 2420 2430 2440
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2450 2460 2470 2480 2490 2500
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2510 2520 2530 2540 2550 2560
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2570 2580 2590 2600 2610 2620
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2630 2640 2650 2660 2670 2680
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2690 2700 2710 2720 2730 2740
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2750 2760 2770 2780 2790 2800
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2810 2820 2830 2840 2850 2860
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2870 2880 2890 2900 2910 2920
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
2930 2940 2950 2960 2970 2980
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
2990 3000 3010 3020 3030 3040
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3050 3060 3070 3080 3090 3100
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
3110 3120 3130 3140 3150 3160
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3170 3180 3190 3200 3210 3220
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
3230 3240 3250 3260 3270 3280
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3290 3300 3310 3320 3330 3340
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
3350 3360 3370 3380 3390 3400
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3410 3420 3430 3440 3450 3460
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
3470 3480 3490 3500 3510 3520
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3530 3540 3550 3560 3570 3580
QYNNM---WGCHKLEFRTIGGTALISTQGSNTWISNPIVTLFTSRDVRTESLAGLMLFL
3590 3600 3610 3620 3630 3640
QIMASPVGFSQPEFTPLXGTMGNAAPQQRIVAGLQGVYRTLSSTLYRPPNIGIN---
3650 3660 3670 3680
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cryla-105.pe RLSHVGRSGFSSVSILIRAPMSWHRGAENFIISDSTIQIPLVKAHITLQSGTIV
Y08920_1 RLSHIGLI-----SASRKKKALNSWTHRSADRNTIEPNSITQIPLVKAFNLSSGAAV
cryla-105.pe VRPGPTGGEDLRKSGPPATNVINNSIPQVRARIAYATTNRLIYTVAGERIFA
Y08920_1 VRPGPTGGDIISRNTCTTGDAVNINPPAQARVRIYAYASTDLQPHITSINGKAING
cryla-105.pe GQFNKWTMDGLTLTFQSFIATNTHTFPMS--SVTWGADTSNGXNYIDRELPVT
Y08920_1 GNFSATNRGEDELTKYFTRTVGTFFPSLELDVOSTFLGAWNSSGNEVINDREFVPVE
cryla-105.pe ATLEAEYNLERAKAVALNFSTINOLGLKNVDVHDIO/SNLVTVLSPFGDEKRELS
Y08920_1 VTVEAEYDFEKAQEKVALTFTSNRGLTKDVKDVIHDOVSNNES-SDFEYFGEVETLF
cryla-105.pe EKVVKHAKRLSDERNLLQDSNFKDINRQPERGWGSSTGITIQGGDDVFKENYVLTSGNFEDE
Y08920_1 EIVKYANELHIERNM
cryla-105.pap
TXN5:AAK66742

Description: Aak66742 bacillus thuringiensis. crylia. 8/2001
Accession/ID: 000000
ID AAK66742 PRELIMINARY; PRT: 719 AA.
AC AAK66742
DT 23-AUG-2001 (EMBLRel. 63, Created)

SCORES Initl: 896 Inltn: 1603 Opt: 1707 z-score: 1881.1 E(): 7.2e-99
>>TXN5:AAK66742 (719 aa)
initl: 1603 initl: 896 opt: 1707 Z-score: 1881.1 expect(): 7.2e-99
Smith-Waterman score: 1723; 42.7% identity in 705 aa overlap
(4-683:36-719)

```

cryla-105.pe      MONNNPNIIECPYNCJNSNVEPVGLGRIETGY      10 20 30
AAK66742      ODKHQSFSSNAKVDKISTDSLKNETDIELQNIINHHEDCLKNSEYVENPFV--SASTIQTG-
10 20 30 40 50 60
cryla-105.pe      TPIDISLSLTQFLSEFFVPGAGFVLGVLDIIMGICGP--SQWDAFVAIOIELQINORIEE      70 80 90
AAK66742      --IGIA---GKIILUGVFFGQASVLSYSLFELGMLPGKGNQWEIFNEHVEELIINKIST
70 80 90 100 110
cryla-105.pe      FARNQAISRLEGLSNLYQIYAESFREWEADPTNPALREEMRIQFNDMNSALTTAIPLEAV      100 110 120 130 140 150
AAK66742      YARNKALTDILKGLGDALAYIHDSILESWSGVRNNTRARSWKVSQYIALEMLVQKLPSPAV
120 130 140 150 160 170

```

Description: 085796 bacillus thuringiensis (subsp. kurstaki). insecticidal protein. 9/2001

protein. 9/2001

[illegible]

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490
cyla-105.pe VRGPGTGDILRTSGGPFATVIVNNGQLPQRIARIVASTNLRIVTVAGERIFA
085796 VROGPGTGDILRTTNGTGDIRVNIKPFAQVRVIRVASTTDIQHTSINKIAINQ
530 540 550 560 570 580
cyla-105.pe GQFNKTMGTGDLTFQSFYATINTATFPMSSGFTVGADTRSSGNEVYIDRFELPVT
085796 GNFSAIMRGEDLDYKTFRTVGFTFPFSLDVOSTFTICANFSSGNEVYIDRFEPVE
590 600 610 620 630 640
cyla-105.pe ATLEAEYNLRKAQNALFTSTNGLGKTNVTDHXIDQVSNLYLSDEFCLDEKRELS
085796 VTYAEAYFEKAOEKVLTFTSTNPRGLTKDVKDHXIDQVSNLYLSDEFYLDKEKELF
650 660 670 680 690 700
cyla-105.pe EKVYKHKRLSDERMLLDQSNFNDINRQPERGWSGTGITIGGDDVFKENYVLTSGTFDE
085796 EIVKYAKQLHIERNM
710
cyla-105.pep
TXN5:C9AA_BACTG

Description: Q99031 bacillus thuringiensis (subsp. galleriae). pesticidal
crystal protein cr
Accession/ID: Q99031
ID C9AA_BACTG STANDARD; PRT; 1156 AA.
AC Q99031; Q03747; . . .

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

SCORES Initl: 457 Inltn: 1750 Opt: 1706 z-score: 1876.8 E(): 1.2e-98
>>TXN5:C9AA_BACTG
inltn: 1750 inl1: 457 opt: 1706 z-score: 1876.8 expect(): 1.2e-98
Smith-Waterman score: 1995; 33.9% identity in 1227 aa overlap
(1-1177:26-1156)

cyla-105.pe MDNNP-----NINECIPYNCISNFEVVLGGERIE
C9AA_BACTG MNQKHGHTIGASGCCASDDVAKYPLANNPYSSALNLSQSSILN--WINIIGDAAKE
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190
cyla-105.pe TGYTPIDISLSTOFLLSSEFVG-AGFVLGVD-IIWGIFGQSDWDAFLVQIEQLINORI
C9AA_BACTG A---VSLGTTIVSLTAPSLTGLISIVDILGKVLGSSSQSISLSDLSIDLIDRV
60 70 80 90 100 110 120 130 140 150 160 170 180 190
cyla-105.pe EEFARQAISLEGSLNLYQVAESFREWEADPTNPALEEMRIQF-----NDMNSALT--
C9AA_BACTG SQSVINDGIADFNGSVLLRYNLYLEALDSWNKNP-NSASAEELRTFRFIADSEFDILIRG
120 130 140 150 160 170 180 190 200 210 220 230
cyla-105.pe --TAIFLFAVQNYQVPLLSVYVOAANHLISLRDVSFQKRWG-FDAATINRYNDLTRL
C9AA_BACTG SLNQSGLARQNAQKILLPSFASAFFHLLLRDATRYGTNMGVYNATPFIYVQSKVLVEL
180 190 200 210 220 230

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[illegible]

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cry1a-105.pe 90 100 110 120 130 140
EFARNQAIISRLGSLNLYQIYVAESFREWEADPTNPALREEMRIQF---NDMNSALT--
X58120_2 120 130 140 150 160 170
SOSVINDGIADFGNSVLLYRNVLKALDSWKNP-NEASAEELRTFRADSEDFRILTRG

cry1a-105.pe 150 160 170 180 190
--TAIPFAVQNVQVFLLSVYQAAHLVLRDVSFQRMG-FDAATINSRYNDLTR
X58120_2 180 190 200 210 220 230
SLTNGSLARQNAQILLPSFASAAFFHLLLRDAYSRTGNGLNATPFFINQSKLVEL

cry1a-105.pe 200 210 220 230 240 250
IGNYTDHAWNYATGLE--RVWGPDSRDWRYNQFRELTLVLIVSLFNVDSRTYPI
X58120_2 240 250 260 270 280 290
IELYIDXCVMYARGFNEUQRGTSATAWLEFHYRREMTLVWLDIVASFSSLDITNPI

cry1a-105.pe 260 270 280 290 300
RTVSQLTREIYTPNPLENFDGSRGSA-----QIEGSISSPHLMDILNSITIV
X58120_2 300 310 320 330 340 350
ETDFGLSRVIYTDPIGFVHRSSLRGESWFSVNRANFSDELAENPSPFWFLNMIIIST

cry1a-105.pe 360 370 380 390 400
DA-----HRGEYWSGHQIMASPVGSGPEFTPLYGTMGNAAPQQRVAQGGQV
X58120_2 410 420 430 440 450 460
GSLTLPVSPSTDRAV-MYGSRDRIISP---ANSQFITEISQHTATQ-----TILGRNI

cry1a-105.pe 470 480 490 500 510
YHTLSSTLYRPPNIGINNQOLSVLDGTGFAYCTSSNLPSAVYKSG-----TYDLSDE-I
X58120_2 520 530 540 550 560 570
FRVDSQACNLNDITYGVN-RAVYHDASE---GSQSVVEGVIKITGIDNPRVQNTIYL

cry1a-105.pe 580 590 600 610 620 630
PPQNNVPPRQGSFHLRSHVSMFRSGF-----SNSSVIIRAPMFSWIHRSAENFIASD
X58120_2 640 650 660 670 680 690
PCENSIDPTPEDYTHILSTIINLTGGLROVASNRRSSLV---MYGWTNKSILARNNTINPD

cry1a-105.pe 700 710 720 730 740 750
SITQILPVKATILQSGTIVVRGPGFTGDIILRTSGPPAYTIIVNNGPQRYRARIY
X58120_2 760 770 780 790 800 810
RITQILPTKVDTRGTSVYNDPGFIGGALLQRTDHSGLVLRQFPLHLRQQYRIRVY

cry1a-105.pe 820 830 840 850 860 870
ASTNLRIYVTVAGERIFAGQFNKMTDGTPLTFQSFVSATINTAFTFPMQSSSTVGAD
X58120_2 880 890 900 910 920 930
ASTNIRLSVNGSFGTI-SQNLPSMTLRLGEDLRVGSFAIRENTSIRPTASPOILTIE

cry1a-105.pe 940 950 960 970 980 990
IFSSGNEVYIDRDELIPVTALEAYNLRAQKAVNALFTSTNQGLKTNVTDYHIDQVS
X58120_2 1000 1010 1020 1030 1040 1050
PSFIRQEVYVDRIEFIPVNPFTREAKEDLEAKKAVASLFTTRD-GLQVNVKDYQVDQAA

cry1a-105.pe 1060 1070 1080 1090 1100 1110
NLVYLSDEFCLDEKRELSEKVKIAKRLSDERNLLQDSNFKDINKQPERGNGSGTITQ
X58120_2 1120 1130 1140 1150 1160 1170
NLVSLSDQGYQYDKOMLEAVRAAKRLSRERLLQDDPFDNTINSTENGKASNGVTIS

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cry1a-105.pe 710 720 730 740 750 760
GGDDVFENYVTLGSGFDCEYCYTYLYOKIDESKLKAFTRYQLRGVIEDSODLEIYSIRYN
X58120_2 760 770 780 790 800 810
EGPPYKGRATQIQLASA-RENYPTYIYQKVDASELKPYTRYLRDGFVKSSQDLEIDLHHH

cry1a-105.pe 770 780 790 800 810 820
AKHETVNVPGT--GSLWPLSAQSPIGKCGEPNRCAPHLEW--NPDLDCSRDGEKCAHHS
X58120_2 820 830 840 850 860 870
KVHLVKNVFNLDVSDIYPPDSCSGINRCQEQOMVNAQLETEHHHPDWC-CE-----AAQT

cry1a-105.pe 830 840 850 860 870 880
HFSLDIDVGCITLNEDELGVWVIFKIKTQDGHARLGNLEFLEKEPLVGEALARYKRAEKX
X58120_2 870 880 890 900 910 920
HEFSSYIDTGLDNSSVDQIGMAIFKVRTTQGYATLGNLELVEVGLSGESLEREQRDNTK

cry1a-105.pe 890 900 910 920 930 940
WEDKEKLEWETNIVYKEAKESVDALFVNSQYDQLQADNTIAMIAADKRVHSIREAYLP
X58120_2 930 940 950 960 970 980
NSAELGRKRAETDRVTDRAKQSNHLFVDYQDQLAPEIGMADIMDAONLVASISDVYSD

cry1a-105.pe 950 960 970 980 990 1000
ELSVTPGVNAIIFEELEGRIFAFSLYDARNVKNQDGNNGLSWNKGVHVDVEEQNQR
X58120_2 990 1000 1010 1020 1030 1040
AVLQIPGNIYEIVTELNSLQOASVLYTSRNAVQNGDFNNGLSDSNATAGASVQODGNTH

cry1a-105.pe 1010 1020 1030 1040 1050 1060
SVLVVPEWEAEVQEVVRCPGXYILRVATYKSGYGGCVTTHIEENNTDELKFSNCVVEE
X58120_2 1050 1060 1070 1080 1090 1100
FLVLSHMDAQVQSQFRVQNPCKYVLRVTAEKVGGSDGYVITRDDAHTHTLTITFNAC---

cry1a-105.pe 1070 1080 1090 1100 1110 1120
EYFPNTVTCNDYTVNOEYGGVATSRNRYNEAPSPADYASVYEKSYTDGERNPCE
X58120_2 1110 1120 1130 1140 1150 1160
-----DYDIN-----GTYYTNT-----

cry1a-105.pe 1130 1140 1150 1160 1170 1180
FNRGYRDTPLPGYVTKLEYFPETDKWIEIGETEGTFIVDSVELLMEE
X58120_2 1180 1190 1200 1210 1220 1230
-----YLTKEVVPHPETQHMVVEVNETEGAFHIDSIEFFVETEK

cry1a-105.pe 1230 1240 1250 1260 1270 1280
TXN5:X62821_1
TXN5:X62821_1

Description: X62821 Bacillus thuringiensis B.thuringiensis cryv gene for
Delta-endotoxin. 5/1
Accession/ID: X62821
=====General comments=====
LOCUS X62821.1 [BTCRYV]
DEFINITION B.thuringiensis cryv gene for delta-endotoxin.

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SCORES Initl: 896 Initn: 1592 Opt: 1701 z-score: 1874.4 E(): 1.7e-98
>TXN5:X62821_1
Initn: 1592 Initl: 896 Opt: 1701 z-score: 1874.4 expect(): 1.7e-98
Smith-Waterman score: 1717; 42.6% identity in 705 aa overlap
(4-683:36-719)

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```
cry1a-105.pe      10      20      30
                  MDNPNINCEIPYCNLSNPEVEVLGGRIETGY
X62821_1          10      30      40      50      60
                  QKHQSFSTAVDKISTDLKATDIELQNLNEDCLKMSVENVEPV-SASTIQG-
cry1a-105.pe      40      60      80      90
                  TPIDISLSITLSEPPFQVPLVGLVDKINGFGP---SNDALFVIGIOLINORIEE
X62821_1          40      60      80      100      110
                  --IGIA---GRITGLDVPFAGQASLSVIFLGENMPKSNQWEIFMEHVEEILNQKIST
cry1a-105.pe      100     110     120     130     140     150
                  FARNQAIISLEGLSNLYOIAVESRENEADPTNREEMRIOPNNKALTATPILFAV
X62821_1          100     110     120     130     140     150
                  YARKALITDLKGLDALAVYHDSLESWENRNTFARAVYKFOYIALELMEVQLPSFAV
cry1a-105.pe      160     170     180     190     200     210     220     230     240
                  QNYQVPLLSVYQAAHLHLSVLRDVSVFQRMGFDAAVINSKNDLTLNIGNTTHAVRM
X62821_1          160     170     180     190     200     210     220     230     240
                  SGEVPLLPYIAQAAHLHLLLRDASIFGKWLSSSEISTFTRQVERAGDSYFQK
cry1a-105.pe      250     260     270     280     290     300     310
                  YNTGLERVGPPDSRWIRYNQFRRELTIVLIVSLFPNYSRTYPIRTVSOLRENTN
X62821_1          250     260     270     280     290     300     310
                  YSTGLANLRGTWASWVRYNQFRREDTLVLDLVALFYSYDTQNYPIKTIQAQITREVSD
cry1a-105.pe      320     330     340     350     360     370
                  QIMASPVGSGEPFTFPLYGTMGNAAPQQRIVAQLGQGVYRTLSLTRYPPNIGIN---
X62821_1          320     330     340     350     360     370
                  QYMMN---WGHKLEFRTIGTILNISTQGSTNTSINPVLPTFTSRDYRTESLAGLNFL
cry1a-105.pe      380     390     400     410     420
                  NOQLSVLDGTEFAYG-----TSSNLPASVYKSGTV--DSLDEIPPNNNVPPROGFSH
X62821_1          380     390     400     410     420
                  TOPVNGVRVDFHFWKTHPTASDNFYYPGYAGIGITQLODSENELPEATGQPNYSYSH
cry1a-105.pe      430     440     450     460     470     480
                  RLSHVSVFGSGFNSSVSIIRAPMFSWIRHSAEFNNIIASDSITQIPLVKAHTLQSGTIV
X62821_1          430     440     450     460     470     480
                  RLSHIGLI-----SASHVKALVYSWTHRSADRTNTEPNISITQIPLVKAFLNLSGAAV
cry1a-105.pe      490     500     510     520     530     540
                  VVGPGFTGGDILRTSGGPFATIVNINGQLPQRYARIRYASTNLRIYTVAGERIFA
X62821_1          490     500     510     520     530     540
                  VVGPGFTGGDILRTSGGPFATIVNINGQLPQRYARIRYASTNLRIYTVAGERIFA
cry1a-105.pe      550     560     570     580     590     600
                  QGFNKTMDTGDLTFQSFYSATINTAFTFPMSSQSFVTGADTFSSGNVYIDRELIPTVT
X62821_1          550     560     570     580     590     600
                  GNFSATMVRGEDLDYKIFRTVGTFTFPFSLDVQYITFTIGNWFSSGNVYIDRELIPTVE
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```
cry1a-105.pe      610     620     630     640     650     660
                  ATLEAEYNLERAQAVNALETSTNOLGKTKNTDYHIDQVSNLAVTVLSDFCLEKRELS
X62821_1          610     620     630     640     650     660
                  VTYEAEYDFEKAQEKVALTFTSPRGKTKVDKHIDQVSNLVSLSLSDFCLEKRELF
cry1a-105.pe      670     680     690     700     710     720
                  EKVKHAKLSIDERNLLQDSNFKNQRPGRMGSGTGITIQGGDDVFKENYVYTLSGTFDE
X62821_1          670     680     690     700     710     720
                  EIVKAKQLHIERNM
cry1a-105.pep
TXN5:CLID_BACTU
Description: Q9xdl1 bacillus thuringiensis. pesticidal crystal protein cryIId
(insecticidal)
Accession/ID: Q9XDL1
General comments:
ID CLID_BACTU STANDARD; PRT; 719 AA.
AC Q9XDL1;
Scores Initl: 888 Initn: 1589 Opt: 1695 z-score: 1867.8 E(): 3.9e-98
TXN5:CLID_BACTU
Initn: 1589 Initl: 888 Opt: 1695 z-score: 1867.8 expect(): 3.9e-98
Smith-Waterman score: 1711; 43.2% identity in 696 aa overlap
(14,683-41,719)
cry1a-105.pe      10      20      30      40
                  MDNPNINCEIPYCNLSNPEVE-VLGGRIETGYTIDLSLSL
CLID_BACTU        10      20      30      40
                  SFSSNATVQKSTDTPLENTMELQNSHEDCLKMSEYSEVPFVSITQIGIA---
cry1a-105.pe      50      60      70      80      90
                  TOFLSEVPGAGFVLGNDLWGIK---GPSQDAFLVQIEQLINQRIEFAFNQAIQR
CLID_BACTU        50      60      70      80      90
                  GATLGLGVFPAGC---SYSTFDELMPKSKSOMEIFMEHVEELINQKISTYARNKALAD
cry1a-105.pe      100     110     120     130     140     150
                  LEGLSNLYQIYASFPNWEAEPNPPREEMRYQFNMSNALTATPILFAVQNYQVPLLS
CLID_BACTU        100     110     120     130     140     150
                  LKGLDALAVYHESLESLENNNTNTPVSKNOYIALELMEVQLPSFAVSGEVEVPLLP
cry1a-105.pe      160     170     180     190     200     210     220     230     240
                  VIVQAAHLHLSVLRDVSVFQRMGFDAAVINSKNDLTLNIGNTTHAVRMNTGLERV
CLID_BACTU        160     170     180     190     200     210     220     230     240
                  IYAAQAAHLHLLLRDASIFGKWLSSSEISTFTRQVERAGDSYFQK
cry1a-105.pe      250     260     270     280     290     300     310     320
                  GPDGRMIRYNQFRRELTIVLIVSLFPNYSRTYPIRTVSOLRENTNIGNTTHAVRM
CLID_BACTU        250     260     270     280     290     300     310     320
                  GTNAESWRVYNQFRREDTLVLDLVALFYSYDTQNYPIKTIQAQITREVSD
cry1a-105.pe      330     340     350     360
                  QGIEGSI-RSPHMLDILNLSITYDAHRGYYSWGHQINMASPVGE
CLID_BACTU        330     340     350     360
                  SFASITWYNNNAPSFTIEAAVVRNPHLLDFLEQVITYLSLSR---WSNTQYMMN---W
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cryla-105.pe	80	90	100	110	120	130
Q9F0P8	110	120	130	140	150	160
cryla-105.pe	140	150	160	170	180	190
Q9F0P8	170	180	190	200	210	220
cryla-105.pe	200	210	220	230	240	250
Q9F0P8	230	240	250	260	270	280
cryla-105.pe	260	270	280	290	300	310
Q9F0P8	290	300	310	320	330	340
cryla-105.pe	310	320	330	340	350	360
Q9F0P8	350	360	370	380	390	400
cryla-105.pe	370	380	390	400	410	420
Q9F0P8	400	410	420	430	440	450
cryla-105.pe	420	430	440	450	460	470
Q9F0P8	450	460	470	480	490	500
cryla-105.pe	480	490	500	510	520	530
Q9F0P8	500	510	520	530	540	550
cryla-105.pe	520	530	540	550	560	570
Q9F0P8	550	560	570	580	590	600
cryla-105.pe	580	590	600	610	620	630
Q9F0P8	600	610	620	630	640	650
cryla-105.pe	620	630	640	650	660	670
Q9F0P8	650	660	670	680	690	700
cryla-105.pe	660	670	680	690	700	710
Q9F0P8	700	710	720	730	740	750

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cryla-105.pe VEVLGGERTYTYTDISLUSLTQFLSEFVPGAFVGLVDIMGIFGP---SQWDAFL
                                     |||:::||:|||||
SEHESIDPTFVSASTIQTGTIGIAGKILGTGVFPFAQIASLYSLFGELMPKGKSQWEIFM
50      60      70      80      90      100
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~~Product Characterization Center~~

001
 Description: 045733 bacillus thuringiensis (subsp. tolworthi). pesticidal
 crystal protein of
 Accession/ID: 045433
 General Comments:=====

ID	CSCA_BACTO	STANDARD	PRT	1157 AA
AC	045733;			

SSCORES Initl: 702 Initn: 2140 Opt: 166 Z-score: 1854.8 E(): 2.1e-97
 >>TXNS:C9CA_BACTO
 initn: 2140 initl: 702 opt: 1686 Z-score: 1854.8 E(): 2.1e-97
 Smith-Waterman score: 2457; 38.7 identity in 1487 aa overlap
 (18-1177:59-1157)

```
SCORES      Inl1: 702          Z-score: 1854.8 E(): 2.1e-97
>>XNN:C9CA BACTO         (1157 aa)
Initn: 2140 Opt: 1666   Z-score: 1854.8 E(): 2.1e-97
Inl1: 702          Z-score: 1854.8 E(): 2.1e-97
Smith-Waterman score: 2457; 38.% identity in 187aa overlap
(18-1177:59-1157)
```

cry1a-105.pe
 MNPNPNCICPYNCLSPVEVPSFETGYNIDITLSLTQFDL
 10 20 30 40
 LASDPNALQNNYKDYLOWTDEYDTSYNPSPSISGRDASTATLVGNGANWDF
 CS9A BACTO

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30      50      60      70      80      90     100
cryla-105.pe SEFVPGAGFVLGVLDIWIWGIFGFSQWDAFLVIQLINORIEFAFNQAISRGESNLN
          :   :   :   :   :   :   :   :   :   :   :   :   :   :   :   :
C9CA_BACTO  SGQI--VSFYQPLNTLMPYNDTAIWFAIPMFQVEELYNQOOITFEAFNNALRGLGGSEF
          90    100    110    120    130    140

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	110	120	130	140	150	160
cr1a-105.pe	QIYAEFRFEADPTNPALREEMRIQFNMSALTTAIPFAVQNVPLSLVVQRAVL					
C9CA_BACTO	NYVQISQNLQADLRNDTENTLSVVRAGFIALDDFNALPFAVQGVPLSLVTAQRAVL					

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cryla-105.pe HLSVLRDVSVCQRGFGDAATINSRNDLUTRLIGNYTHAVRYNVTGLERWVGPSRDWI  
| | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
HLLLKDASIFEGWGFTQGSIPTDYDRQLELTAKNYTCYTCTWTNGTLDRLGRGNTESWL
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210      230      240      250      260      270      280
cry1a-105.pe RYNOFRRETLTVLDIVLGFNDSTYPIRVLSQLTREITYTPVLENF---GSFR---
          |||:|||||:|||||:|||||:|||||:|||||:|||||:
C9CA BACTO  RYHOFRRRETLTVLDVVALFFYDVRVLYFTGNSPOLTREYVTDPIVFNPPANGLCRWG
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C9CA_BACTO  EDS--YGLITTT---RATINGPVDGNRIESTADVDFRSALIGLYGNVRSFVPGLEN-
cryla-105.pe  FTFPLLYGTMGNAAPQRIVAQLG-QGYRTLTSTLYRPFNINN-QQLSVLDCTEAT
330          340          350          360          370          380          390

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[illegible]

cr1a-105.pe ---PMFSMIHRSAEFNMI IASDSITQIPLVKAHTLAGSTTVVVRGPGTGGDILRTSGCP
C9CA_BACTO GSUPTVWTRRDVDLANNITIPNRI TQLPVLKAPASGTVLKGPGTGGGILRTTNGT
500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe FAYIWININGOLPORYPARIRASTINRIYTVVAGERIFAQOFNKMTGDDPLTQFSF-
C9CA_BACTO FGLRTVYNSPLTOOYLVRKFASTGFNSIRLGVGSGDVLGSGTNNRQOELTVESFF
570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe -----SVATINTAFTPMGSSFTVGADTFSGNGEVIYDRFELIPVATLEAEYNLRAQ
C9CA_BACTO TREFTTGFNPFFITQAOELITVNAEGVSTUGGEYVIDRAIEIYVWPNPAREADELEAK
620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe KAVNALFTSTNGLKTNTVDYHIDVSNLVTYISDFCLDEKRELSKVAKHRLSDER
C9CA_BACTO KAVASLFTTRD-GLQVNVTDYQVQAAANVCLSDSQYGHDKMLLEAVRAAKRLRER
680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe NLLQDSNFKDINRQPERGCGSGTITQGGDDVFKENVNLTSGTDFCEPTYLYXQKIDES
C9CA_BACTO NLLQDDPFNTINSTENGKASNGVVISGGFFKGRALQASA-RENVPTYIYQKVQDAS
740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe KXWPFYQYQLGYEDSODLEIYSIRYNAKHETVNVNFGTSLWPLSAQSPICKCEPNRC
C9CA_BACTO VLKPYTNIRLNGFVKVSSODLEIDLHHKHVHLVKNVPDNL-----VSDTYSQSGSGNIR
790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe APHLNFDLDCSDRQKCAHSHHSFELDIDVCGTDLNEDLGVMVFIKFIQTQDGHARL
C9CA_BACTO DQGHQVMDQDAFTVQVCCENQTHFFSYINTGDLNASVDGIGWVLKVRTTGYATL
860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe GNLEPLEKPELDESARVYKAKKDRKRSFENINVIYKEAKESVALFVNSQYDOL
C9CA_BACTO GNLEAVEGVLGSESIREDQDNKAKMDEGRKRAIDRVTAQAQAINHLFVDYQDOOL
910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe QADTNIAHIAADKRVHSIREAYLPESQVTCVGNAMIPEREGEFTNSESIDARNVLKN
C9CA_BACTO NFEIGLAEINAEANLVYESISGVYSDTLQLQIPNYNYLTSLSDRLQRYLYISRVON
970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe GDFNNGLSCNWVKGHVDVEENORSVLVYPEVAEVSQEVLPFSGYLILYKFGY
C9CA_BACTO GDFNGLSDSNWTTMDASVQDQGNMH-FLVLSHMDAQVSQQLRVNPNKVDYRVTAKEA
1030 1040 1050 1060 1070 1080 1090 1100 1110
cr1a-105.pe GEGCVTHIEENNTDELKSNCEBEEIYNNVTCTNDITYTNQOEEYGAGIYRRNGYNAEP
C9CA_BACTO GDCYVTRDGAHQHQTETTNAC-----DYVDN-----GTYYDN-----
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cry1a-105.pe LSSTLHRRPNTGIN---NQQLSVLDGTFAIG-----TSSNLPASVVRKSGT--VDSL
AF056933_1   TSDRFYTESWAGLNLTQPVNGVPRVDFHMKFTPLFIASDFFYVLGAGVYQLQDSE
400          410          420          430          440          450
cry1a-105.pe DEIPPNNVPPROGFSHRLSHVSMFSGSNSSVSIIRAPMFWSHTRSAEPNIIASDS
420          430          440          450          460          470          480          490          500
AF056933_1   NELPPEITQPNVESYSHRLSHGLI-SG-----SHVKALVSWHTRSADETNTEPFS
460          470          480          490          500
cry1a-105.pe ITQIPLVKANTLQSGTIVVRGPGFTGDIILRTTSGGPFAYTIVNINGQLPQRYRARIYA
480          490          500          510          520          530          540          550          560          570          580          590
AF056933_1   ITQIPLVKAFNLSGAAVVRGPGFTGSHILRTKSGTFGHRVNNINPPFAQRYVRWMSYA
510          520          530          540          550          560
cry1a-105.pe STTNLRIYTVVAGERIFAGQFNKMTGDTGDLRTQFSVATINTAFTFPMSSQSFVVGADT
540          550          560          570          580          590
AF056933_1   STTDLPHTISINGKAINQNFESATPMNRGEDLDYKTRFTVGFTTFPFSQSDVSTFTIGAWN
570          580          590          600          610          620
cry1a-105.pe FSSGNEVYIDRELIPVTATLEAYNLEAKVNAALFTSTNQLGKTNVTDYHIDQVSN
600          610          620          630          640          650
AF056933_1   FSSGNEVYIGRIEYFVPEVYEAEDYFEKAQSKVTALEFSTNPRGLKTDVXDYHIDQVSN
630          640          650          660          670          680
cry1a-105.pe LVTVLSDEFCLDEKSELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITQG
660          670          680          690          700          710
AF056933_1   LVESLSDELVDLEKRELFEIVKVAQHIERNM
690          700          710
cry1a-105.pe GDDVFKENVYVLTSGTFDECYPTLYLQKIDESKLKAFTRYQLRGVIEDSQDLIYSIRYA
720          730          740          750          760          770
cry1a-105.pe
TXN5: CLIC_BACTU

Description: O87404 bacillus thuringiensis. pesticidal crystal protein c
(insecticidal
Accession/ID: O87404
=====General comments=====
ID CLIC BACTU STANDARD; PRT: 719 AA.
AC O87404; . . .

SCORES      Init1: 862      Initn: 1515      Opt: 1604      Z-score: 1767.4      E(): 1.5e-92
>>TXN5: CLIC_BACTU
Initn: 1515      Init1: 862      Opt: 1604      Z-score: 1767.4      expect(): 1.5e-92
Smith-Waterman score: 1610;      41.9% identity in 663 aa overlap
(51-683;76-719)

cry1a-105.pe VEVLGGERIETGYTPIDISLTSLSLTQFLLSEFVPGAGVGLVDIIWIGFGP---SOWDAFL
30          40          50          60          70          80          90          100
CLIC_BACTU   SEHSIDDFVSASITQTIIGTAGILGCVFPFQIQIASLVSFILGELPWKSKSOWEIFM
50          60          70          80          90          100

cry1a-105.pe VQIQLINRIEERFARNOAISREGLSNLYQIYAESFFRENEADPTNPALFREEMRIQFNMD
80          90          100          110          120          130

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1090      1100      1110      1120      1130      1140
cryla-105.pe AYTNRNGYNEAPSVADYASVYEKSYTDGRNRCPEFNRGYRDYTPLPVGYVTKLEY
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
C8CA_BACTP VLST-----DOTS-----YITTKVTF 1130
                                         1120

1150      1160      1170
cryla-105.pe FPETDKWIEIGETEGTFIVDSVELLMEE
:  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
C8CA_BACTP TPTEQWIMDMSETEGVNFVSEVELVEE 1160
                                         1140      1150

cryla-105.pep
TXNS:U04366_1

Description: U04366 Bacillus thuringiensis Bacillus thuringiensis japonensis
Buibui CryIII de
Accession/ID: U04366
=====General comments=====
LOCUS      U04366_1 [BTU04366]
DEFINITION Bacillus thuringiensis japonensis Buibui CryIII delta-endotoxin
(18-1177:59-1160)

SCORES      Initn: 503      Initn: 1400      Opt: 1542      z-score: 1695.8      E(): 1.5e-88
>>TXNS:U04366_1
      initn: 1400      initl: 503      opt: 1542      z-score: 1695.8      expect(): 1.5e-88
Smith-Waterman score: 2142;      34.8% identity in 1200 aa overlap
(18-1177:59-1160)

cryla-105.pe      10      20      30      40
U04366_1      MNNPNINCEIPYNCUSNPEVEIGGERIETGYTPIDISLSLQFL
30      40      50      60      70      80
LANDQNTNTLQNNYKDYLMKTESTNAELSRNPGTFISAQDAVGTG---IDIVTIIISGLG
110      120      130      140      150      160      170      180      190      200
cryla-105.pe      SEFVPGAGFVLGDVIWGIQFSGQ---WDAFLVQLEQLINORLEEFARNQALSLGL
30      40      50      60      70      80      90      100
U04366_1      ---IPVLGEVFSILQSLGILLNSNNENVQIFMNRVEELIDKILDSVRSRAIDLANS
110      120      130      140      150      160      170      180      190      200
cryla-105.pe      SNLYQIYAESFREWEADPTNPALEEMRIQFDMNSALTTAIPLFAVONYQVPLLSVYVQ
30      40      50      60      70      80      90      100      110      120      130      140      150      160
U04366_1      RIAVEYQNALEDKWKPHSTRSAAVLKVERFGNAEALIRTNMGSSQTNVETPLPPTAQ
110      120      130      140      150      160      170      180      190      200
cryla-105.pe      AANLHLVLRDVSFGQKWFDAATINSYNDLRLTGNTDIAVRWNTGLGRWGPDS
170      180      190      200      210      220
U04366_1      AASLLLRWDVQIVGKEWGPQNDIDLFYKEQVSYTRYARSDHCVMYNAGLNKLRTGA
210      220      230      240      250      260
cryla-105.pe      RDMVNRQFRRELTITVLIDIVSFLFPNDSRTVPYRTISQLTREIYNPVLNFDGSPR--
230      240      250      260      270      280
U04366_1      KQWVDNRFRRERNWMLDLVALFRNYDARIYPLETNAELTREIFTPDVGSVYTGOSSTL
270      280      290      300      310      320
cryla-105.pe      290      300      310      320
U04366_1      -----GSAQIGESIRSPHMLDILNSITIIDAHRG---EY--YWSGQHWASP
330      340      350      360      370      380
ISWDMIPALSPFSFTLENLRKPRDFTLLQIEIRMTYSFRQNGTEIYNNYWGQGLFTLSY
330      340      350      360      370      380

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230      240      250      260      270      280
cry1a-105.pe WIDYNGFRBELTLDIVLSIFPNYSRTPYRTSQTREIYNPV-----LENFDGSR
U04365_1      WIDYNGFRBELTLDIVLSIFPNYSRTPYRTSQTREIYNPV-----LENFDGSR
270      280      290      300      310      320
cry1a-105.pe GSAQGI-----EGSIRSPHLMILNSITIVTD-----AHRGYVMSGHQMASPGVGSPE
U04365_1      GSAQGI-----EGSIRSPHLMILNSITIVTD-----AHRGYVMSGHQMASPGVGSPE
330      340      350      360      370      380
cry1a-105.pe FTPLPYGTGNNAAPQQRIVAGLQGGVYRTLSSTL-----YRRFNGIGNNQLSVL
U04365_1      FT-QMGTGNQLQSTNF-DFTNYDIYKTLNSGAVLLDIVPGYTYTF-FGMPETEFPMV
390      400      410      420      430      440
cry1a-105.pe DGTETAYGTSSNLPASVYKSGTVDSLDELPQNNVPPROGTFSHLSHVMSFRSGFSNS
U04365_1      DGTETAYGTSSNLPASVYKSGTVDSLDELPQNNVPPROGTFSHLSHVMSFRSGFSNS
450      460      470      480      490      500
cry1a-105.pe SVSIIIRAPMFMSIHRSAEFNIIASDSITQIPLVKAHTLQSGTVVVRGPGFTGGILART
U04365_1      SVSIIIRAPMFMSIHRSAEFNIIASDSITQIPLVKAHTLQSGTVVVRGPGFTGGILART
510      520      530      540      550      560
cry1a-105.pe SG-GPAYTIVNINQLPQRVARIYASTTNRILYTVVAG-ERIFAGQNKMTGTD--
U04365_1      SG-GPAYTIVNINQLPQRVARIYASTTNRILYTVVAG-ERIFAGQNKMTGTD--
570      580      590      600      610      620
cry1a-105.pe PLTFQSFVATINTAFTFPMSS--SFTVGADTFSSGNEVVIDRFLIPVATLEAYNL
U04365_1      PLTFQSFVATINTAFTFPMSS--SFTVGADTFSSGNEVVIDRFLIPVATLEAYNL
630      640      650      660      670      680
cry1a-105.pe ERAQKAVNALFTSTNQLGLKTNVDYHIDVSNLVYLSDEFCLDEKRELSKVKHAKRL
U04365_1      ERAQKAVNALFTSTNQLGLKTNVDYHIDVSNLVYLSDEFCLDEKRELSKVKHAKRL
690      700      710      720      730      740
cry1a-105.pe SDERNLQDSNFKINRQPEKGGSGTIGQDDVFNKENYVTLSTGDF---ECYPTYL
U04365_1      SDERNLQDSNFKINRQPEKGGSGTIGQDDVFNKENYVTLSTGDF---ECYPTYL
750      760      770      780      790      800
cry1a-105.pe YQKIDESKLKATRYQLRGYIEDSQLEIYSIRYNAKHETVNVPGTSLMPLSAQSPTGK
U04365_1      YQKIDESKLKATRYQLRGYIEDSQLEIYSIRYNAKHETVNVPGTSLMPLSAQSPTGK
810      820      830      840      850      860
cry1a-105.pe YQVEGVGLKPYTRRLRGLFVGSQGLEIYTHRTNRIKVNVD--DLLP--DVPPVNN
U04365_1      YQVEGVGLKPYTRRLRGLFVGSQGLEIYTHRTNRIKVNVD--DLLP--DVPPVNN
870      880      890      900      910      920
cry1a-105.pe YQVEGVGLKPYTRRLRGLFVGSQGLEIYTHRTNRIKVNVD--DLLP--DVPPVNN
U04365_1      YQVEGVGLKPYTRRLRGLFVGSQGLEIYTHRTNRIKVNVD--DLLP--DVPPVNN
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860      870      880      890      900      910
cry1a-105.pe DGHARLGNLEFLEPGLVGEALARVYRAEKKWRDKREKLEWETNIVYKAKESVDALFN
U04365_1      DGHARLGNLEFLEPGLVGEALARVYRAEKKWRDKREKLEWETNIVYKAKESVDALFN
920      930      940      950      960      970
cry1a-105.pe SQYDQLQADNTIAMIHAAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDA
U04365_1      SQYDQLQADNTIAMIHAAADKRVHSIREAYLPELSVIPGVNAAIFEELEGRIFTAFSLYDA
980      990      1000      1010      1020      1030
cry1a-105.pe RNVIKNGDFNGLSCWNVKGVHVDVEEQNNQSRVSVLVPWEAEVSQEVVPCPGXYLRVT
U04365_1      RNVIKNGDFNGLSCWNVKGVHVDVEEQNNQSRVSVLVPWEAEVSQEVVPCPGXYLRVT
1040      1050      1060      1070      1080      1090
cry1a-105.pe AYKEGEGECVTIHEIENNTDELKFSNCVEEIIYFNNTVTCNDYTNQBEYGAITSNR
U04365_1      AYKEGEGECVTIHEIENNTDELKFSNCVEEIIYFNNTVTCNDYTNQBEYGAITSNR
1100      1110      1120      1130      1140      1150
cry1a-105.pe GYNEAPSVADYASVYEEKSYTDGGRNCPENRGVRYDTPLPVGYVTELEYFPETDKV
U04365_1      GYNEAPSVADYASVYEEKSYTDGGRNCPENRGVRYDTPLPVGYVTELEYFPETDKV
1160      1170      1180      1190      1200      1210
cry1a-105.pe WIEIGETEGTFIVDSVELLMEE
U04365_1      WIEIGETEGTFIVDSVELLMEE
1220      1230      1240      1250      1260      1270
cry1a-105.pe WIEISETGTFYIESVELIVDE
U04365_1      WIEISETGTFYIESVELIVDE
1280      1290      1300      1310      1320      1330
cry1a-105.pe WIEISETGTFYIESVELIVDE
U04365_1      WIEISETGTFYIESVELIVDE
1340      1350      1360      1370      1380      1390
cry1a-105.pe WIEISETGTFYIESVELIVDE
U04365_1      WIEISETGTFYIESVELIVDE
1400      1410      1420      1430      1440      1450
cry1a-105.pe WIEISETGTFYIESVELIVDE
U04365_1      WIEISETGTFYIESVELIVDE
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Description: Q45705 bacillus thuringiensis (subsp. kumamotoensis). pesticidal
crystal protei

Accession/ID: Q45705

ID C8BA_BACUK STANDARD; PRG; 1169 AA.

AC Q45705; . . .

SCORES Initl: 801 Initn: 2006 Opt: 1542 z-score: 1695.8 E(): 1.5e-88
>:XNS:C8BA_BACUK
initn: 2006 initl: 801 opt: 1542 z-score: 1695.8 expect(): 1.5e-88
Smith-Waterman score: 2454; 39.1% identity in 1190 aa overlap
(18-1174:59-1166)

CRY1A-105.pe MDNPNINECIPYCNLSNDEPVEVLGGERIETGYTPIDISLSLTQELL

C8BA_BACUK FANEPTNALQNDYKDYKMSAGNVSEYFGSPSEVFLSEQDAVAKAA---IDIVGKLLTGLG

CRY1A-105.pe SEFY-PGAGFVLGLVDIITWIFGFSQMDAFLVQIQELINQRIEFAFNQAISRLGLSNL

C8BA_BACUK VPFVGVISLYLTQILDILWPSKQSQWEIFMGSQVEELINQKIAEYASNKALSELEGNN

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[illegible]

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AF132928_1 ITWDVATVREMTDILVDLVATFFPYDIRRPRGVELEUTREVYTS---LDHLT-----
240 250 260 270 280
cry1a-105.pe AQSSEGISPRDILINSITVDA-HRGEVYMSGHQIMASVPVSGSGPEFTFPIYGTMG 340
AF132928_1 -----RPPGLFVLSDELFTESWEGVL-SG--IRESKV-YTGNOF-FTMKNIYG 330
320 330
cry1a-105.pe NAAPQORIWAQLOQVRSSTLHFGN-IGINNQLSLDGTTEFAYGTSSNLPASV 400
AF132928_1 NTRLSKQLITLLPCEFWTHS1-NRPFOTLAGN-KLXSLKOKNFTTFKNDNE----- 380
340 350 360 370 380 390 400
cry1a-105.pe YRKSGTVDLSLDEIPQNNVPPROG-----ESRLSHVSNRSGFSNSVSLRAPM 450
AF132928_1 YQKNFNVNQNE-POETINYPNDYGGNSOKFKHNSHPULIHKLEFAYTHSIF--A 440
390 400 410 420 430 440 450
cry1a-105.pe PSWTHSABENNIISADSITQIPLVKAHTLOSCTTVVRGPGFTGGNLLSTSGGKAYV 500
AF132928_1 LGWTHSVNSQNLISESVSTQIPLVXAYEV-TNNSVIRGPGFTGGNLLSTSGGKAYV 500
460 470 480 490 500
cry1a-105.pe VNINGQLPQRYRARIYASTNLRIYTV---AG---ERIPAGQFNKMTDGTDPITFOS 560
AF132928_1 SSL-----KKYALSIFYAANNAIAVSIDVGDGAGVLLQPTFSRKGNNFTIQD-LNYKD 550
520 530 540 550 560
cry1a-105.pe PSYATINTATFFPMQSSFT--VGNATFSSGNEVYIDRELLIPVTATLEAYNLERAAQA 620
AF132928_1 FOYHTLLVDLELPESEEIHLKREDDEYEGVILLIDKLEFKPIDENVYEMNLEKAKKA 610
570 580 590 600 610
cry1a-105.pe VNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDDEFCLDKELSEKVKHAKRLSDERNL 680
AF132928_1 VNVLFINATN-ALKMDVTDYHIDQVANLVEICISDLYAKEKIKFTPCIKFAKLSQARNL 670
620 630 640 650 660 670
cry1a-105.pe LODSNFKDINRQPERGWSGTITIQGDDVFKENVYLSGTFFDCPYTLYOKIDESKL 740
AF132928_1 LSDPNFNLN--AENSWTANTGVITIEGDPYIKRAIQLSAARDENFTYLYOXIDESLL 730
680 690 700 710 720 730
cry1a-105.pe KAFTRYQLRGVIEDSDLEIYSIRYNNAKHETVNVNPGTSGSLMPLSAQSPIGKC----- 790
AF132928_1 KPYTRYQLRGVIEGSDLELDLVRYGATDIWNVNPG--DLEILYSAPINPCIEITRLD 780
740 750 760 770 780 790
cry1a-105.pe ---GEPNRCAPHELEWNPDLDCSRGDKCAHSHHSLDIDVGTDLNEDLGVNVIPIK 850
AF132928_1 TTCGALDRCKQSNVNSAADVR---PDQVNGDPAHAFSHFDITGTTDNRNGLGIWIIKIA 840
800 810 820 830 840 850
cry1a-105.pe TQGHARLGNLEFLEKPIVNGEALARKVAKKKV-RKREKLEWNIYVYKESVDAL 910
860 870 880 890 900 910

AF132928_1 TPDVATFGNLELIELGELGSLGEALAQVORKEQKMGKNTTQKRE-EAAKLYAAAKQTINQL 850 860 870 880 890 900
cry1a-105.pe FVNSQVDLOQADTNIAMHAADKRVHSIREAYLPSELSVIICVNAAFEELEGRIETAFSL 920 930 940 950 960 970
AF132928_1 FADSOQTKLRFDFTESNLSADKLVIYKIRDVYSEVLSVIFGLNLYDFMELENRIONALIDL 910 920 930 940 950 960
cry1a-105.pe YDARNVTKGDFRNGCLSMVVKGHVDVEQNNORSVLVPEWEAEVSEVVRVCPGRGYIL 980 990 1000 1010 1020 1030
AF132928_1 YDARNVTVNGEFRNGLANWMASSNTEVR-QIOAHPCWYSLGWNAAQVAQSLNVKPDHGVVL 970 980 990 1000 1010 1020
cry1a-105.pe 1040 1050 1060 1070 1080 1090
AF132928_1 RVTAAYKEGEGCVTIHEIENNTDELKFCNVCVEEIIYPNNTVTCTNDYVNOEEYGGAYIS 1030 1040 1050 1060 1070 1080
cry1a-105.pe RVTAAYKEGEGCVTIHEIENNTDELKFCNVCVEEIIYPNNTVTCTNDYVNOEEYGGAYIS 1030 1040 1050 1060 1070 1080
AF132928_1 RVTAAYKEGEGCVTIHEIENNTDELKFCNVCVEEIIYPNNTVTCTNDYVNOEEYGGAYIS 1030 1040 1050 1060 1070 1080
cry1a-105.pe RNRGYNAPSVADVASVYEKSYTDGRNCFENRGYRDYTPLPVGVYVTKVELEVPET 1100 1110 1120 1130 1140 1150
AF132928_1 SN-----ELAA-----1070 1070 1080
cry1a-105.pe DKVWIEIGETEGTIVDSVVELLMEE 1160 1170
AF132928_1 DKVWIEIGETEGTIVDSVVELLMEE 1160 1170
cry1a-105.pe DKVWIEIGETEGTIVDSVVELLMEE 1160 1170
TXNS-CSAA_BACTF
Description: Q9X682 bacillus thuringiensis (subsp. finitimus). pesticide
crystal protein, cr
Accession/ID: Q9X682
ID CSAA_BACTF STANDARD; PRT; 1109 AA.
AC Q9X682;
=====General Comments=====
SCORES Initl: 519 Initn: 1580 Opt: 1625.5 E(): 1.2e-84
>>TXNS:CSAA_BACTF
Initn: 1580 Initl: 519 Opt: 1478 Z-score: 132.5 Expect(): 1.2e-84
Smith-Waterman score: 1884; 34.3% identity in 1204 aa overlap
(18-1177:23-1109)
cry1a-105.pe MDNNPINECPNCLNPEVVLGGERLTCGTFIDISLSTOFLLSFV-PSA 10 20 30 40 50
CSAA_BACTF NAQTYIKIGVQSTEVNSSEIFNPEVDSSTVAVVSAGIWL-VETILTA 10 20 30 40 50
cry1a-105.pe GFV-LG-LVDIIMG-I--FGPSQ-WDAFLVQIEQLINQRIEEFARNOAIS-EGNSLYO 60 70 80 90 100
CSAA_BACTF VLISFGTLAPLVNDDPEDPKTKINQFMKHGDELNLOTISTAVKETALAHNGFROLD 110 120 130 140 150 160
cry1a-105.pe YAESFREMEADPTNPALREEMRIQFDMNSALTITAIPLFAVQNVPLLSVTVQANLHL 110 120 130 140 150 160

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Q45789 RLSHVSFMRSGFNSVSIIRAPMFSWIHR
10 20 30
cryla-105.pe SAEFNNIIPSSQITQIPLVKHAHTLOSQTIVVRGPGFTGGDILRTSGGPFAYTIVNINGQ
460 470 480 490 500 510
Q45789 SAEFNNIIPSSQITQIPLVKHAHTLOSQTIVVRGPGFTGGDILRTSGGPFAYTIVNINGQ
40 50 60 70 80 90
cryla-105.pe LPQYRVRIRYASTNLRVTVVASHKFAQFPNKITQTSPLTTFQSFYATINTATFP
520 530 540 550 560 570
Q45789 LSQYRVRIRYASTNLRVTVVASHKFAQFPNKITQTSPLTTFQSFYATINTATFP
100 110 120 130 140 150
cryla-105.pe MSQSSFTVGADTFSSGNEVVIDRFELIPVATLEAEVNLERAKAVNALFTSTNOLGKLT
580 590 600 610 620 630
Q45789 NGSSVFTLSAHVFNAGNEVVIDRFELIPVATLEAEVNLERAKAVNALFTSTNOLGKLT
160 170 180 190 200 210
cryla-105.pe NVTDYHIDOVSNLVTYLSDFCLDEKRELSKVKHAKELSDERNLLQDSNFKDINROPER
640 650 660 670 680 690
Q45789 NVTDYHIDOVSNLVTYLSDFCLDEKRELSKVKHAKELSDERNLLQDSNFKDINROPER
220 230 240 250 260 270
cryla-105.pe GWGSGTGTITQGGDDVFKENYVTLGTFDECYPTLYYOKIDESKLFKAFTRYOLRGYIEDS
700 710 720 730 740 750
Q45789 GWGSGTGTITQGGDDVFKENYVTLGTFDECYPTLYYOKIDESKLFKAFTRYOLRGYIEDS
280 290
cryla-105.pe Description: M84650 synthetic construct Synthetic Bacillus thuringiensis
TXN5:M84650_1
Accession/ID: M84650
LOCUS M84650_1 (SYNCRV3ATX)
DEFINITION Synthetic Bacillus thuringiensis tenebrionis crystal toxin (Cry
Q45789 M84650_1 (SYNCRV3ATX)
DEFINITION Synthetic Bacillus thuringiensis tenebrionis crystal toxin (Cry
cryla-105.pe Scores Initl: 467 Initn: 832 Opt: 1242 z-score: 1369.1 E(): 2.4e-70
TXN5:M84650_1
>TXN5:M84650_1
Initn: 832 Initl: 467 Opt: 1242 z-score: 1369.1 expect(): 2.4e-70
Smith-Waterman score: 246; 56.6% identity in 569 aa overlap
(56-607;14-596)
cryla-105.pe CRYTGTGTIDISISGTFLLSEFVPGAGFVLGVLDIINGIFGSPQSDAFVQIEOLIN
30 40 50 60 70 80
M84650_1 TTKDVIQKGSVWEDLLGVVWVGGALNSVTYTNLTINWPSDD--WKAFMEQVEALWD
20 30 40 50 60 70
cryla-105.pe ORIEEFARNQAIISRLGSLSNVYKVAESFEVDPDT--NPADSEEMRIQFNDMSALT
90 100 110 120 130 140
M84650_1 OKIADYAKKALAELOGGNVEDWISLSSWQKQNVSSRNPHSQSIRLIFSQAESHER
80 90 100 110 120 130
cryla-105.pe TAIPLFVQNVQVPLLSVIVQANLHLSVLRDVSVEGQNGFDAA--INSRVNDLNLIGH
150 160 170 180 190 200
M84650_1 NSMPSFAISGVEYLFVLTYYAQANLHLSVLRDVSVEGQNGFDAA--INSRVNDLNLIGH
140 150 160 170 180 190
cryla-105.pe YTDHVRVYNTGLERVWGSPDSDWIRYNQFRELITVLDDIVSLFPNDSTYLRVVS
210 220 230 240 250 260
M84650_1 YTDHVRVYNTGLERVWGSPDSDWIRYNQFRELITVLDDIVSLFPNDSTYLRVVS
210 220 230 240 250 260
cryla-105.pe LTREYVYNPLV--ENFDGFRGSAQIGESIRSPHMDLNSITTYDAHGEY-----
M84650_1 LTREYVYNPLV--ENFDGFRGSAQIGESIRSPHMDLNSITTYDAHGEY-----
270 280 290 300 310

©01 Proprietary Information

Description: X16315 Bacillus thuringiensis Bacillus thuringiensis aizawai ICI
delta endotoxin

Accession/ID: X16315

LOCUS X16315_1 (BTTOXDAL)

DEFINITION Bacillus thuringiensis aizawai ICI delta endotoxin gene fragment.

SCORES Initl: 1355 Initn: 1355 Opt: 1355 z-score: 1498.4 E(): 1.5e-77
>TXN5:X16315_1
Initn: 1355 Initl: 1355 Opt: 1355 z-score: 1498.4 expect(): 1.5e-77
Smith-Waterman score: 1355; 71.7% identity in 297 aa overlap
(429-725;1-297)

cryla-105.pe AVYRKGTVDSLEIPQNNVPPRQGFHRLSHVSMFSGFNSVSIIRAPMFSWIHR
400 410 420 430 440 450
X16315_1 RLSHVSFMRSGFNSVSIIRAPMFSWIHR
10 20 30

cryla-105.pe SAEFNNIIPSSQITQIPLVKHAHTLOSQTIVVRGPGFTGGDILRTSGGPFAYTIVNINGQ
460 470 480 490 500 510
X16315_1 SAEFNNIIPSSQITQIPLVKHAHTLOSQTIVVRGPGFTGGDILRTSGGPFAYTIVNINGQ
40 50 60 70 80 90

cryla-105.pe LPQYRVRIRYASTNLRVTVVASHKFAQFPNKITQTSPLTTFQSFYATINTATFP
520 530 540 550 560 570
cryla-105.pe LPQYRVRIRYASTNLRVTVVASHKFAQFPNKITQTSPLTTFQSFYATINTATFP
520 530 540 550 560 570

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M84650_1 LTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTFRFGPGYYGNSFN
260 270 280 290 300 310

cryla-105.pe YSGHQIMASVFGSGPEFTFLYGTMGNAAPQRIVAQLGQGVYRTLSST-LYRRPFI
320 330 340 350 360 370
M84650_1 YSGNYVSTRSGSNDIITSFPYGNK-SSEPVQNLFFN-GEKYRAVANINLAWPFSV
320 330 340 350 360

cryla-105.pe --GINNQLSVL-DGTEFAYGTSSNLPSAVYKSGTV--DSLDEIPPNVNNVPRQGFH
380 390 400 410 420
M84650_1 YSGVTKEVFSQYNDQIDEA-STQYDSK--RNVGAVSWDSIDQLPPTIDEPLKGYSH
370 380 390 400 410 420

cryla-105.pe RLHSVMSRSGFSNSSVIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTV
430 440 450 460 470 480
M84650_1 QNYVMCFLMQSGRGTI-----PVLITWTKSVDFNNMDSKKITQLPLVKAYKLGSGASV
430 440 450 460 470

cryla-105.pe VRGPGFTGGDILRRTSGGPFATYIVNGLQPPQRYRARIYASTNLIYTVAGERIFA
490 500 510 520 530 540
M84650_1 VAGPRFTGGDIIOCTENGSAATYVTPDVSYQKRYARHYASTSQITFTLSLDGAPFNG
480 490 500 510 520 530

cryla-105.pe GGFNKTMDGDTLTFQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVYIDREFLIPVT
550 560 570 580 590 600
M84650_1 YYFDKTIKNGDITLYSNFLASFTPE--LSGNNLQIGVGLSAGDKVYIDKIEFIPVN
540 550 560 570 580 590

cryla-105.pe ATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLTVLSDEFCLDEKRELS
610 620 630 640 650 660

cryla-105.pep
TXN5:C3AA_BACTT

Description: P07130 bacillus thuringiensis (subsp. tenebrionis), bacillus
thuringiensis (subs
Accession/ID: P07130
ID C3AA_BACTT STANDARD; PRT; 644 AA.
AC P07130; P21255; . . .

=====General comments=====
TXN5:Q9S6N9

SCORES Initl: 467 Inltn: 832 Opt: 1242 z-score: 1368.6 E(): 2.5e-70
>>TXN5:C3AA_BACTT
Inltn: 832 Initl: 467 Opt: 1242 Z-score: 1368.6 expect(): 2.5e-70
Smith-Waterman score: 1246; 36.6% identity in 569 aa overlap
(56-607:91-643)

cryla-105.pe GERIETGYTPIDISLSLTQFLSEFVPGAGFVLGLVDIWIWIFGFSQWDAFLVQIEQLIN
30 40 50 60 70 80
C3AA_BACTT TTKDVIQKGISVVGDLGLGVVFPFGGALVSFYTNFLNTWPSEDP--WKAPMEQVEALMD
70 80 90 100 110

cryla-105.pe QRIEFARNQAIIRLEGLNLYQIYAESFREWADPT---NPALREENRIQFNQMSALT
90 100 110 120 130 140
C3AA_BACTT QKIADYAKNALAELOGLNQNVEDYVSALSSQKNPVSRRNPVSGRIRLEFSAESHFR
120 130 140 150 160 170
```

```
cryla-105.pe TAIPLFAYQVQVPLLSVVVQAANLHLSVLVDVSVFGQMGDAATINSRYNDLTRIGN
150 160 170 180 190 200
C3AA_BACTT NMPFSALSGYEVLELFTTAAQANATHFLKDAQIYGEWGEKEDIAEFYKROLKLTQE
180 190 200 210 220 230

cryla-105.pe YTDHARVYNTGLERWQSDRDWIRYNOFRRELITVLVDIVSLFPNYSRTYPIRTVSQ
210 220 230 240 250 260
C3AA_BACTT YTDHCVKYNVGLDKLGGSSYESWVNFNRVREMTLTVLDLIAFLFLYDVELYKPKVTE
240 250 260 270 280 290

cryla-105.pe LTREIYTNVL--ENFDGFRGSAQIGSIRSPHLMILNSITTYTDAHGEY-----
270 280 290 300 310
C3AA_BACTT LTRDVLTDPIVGVNNLRG-YGTTFSNIENYIRKPHLFDYLHRIQFHTFRFGPGYYGNSFN
300 310 320 330 340 350

cryla-105.pe YMSGHQIMASVFGSGPEFTFLYGTMGNAAPQRIVAQLGQGVYRTLSST-LYRRPFI
320 330 340 350 360 370
C3AA_BACTT YMSGNYVSTRSGSNDIITSFPYGNK-SSEPVQNLFFN-GEKYRAVANINLAWPFSV
360 370 380 390 400 410

cryla-105.pe --GINNQLSVL-DGTEFAYGTSSNLPSAVYKSGTV--DSLDEIPPNVNNVPRQGFH
380 390 400 410 420
C3AA_BACTT YSGVTKEVFSQYNDQIDEA-STQYDSK--RNVGAVSWDSIDQLPPTIDEPLKGYSH
420 430 440 450 460 470

cryla-105.pe RLHSVMSRSGFSNSSVIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTV
430 440 450 460 470 480
C3AA_BACTT QNYVMCFLMQSGRGTI-----PVLITWTKSVDFNNMDSKKITQLPLVKAYKLGSGASV
480 490 500 510 520 530

cryla-105.pe VRGPGFTGGDILRRTSGGPFATYIVNGLQPPQRYRARIYASTNLIYTVAGERIFA
490 500 510 520 530 540
C3AA_BACTT VAGPRFTGGDIIOCTENGSAATYVTPDVSYQKRYARHYASTSQITFTLSLDGAPFNG
530 540 550 560 570 580

cryla-105.pe GGFNKTMDGDTLTFQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVYIDREFLIPVT
550 560 570 580 590 600
C3AA_BACTT YYFDKTIKNGDITLYSNFLASFTPE--LSGNNLQIGVGLSAGDKVYIDKIEFIPVN
590 600 610 620 630 640

cryla-105.pe ATLEAEYNLERAKAVNALFTSTNQLGKTNVTDYHIDQVSNLTVLSDEFCLDEKRELS
610 620 630 640 650 660

cryla-105.pep
TXN5:Q9S6N9

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

SCORES Initl: 467 Inltn: 832 Opt: 1242 z-score: 1368.5 E(): 2.6e-70
>>TXN5:Q9S6N9
Inltn: 832 Initl: 467 Opt: 1242 Z-score: 1368.5 expect(): 2.6e-70
(652 aa)
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U04364_1 REETDRYMASNOARLYADYQOQLNPDOVEITDLTAQDLIOSIPVYNEMFPEIPGM
940 950 960 970 980 990

cry1a-105.pe WAAFELESEIPTFSLIDANIKNGDFNGLSQWYKGVHVDVEEQNORSVLVVPBW
960 970 980 990 1000 1010

U04364_1 NYTRFELSRLQOAMLDQDNALPNSDFNGLSNWNAIPGVEVQ-QINHTSVLIPNW
1000 1010 1020 1030 1040 1050

cry1a-105.pe EAEVSQEVCPGCGMLNTAYKGSFECVWTHEINNTRELKFSNCVEEIEYNNTV
1020 1030 1040 1050 1060 1070

U04364_1 DEQVSQFTVQPNQVILVLRNARGVNGVGSIRACGNSQENLPSA-
1060 1070 1080 1090 1100 1110

cry1a-105.pe TCNDVTNQEEYGAXTSRNGVNEAPSPVPAVYASVEEKS-
1080 1090 1100 1110 1120 1130

U04364_1 --SDYDTN-
1100 1110 1120 1130 1140 1150

cry1a-105.pe TPLPGVYTKLEFFPETDKVMEIGETEGFIVDSVELLMEE
1140 1150 1160 1170

U04364_1 -----GYITKTVTFIPYIDQMWIEISETEGTFYESVELIVDE
1120 1130 1140 1150

cry1a-105.pe
TXNS: C8AA_BACUK

Description: Q45704 bacillus thuringiensis (subsp. kumamotoensis). pesticial
crystal protein
Accession/ID: Q45704
ID C8AA_BACUK
AC Q45704;

=====
General comments
STANDARD; PRT; 1157 AA.
=====
Smith-Waterman score: 2564; 39.4% identity in 1211 aa overlap
(4-1174:39-1154)

SCORES Init1: 601 Initn: 1940 Opt: 1223 z-score: 1343.8 E(): 6.1e-69
>>TXNS: C8AA_BACUK
initn: 1940 init1: 601 opt: 1223 z-score: 1343.8 expect(): 6.1e-69
Smith-Waterman score: 2564; 39.4% identity in 1211 aa overlap
(4-1174:39-1154)

cry1a-105.pe
C8AA_BACUK YEIIDATPSTSVSSDSNRYPFANEPTDALQNNYKDYLMKSGENPEL--FGNPETFISS
10 20 30 40 50 60

cry1a-105.pe
C8AA_BACUK MDNPNINECIPYNCISNLEVEVLGGERIETGY
10 20 30

cry1a-105.pe TPDISLSITQLLSEF-VPCAGFVLGLVDIIWIGIFGSPQ----WDALVQLIQLINORI
40 50 60 70 80

C8AA_BACUK STIQTGIGIVGILGALGVFPASQIASFYSFVIGQLWNPFSVDIWEINERVELVDQKI
70 80 90 100 110 120

cry1a-105.pe EFARWCAISRLEGLSNLQVAYESPREMEADPTNAPLRBMRIOFNDMMNSALTAIPLF
90 100 110 120 130 140

C8AA_BACUK EKVYKALAEKLGKGNALDVQOSLEDWLENPDARTSVSVNOFTALDLNVSIIPSF
130 140 150 160 170 180

cry1a-105.pe AVQNYQVPLLSVYQAAANLHLSVLRSVDFGQWGFDAATINSRYNDLTGLIGNYTHAV
150 160 170 180 190 200

C8AA_BACUK AVSGHEVLLAVYAQAVNLHLLLEDASIFGEEMGFTPGCEISRFRNQVOLTAEYSYDCV
190 200 210 220 230 240

cry1a-105.pe RMYNTGLERWGPDSRDMIRYNQFRRELTITLVDIVSLFPNYSRTPPIRVISQLTREIY
210 220 230 240 250 260

C8AA_BACUK KWKYIGLDKLGKTTSKSNLWVHQFRREMTLLVLDLVALEPNYDTHMYPIETIAQLTRDY
250 260 270 280 290 300

cry1a-105.pe INPVLENFDGFR-----GSAQGI-----EGSIRSPHLMIDILANSITIVDAHRG-----
270 280 290 300 310

C8AA_BACUK TDPIAFINIVTSTGFCNPNWTHGILGFYEVENNVIRPFLFDILSSVEINIS--RGGITLN
310 320 330 340 350 360

cry1a-105.pe --EY--YWSGHQIMASGVGSGPFEFTFLYGTMGNAAPQORIVAQLGQGVYRTLSSTLYR
320 330 340 350 360

C8AA_BACUK NDAYINYASGHTLKYRTADSTVTVT-----ANYGRITSEKNSFALEDRIIFE-INSTVA-
370 380 390 400 410

cry1a-105.pe RPFNIGINNQOOLSVLDGTEF--AYGTSNLPSSAVYKSGTV-----DSLDEIPPN
370 380 390 400 410

C8AA_BACUK --NLANYQAYGVPGSMFHMVKRGTSIT--AYLSKTHALQOGTOVYSSDEIP-LD
420 430 440 450 460 470

cry1a-105.pe NVVPRQGFSHRLSHVSMFSGFS-NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPL
420 430 440 450 460 470

C8AA_BACUK ITVPRVRESYSHRLSHIT--SHSPSKNGSAYGVSPFVFWTHISADLANITYSDKITQIPA
480 490 500 510 520 530

cry1a-105.pe VKAHTLQSGTVVSPGFTGGDILRRTSQGPFAVTIYVINGQLPQRYRARIYASTNLRL
480 490 500 510 520 530

C8AA_BACUK VKGSMAYVSGVQGFETGGDILKRTNPSILGTFAVTVNGSLSQRYRARIYASTIDFE
540 550 560 570 580 590

cry1a-105.pe IYVTVAGEIFAGQFNYDTGDPLEQSNSTATINTAFTFPMSSQSFVAGATFFSGNE
540 550 560 570 580 590

C8AA_BACUK --FTLYLGDTFEKNFNKNTWNAFALTYETFFASNTIDFQFRETQDKILLSMGDFSSQGE
600 610 620 630 640 650

cry1a-105.pe VIIDRELPVATLAEYKREKAVQVAFNNOIGLKNVYHVIDOVSNLVTVLS
600 610 620 630 640 650

C8AA_BACUK VIIDRIEIPVDTEYAEQDLEAKRENVALLFTNIDGLRPGVTDEYVQAANLVECLS
660 670 680 690 700 710

cry1a-105.pe DEFCLDEKRESEKVKHAKRLSDERNLLQDSNFKDINPDERGNGSGTGITQGGDNVFN
660 670 680 690 700 710

C8AA_BACUK DDLYPNEKRLLFDAVREAKRLSGARNLLQDPDFQIN--GNGMNASTGMEFPAVFK
710 720 730 740 750 760

cry1a-105.pe ENYVTVSGTFD--ECYPTTYLYQKIDESKLFKAFRIQURGVIEDSOLEIYRIRNAKHE
720 730 740 750 760 770

C8AA_BACUK GRYLRLFGAREIDTETPTTYLYQKVEEGLKPYRYLRGVGSSQGLEIYTIHQDRI
770 780 790 800 810 820

cry1a-105.pe TVNYPGSGIWLPLSAQSGTIGKGFENPCAPHEWNPDLDCSRDGEKCAHSHHSFLDID
780 790 800 810 820 830

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Accession	Gene	Strain	Gene	Strain			
C3BB_BACTU	KAPFAQVEVLIDKKIEEVAKSKALAELOGLQNNFEDYNALNSWKTPISLRSKRSQDRI	110	120	130	140	150	160
cryla-105.pe	Q-FNDMNSALTTAIPLEAVQNYQVPLLSVYQAAHLHSLVLRDVSVFQORMGFAAATIN	140	150	160	170	180	190
C3BB_BACTU	RELFSQAEHSFRNSMPSFAVSKPEVLFLPTFYAAANTHLLKLLKDAQVFGEMGYSSDA	170	180	190	200	210	220
cryla-105.pe	SRYNDLTRLIGNYTHAVRWNTGLEKVMGPGSRDWIRYNOFRRELTTLVDIVLSLFPNY	200	210	220	230	240	250
C3BB_BACTU	EYFHRQLKLTQQYDHCYCNWYNGVLGRSTDAWVKNFRFEMTLTVLVDIVLFPFY	230	240	250	260	270	280
cryla-105.pe	DSRTYPIRTVSOLTRIEYTNVLE-NFDSGFRSGAQGLEGSIRPRLMDIANSITIYTD	260	270	280	290	300	310
C3BB_BACTU	DIRLYSGVKEIUTRDIIFDIFSLNTLQBYGPTFLSISSIRKPHLFDLYLOGEPHRL	290	300	310	320	330	340
cryla-105.pe	HRGEY-----YMSGHQIMASPVFGSGPEETPLVGTGTMGNAAPQORIVAGLQGVYRTLS	310	320	330	340	350	360
C3BB_BACTU	QPGYFGKDSFNYSWGNVYETAPISGSKTTITSPFYGDK-STEPYQKLSFD-GQYKVRTIA	350	360	370	380	390	400
cryla-105.pe	ST-LYRRP-----FNIGINNQQUSVLVDGTGFAYGTSNLSPAVYRKSGTV---DSLDEIPPQ	370	380	390	400	410	420
C3BB_BACTU	NTDVAAMPNGKVLYGVTKVDFSQYDDQK--NETQTQYDSKRNGHVSQAQSDIDQLPPE	410	420	430	440	450	460
cryla-105.pe	NNVVPYRQGFSEHLSHVSMERSGFSNSVSIIRAPMFWHSIRSAEENNIASDSITQIPL	420	430	440	450	460	470
C3BB_BACTU	TIDPLEKAYSHQLYAECLMQDRRGTI-----PFTWTRHSDVFNTTIDAEKIIQLDLPV	470	480	490	500	510	520
cryla-105.pe	VKANTLQSGTTVVRGPGFTGSDILR-RTSGGPFAYTVINNGQ-LPORYEARIRYASTTN	480	490	500	510	520	530
C3BB_BACTU	VKAVALLSSGASIIIEGGFTGGNLLFLKESNSIAKFKVTLNSAALLQRYRVRIRYASTTN	520	530	540	550	560	570
cryla-105.pe	LRIYTVVAGERIPAGQFNKMTDGDPTFGSPSIATINTATTFPMSSOSTGVAUTFGSG	540	550	560	570	580	590
C3BB_BACTU	LRLFLVQNSNNDFLVIYINKTNKDDDLTYQTFDLATTNSNGFGSGDKNEIILIGAESFVSN	580	590	600	610	620	630
cryla-105.pe	NEVVIDREFLIPVATLEAYENLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVTY	600	610	620	630	640	650
C3BB_BACTU	EKIYVDKIEFIPVOL	640	650				
cryla-105.pep							
TXN5:A07234_1							

Description: A07234 *Bacillus thuringiensis* B.thuringiensis (strain PGS12008)

Gene: 10/1993

Accession/ID: A07234

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

LOCUS A07234.1 [A07234]

DEFINITION: B.thuringiensis (strain PGS1208) gene. . . .

SCORES Initl: 414 Initn: 1072 Opt: 1168 z-score: 1286.8 E(): 9e-66
>>TXNS:A07234_1
Initn: 1072 Initl: 414 Opt: 1168 z-score: 1286.8 expect(): 9e-66
Smith-Waterman score: 1246; 35.4% identity in 636 aa overlap
(1-607:29-650)

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

cryIa-105.pe

A07234_1

A07234_1 ASIIEGPGTGNLLFLKESNSIAKFKVTLNSAALLQRYVRIRYASTTNLRLFVQNSN

cryIa-105.pe ERIAGOFNKMTDGTPLTFQSFYATINTAFTFPMSSQSFVAGDTFSSGNEVYIDRFE

A07234_1 NDLVIYINKTMDGLTYOTFDFATSNMCMGFGSDTNDIIGAESFVSNKXIYDKIE

cryIa-105.pe LIPVTATLAEYNLEAKVANNALFTSTNGLKINVTYDHYDIDQVSNLVTYLSDEFCLDE

A07234_1 PIPVQ

cryIa-105.pe

TXNS:C3BA_BACTO

Description: P17969 bacillus thuringiensis (subsp. tolworthi). pesticidal

Accession/ID: P17969

ID C3BA_BACTO

AC P17969;

General comments:

STANDARD; PRT: 659 AA.

SCORES Initl: 414 Initn: 1072 Opt: 1168 z-score: 1286.8 E(): 9.1e-66

>>TXNS:C3BA_BACTO

Initn: 1072 Initl: 414 Opt: 1168 z-score: 1286.8 expect(): 9.1e-66

Smith-Waterman score: 1246; 35.4% identity in 636 aa overlap

(1-607:37-658)

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

cryIa-105.pe

C3BA_BACTO

Description: U31633 Bacillus thuringiensis coleoptera-toxic protein (cry3Bb2) gene, . . .

Accession/ID: U31633

LOCUS U31633.1 BACILLUS THURINGIENSIS COLEOPTERA-TOXIC PROTEIN (CRY3BB2) GENE, . . .

DEFINITION Bacillus thuringiensis coleoptera-toxic protein (cry3Bb2) gene, . . .

SCORES Init1: 412 Initn: 1067 Opt: 1167 z-score: 1285.7 E(): 1e-65
>TXNS:U31633_1
Initn: 1067 Init1: 412 Opt: 1167 z-score: 1285.7 expect(): 1e-65
Smith-Waterman score: 1242; 36.7% identity in 580 aa overlap
(51-607:82-650)

cry1a-105.pe VEVLGGERIETGYTPIDISLSLQFLSEVPAG---FVGLVDIINGIPGSG---W

U31633_1 SSTEVLDSNVTVDAGVTGIGSVVQILGVGVFPAGALTFYQSFLDTIY---PSDADPR

cry1a-105.pe DAFVLQELQINRIEFARNQAIISRLGLNLYQIYAGSFREMDADIN-PALDEEMK
U31633_1 KAFMAQVEVLIDKKIEEYAKALAEQLQGNLFEDIVNALSKWTKPLSRSRSODRI

cry1a-105.pe Q--FNDWMSALTATPLFAVQVQVPLLSVYVQAANLHLSVLDVSFGQRMGFAATIN
U31633_1 RELFSQAESHERNSMFSFAVSKFEVLPLPTVAQAANTHLLLDQAQVGEWGYSSDDVA

cry1a-105.pe SRYNDLTILIGNYTHAVRWYNTGLERVWGPDSRDNRKYNQFRETILTVLDIVSLPNY
U31633_1 EFYRLQKLQTYTHCVWYVNVGLNGRLGSGTYDAWVKFNRFRREMTLVLDLVLFFFY

cry1a-105.pe DSTYPIRTVQSLTRELYTNPVLE-NFDGSRGSAQGEISIRSPHLMILNSITIVIDA
U31633_1 DVFLYSGKGVKIELTRDIFDPIFSNLQEQYPTFLSIENSIRKPHLFDYLOGIEFHTL

cry1a-105.pe YWSGHQIMASPVGSGPEFTFPLGYTGNAAPQQRIVAQLOQGVYRILS
U31633_1 QPVGSGKDSFNWNGVYVETRPISGSKTITSPFYGDK-STEPVQKLSFD-QQKYRTIA

cry1a-105.pe ST-LYRRP---FNIGINNQLSVLDGTEPAYCTSNLPSAVYRKSQVDSLDPEIPNNN
U31633_1 NTPVAAPNGKIYFGVTQVDFSDQYDQKNETSIQITQISKRNNHGVGAQDSIQQLPPTID

cry1a-105.pe VPRQGFSLHLSVMSFERSGFSNSSVSLIRAPMFSWIHRSAEFNIIASDITQIPLVKA
U31633_1 EPLKAYSHQNLPAECFLMQDRGTI-----PFFTWTHRSVDFTTDAEKITQLPVVKA

cry1a-105.pe HTLOSGTIVVRGPGFTGDDILR-RTSGGPAYTIVNNGQ-LPQRYARIRYASTINLRI

U31633_1 YALSSGASIIIEGPGTGCNLLFLKSSNSIAKFKVTLSAALLQVRVIRVASTINLRL

cry1a-105.pe YVTVAGERIFAGQFNKMTDGTGDLTTFOSFYATINTATFFMSOSSFTVGDATFSSGNEV
U31633_1 FVQNSNDFVIYINKTNWIDDLTYOTFDLATINSMGFGSDTNELIIGAESFVSNEKI

cry1a-105.pe YIDREFELIPVATLEAEYNLEBRAKAVNALFTTNGLGKTNVTDYHIDQVSNLVTYLS
U31633_1 YIDKIEFIPVQL

cry1a-105.pe
TXNS: CABA_BACTI

Description: P05519 bacillus thuringiensis (subsp. israelensis). pesticidal

Accession/ID: P05519

ID CABA_BACTI STANDARD; PRT; 1136 AA.

AC P05519; PI6479; PI1782;

SCORES Init1: 571 Initn: 1667 Opt: 1126 z-score: 1236.8 E(): 5.5e-63
>TXNS:CABA_BACTI
Initn: 1667 Init1: 571 Opt: 1126 z-score: 1236.8 expect(): 5.5e-63
Smith-Waterman score: 1898; 33.5% identity in 1198 aa overlap
(34(117):43-1156)

cry1a-105.pe NPNINECTPNCLENPEVEVLGGERIETGYTPIDISLSLQFLSEVPAGFVL---G
CABA_BACTI GSNAKATVADMLANENNQYGVNPAANSSSVSTALKVAGALKFVNPAGTTLVLSA

cry1a-105.pe LVDIINGVFGSG---VNAFLVQELQINRIEFARNQAIISRLGLNLYQIYAGSFRE
CABA_BACTI VLPILFNTPTSERVANDYTTIGNLIDSTYTVAVRIDANAKMTVVKDYLDQYTKENT

cry1a-105.pe WEADPTNPALREMRIOFNNKNSALT-TAIFPAVQVQVPLLSVYVQAANLHLSVLRDV
CABA_BACTI WKPEPNQSYRTAVITQFNLTSAKRENAVFSNAGVYELLPLPVAQVANFNLLIRDG

cry1a-105.pe SVFGQRMGFAATINRYNDLTILIGNYTHAVRWYNTGLERVWGPDSRDNRKYNQFRETILTVLDIVSLPNY
CABA_BACTI LINAQWLSARSAGQLYNTWVQVTEYIAHSITVYNGKSDVSNKSNQVNDYKRE

cry1a-105.pe LTLVLVDIVSLFNFVDSTYPIRTV-----SOLTREIYNTPVLENFDSFGSAQGE
CABA_BACTI MTIOVLIDIALFASVDPRYPADKIDNTKLSKTETREIYIALV-----ESPSSKATAE

cry1a-105.pe GSI-RSPHLMILNSITIVIDA-HRGEYVWSGHQIMASFPVSGPFTFPLFYTGMAAP

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C4BA_BACTI AALTRDVHLFTWKLKRVDFWNTIYQDLRELSANKIGFSYNTSSAMQES-GIYGSSGFGSN
310 320 330 340 350 360
cry1a-105.pe QQRIVAAQGGVYTLSTLYRFPNIGINNOQLSGVDGTFEYAGTS-SNLFSAVYRKS
350 360 370 380 390 400
C4BA_BACTI LTHQI-QLNSNVYK-SITDTSFNS-RVTGMDFKTGDLTGLASYNISNITPTPEGI-RTTF
370 380 390 400 410 420
cry1a-105.pe TVDSLETPQNNVPPROGFSRHLRSHVSMFSGFSSNSVSIIRAPMFWIHRSEFNII
410 420 430 440 450 460
C4BA_BACTI FGSINENTP--NOPTVNDYTHILSYIKTDVIDYNSNRVS-----FAWTHKIVDPNNQ
430 440 450 460 470
cry1a-105.pe IASDSITQIPLVKAHTLQSGTIVVRGFTGGDILRRTSGGPFAYTI-VNINGQL---PQ
470 480 490 500 510 520
C4BA_BACTI IYDAITQVPAKSNFLNATAKVIKGFHTGGDLVALTSNGTSLGRMEIOCKTSIFNDPT
480 490 500 510 520 530
cry1a-105.pe R-YRARIPTASTNIRIYVAGERIFACQFNKMTD-GDP-----LTFQSFYATIN
530 540 550 560 570
C4BA_BACTI RSYGLRIYAANSPIVLNVSVLQGVSRGTITSTESTFSRPNIIPTDLKYEFPYKDPF
540 550 560 570 580 590
cry1a-105.pe TATFFPMOSS---FTVGADTF--SSGNEVYIDRELIPIVATL--EAB-VNLEBAOKAV
580 590 600 610 620
C4BA_BACTI DAIV-PMRLSSNQILITAIQPLNMTSNQVIIDRIEIIPIITQSVLDETENQLESEREV
600 610 620 630 640 650
cry1a-105.pe NALFTSTNOLGKNTVDYHIDQVSNLTVLSDFCLDEKRELSKVKHAKLSERNLL
630 640 650 660 670 680
C4BA_BACTI NALFTNDKDALNGTIDYDIDQANLVECISEELYPKMKMLLDLVEKNAQLSGSRNL
660 670 680 690 700 710
cry1a-105.pe QDSNFKDINRQPERGWSGTITIQSGDDVFKENVTLTGTFD---ECYPTVLYOKIDES
690 700 710 720 730 740
C4BA_BACTI QNGDFESATL---GWTSNDITIQEDDPIFKGHLHMSGARDIDGTIPTTPIFOKIDES
720 730 740 750 760
cry1a-105.pe KLAFFRYQLRGYIEDSQDLEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPN
750 760 770 780 790
C4BA_BACTI KLPFTYRLVLRGFGSSKDVLEVVSRYGEEIDAINVPADNLVLYSTFD-----CEGSN
770 780 790 800 810 820
cry1a-105.pe RC-----AP-HLEWFPDLDCSR--DGEK---CAHSHHFSLDIDVCGTDLNEDLGVWVIF
800 810 820 830 840
C4BA_BACTI RCTSAVPANIGNTSDMLYSQYDTGCKHVVC-QDSHQFSGFTIDTGALDNTENIGVWYMF
830 840 850 860 870 880
cry1a-105.pe KIKTOGHARLGNLEFLEKPLVGEALARYKAEKWKEDKKEKLEWETNIVYKEAKESVD
850 860 870 880 890 900
C4BA_BACTI KISSPDGASLNLNLEVEIEGPDIGDEALSRVHKMEKMNWDQMEAKRSETQQAQYDVAKAID
890 900 910 920 930 940
cry1a-105.pe ALFVNSQYDQLQADNTIAMIHAAQKRVHSIRAYLPESLVTGPGVNAIIEEGRIFTAF
910 920 930 940 950 960

C4BA_BACTI ALFTNVQDEALQFDTLLAQIYAEYLQSIPIYVNDMLSDVPGMNYDIYVELDARVAQAR
950 960 970 980 990 1000
cry1a-105.pe SLYDARNVTKGDFNGLSCWNYKHVDVVEEQNNQSRSLVVPPEAEVSEQVYRCPGRGY
970 980 990 1000 1010 1020
C4BA_BACTI YLDTYRNIKNGDFTQGVGMGHVYTGNAVQ-QIDGVSVLVLSNWSAGVSQNVHLQHNGY
1010 1020 1030 1040 1050 1060
cry1a-105.pe ILRVTAKEGVEGCVTHIEIENNTDELAFNSCVHEEILYPNNTVTCNDYTVNQBEYGGAY
1030 1040 1050 1060 1070 1080
C4BA_BACTI VLRVIARKEGPGNGYVLMDCENQEKLTFTSCEE-----
1070 1080 1090
cry1a-105.pe TSNRNGYNEAPSPADVASVVEEKSVTDGRRNCPENRGYRDTPLPVGYVYTKLEYFP
1090 1100 1110 1120 1130 1140
C4BA_BACTI -----GYITKIVDVFP
1100
cry1a-105.pe ETOKVWIEIGETEGTFIVDSVELLMEE
1150 1160 1170
C4BA_BACTI DTDVRIEIGETEGSFVIESIELICMNE
1110 1120 1130
Description: X07423 Bacillus thuringiensis israelensis
bt8 gene for 13
Accession/ID: X07423
=====General comments=====

LOCUS X07423.1 [BTTOXD2]
DEFINITION Bacillus thuringiensis israelensis bt8 gene for 130 kDa crystal . . .

SCORES Init1: 571 Initn: 1667 Opt: 1126 Z-score: 1236.8 E(): 5.5e-63
>>TXNS:X07423.1
Initn: 1667 Init1: 571 opt: 1126 Z-score: 1236.8 expect(): 5.5e-63
Smith-Waterman score: 1898; 33.5% identity in 1198 aa overlap
(34-1177:43-1136)

cry1a-105.pe NPINCEIPYNCLSNPVEVLGGERETGCTPIDISLSLTQFLLEFPVAGFVL---G
10 20 30 40 50
X07423.1 GSMKNTNYKDLAMCENNQYGVNPAINSVSTALKVAGAILKFWNPAGTIVTLVLSA
20 30 40 50 60 70
cry1a-105.pe LVDIWIGIFGSPQ--WDAFVIEQIQLINQRIEFPARNQAIISRLGLSLNLYQIYAESFRE
60 70 80 90 100 110
X07423.1 VLPILMPTTPTPERVWVNDFTNTGNLIDQTVAYVRTDANAKMTVVKDYLDQYTTKENT
80 90 100 110 120 130
cry1a-105.pe WEADPTNPALREERNRIQNDMNSALT-TAIPFAVQNYQVPLISVYVQANLHLSLRDV
120 130 140 150 160 170
X07423.1 WKPEPNQSYRTAVITQFNLTSAKRETAIVYFNSVYELLPLFIYAQVAFNELLIRDG
140 150 160 170 180 190
cry1a-105.pe SVFGQWGFDAATINRSYNDLTLIGNYTHAVRWYNTGLERVWGPDSRDWIRYNQFRRE
180 190 200 210 220 230

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X07423_1  LINAQWLSAAGAGQOLYNTMVQYTKYIAHSITWNKGLDVLANKNGOWITFNDYKRE
200 210 220 230 240 250
cry1a-105.pe  LIAVLDISGQVDSRYAIPN-----SOLTRFYNPVLENDGSRGSAQIE
260 270 280
X07423_1  MTISGLSLALFAP  QPRVPADKIDWTKSKTEFRIEYIALV-----ESPSSKSIATALE
290 300
cry1a-105.pe  GSI-RSPHLDIILGIIITVDA-HRSGYGHQIQINSPGSGPEFTFLYTGMAAP
310 320 330 340
X07423_1  AALTRDVHLEFTLWKRVDFPNTNMODLRASANKGFSYTNSSAOKES-GIYSSSGFGSN
350 360 370 380 390 400
cry1a-105.pe  QQRIVAQLOGCVIRTLSSLYRRPNIGINNOLSVLDGTFAYGTS-SNLSRANRKSQ
410 420 430 440 450 460 470 480
X07423_1  LTHQI-QLNSNYKT-SITDTSSPN-RVTMDP-KTNGTILASYNIPYIPEGL-RYTP
490 500 510 520 530
cry1a-105.pe  TVDSDEIPQNNVNPFGFSGHRLSHVSMRSGFNSVSIIRPMPFWHRSEFPA
540 550 560 570 580 590
X07423_1  FQFSINENTP---NQPTVNDYTHILSYIKTDVYDYNRVS-----FANTHSVDPNNO
600 610 620 630 640 650
cry1a-105.pe  IASDSITQIPVLAHTLQSGTIVRGPGFTGGDLIRTSGGFPAYTI-VNINGOL---PC
660 670 680 690 700 710
X07423_1  IYTDATITQVPAKSNFLNATAKIVKPGHGTGGDLVALTSNGTSLGRMEIQCKTIFNDPT
720 730 740 750 760 770
cry1a-105.pe  R-YRARIYASTNLRIVTVAGERIFAGQFNKMDT-GDP-----LTFQSPSYATIN
780 790 800 810 820 830 840
X07423_1  RSYGRIRYAANSPIVLNVSIVLQVSRGTTISTESTFSRPNNIIFTDLKVEERYKDPF
850 860 870 880 890 900 910
cry1a-105.pe  TAFTEPMSQSS---FTVGADTF--SSGNEVIDRFELIPVTATL--EAF-YNLERAQAV
920 930 940 950 960 970 980
X07423_1  DAIV-PMRLSSNQLITIAIQPLNMTSNNOVIIDRIEIIPIITQSVLDETENQNLSEREV
990 1000 1010 1020 1030 1040 1050
cry1a-105.pe  NALFTSTNQLGKNTVDIHDQVSNLVTYLSDFCLDEKRELSKVKHAKLSERNLL
1060 1070 1080 1090 1100 1110
X07423_1  NALFTNDKADALNTGTYDIDQAAALVECISEELYPERKMLLLDEKVNKAKLSRSNVL
1120 1130 1140 1150 1160 1170
cry1a-105.pe  QDSNFKDINRQPERGWSGTGTTIQGGDDVDFKENYVTLSGTFD---ECPTYLYQKIDES
1180 1190 1200 1210 1220 1230 1240
X07423_1  QNGDFESATL-----GWTTSNIIQEDDPIFKGHVYHMSGARDIDGTIPTPIVIFQKIDES
1250 1260 1270 1280 1290 1300 1310
cry1a-105.pe  KLAFTRYOLRGYIEDSQDLIEYSIRYNAKHETV-NVFGT-GSLWPLSAQSPFGKCGEPN
1320 1330 1340 1350 1360 1370 1380
X07423_1  KLAFTRYLVRGVGSSKDVSLVSRVYGEIDAIIMNVPADLNYLPSTFD-----CEGSN
1390 1400 1410 1420 1430 1440 1450
cry1a-105.pe  RC-----AP-HLEWNPDLDCSR--DGEK---CAHSHHFSDDIDVGCITDLNEDLGVWVIF
1460 1470 1480 1490 1500 1510 1520
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X07423_1  RCETSAVPANIGNTSMLYSQYDTGKKHVVC-QDSHQFSFTIDTGDALTNENIGVWVWF
830 840 850 860 870 880
cry1a-105.pe  KIKTODGHARLGNLEFLBEKPLVGEALARKVGAEKKWKREKLEWETNIYVYKEAESVD
890 900 910 920 930 940
X07423_1  KISSPDGYASLDNLEVEIEGPIDEGALSRYKHMEKWKMDQMEAKRSETQOAYVAKQALD
950 960 970 980 990 1000
cry1a-105.pe  ALFVNSQYDQLOQADNIAMIRHAAKRVHSIREAYLPELSVIPGVNAAIIFEELEGRIFTAF
1010 1020 1030 1040 1050 1060
X07423_1  ALFTNVODEALQDFDITLAIQVAYLYVQSIPYVYNDWLSDFPGMNYDIYVELDARVAQAR
1070 1080 1090 1100 1110 1120
cry1a-105.pe  SLYDARNVIRKNGDFNGLSCMNVKGVHDVEEQNNQSRSLVLPPEWAEVSEVRVCPGRGY
1130 1140 1150 1160 1170 1180
X07423_1  VLYDTRNIIKNGDFTQGVGMHVTGNADVQ-QIDGVSIVLVLSNSAGVSQNVHLQHNHY
1190 1200 1210 1220 1230 1240
cry1a-105.pe  ILRVYAKREGGEGCVTTHIEINWTDLXKSNVVEEIIYPNNVTICNDYTVNQVEYGGAY
1250 1260 1270 1280 1290 1300
X07423_1  VLRVIAKKEGPGNGYVTLMDCEENQEKLTFTSCEE-----
1310 1320 1330 1340 1350 1360
cry1a-105.pe  TSNRGYNAPSPADVASVYEKSYTDGRRNCFENRGYRDYTPLEGVYVTKLEYFP
1370 1380 1390 1400 1410 1420
X07423_1  DVAWRVRSYSGTESGTFYSIELICMNE-----GVITKTVDFP
1430 1440 1450 1460 1470 1480
cry1a-105.pe  ETDKWIETSETGTFIVDSVELLMEE-----
1490 1500 1510 1520 1530 1540
X07423_1  DVAWRVRSYSGTESGTFYSIELICMNE-----GVITKTVDFP
1550 1560 1570 1580 1590 1600
cry1a-105.pep
TXN5:X07082_1
Description: X07082 Bacillus thuringiensis Bacillus thuringiensis gene for 130
kDa delta-endo
Accession/ID: X07082
LOCUS X07082.1 (BTITOX)
DEFINITION Bacillus thuringiensis gene for 130 kDa delta-endo toxin;
=====General comment=====
SCORES Initl: 571 Initn: 1666 Opt: 1126 Z-score: 123.6 E(1) 5.6e-63
>>TXN5:X07082_1
Initn: 1666 Initl: 571 Opt: 1126 Z-score: 1236.8 expect(1) 5.6e-63
Smith-Waterman score: 1897; 33.5% identity in 1194 aa overlap
(34-1177:43-1136)
cry1a-105.pe NPAINCIPYNCLSNPVEVLGGRIETGVTPIDISLSLTQFLISFVSRGMLN---G
10 20 30 40 50 60 70 80 90 100 110
X07082_1 GSMKNTNYKDLAMCENNOQYGVNPAINSVSSVSTALVAGAILLKFNPPAGTIVAVSA
20 30 40 50 60 70 80 90 100 110
cry1a-105.pe LVDIWIGIFGSPQ---WDAFLVQIEQLINQRIEERFARNQALREGLSNLYQIYAESPRE
60 70 80 90 100 110
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X07082_1  VLPILPMTPTPTPERVWDFMTNTGNLIDQITVAVRTDANAKMTVVVKYLDQYTKENT
80 90 100 110 120 130
120 130 140 150 160 170
cry1a-105.pe WEADTPNALREERIRIENDNSALT-TAIPFAVQNVPLSVVVOANLHLVLSDV
120 130 140 150 160 170
X07082_1 WKREPNQSYRTAVTQFNLTSAKRETAVFSNVLGVVELLLPITIAQVANFNLLIIDG
140 150 160 170 180 190
180 190 200 210 220 230
cry1a-105.pe SVFGQWGFDAATINSRYNDLTRIGNYTHAVRWYNTGLERVMGPDSDWIRYQPRRE
180 190 200 210 220 230
X07082_1 LINAQWLSLRSGDOLYNTMWQYTKETIAHSITWYKNGLDVLRNKSNGQWITFNDYERE
200 210 220 230 240 250
240 250 260 270 280 290
cry1a-105.pe LTLVLDIVLSPNDSTYPIRTV-----SOLTREIYTNPVLENFDSFRGSAOGIE
240 250 260 270 280 290
X07082_1 MTIQVLDIILFASVDPRIYPADKIDNTKLSKTEPTREIYALV---ESPSSKIAALE
260 270 280 290 300 310
290 300 310 320 330 340
cry1a-105.pe GSI-RSPHMDLISITIIYDA-HRGEYYWMSHOIMASPVGFSPEFTFLYGTWGNAP
290 300 310 320 330 340
X07082_1 AALTRDVHLFTWLKRVDFWNTIYQDLRFSLANKIGFSYNSSAMQES-GIYGSGPGSN
310 320 330 340 350 360
350 360 370 380 390 400
cry1a-105.pe QQRIVAQCGGYRTLSLTYRRPFNIGINNOQLSVLDGTEFAYGTS-SNLPSAVYKSG
350 360 370 380 390 400
X07082_1 LTHQI-OLNSNVYKT-SITDTSPSN-RVTKMDFKIDGTLASVNSNIPTPEGI-RTTF
370 380 390 400 410 420
410 420 430 440 450 460
cry1a-105.pe TVDSLEIPQNNVPFQGFSLHVSFMRSGFSNSVSIIRAPMFSWIRHSAEFNNI
410 420 430 440 450 460
X07082_1 FGSTENETP---NQPTVNDYTHILSYIKTIDVIDNSNRVS-----FAMTHKIYDPNNQ
430 440 450 460 470 480
470 480 490 500 510 520
cry1a-105.pe IASDSITQIPLVKAHTLQSGTIVVRGFTGGDILRRTSGGPFAYTI-VNINGQL---PQ
470 480 490 500 510 520
X07082_1 IYTDALTQVPAVKSNFLNATAKVIKGFHTGSDVALTSNGTSLGRMEIQCKTISIFNDPT
480 490 500 510 520 530
530 540 550 560 570 580
cry1a-105.pe R-YRARIYASTNIRIYTVAGERIFAQENKTMDT-GDP-----LTFQSFYATIN
530 540 550 560 570 580
X07082_1 RSYGLRIYAANSPIVLNVSVLQGVSRGTITISTESTFSRPNIIIPDLKLYEYFRYKDPF
540 550 560 570 580 590
590 600 610 620 630 640
cry1a-105.pe TATFFPMSSQSS---FTVGADTF---SSGNEVYIDRELPITVATIL---EAE-YNLERAQAV
590 600 610 620 630 640
X07082_1 DAIV-PMRLSSNQIITIAQIPLMNNSNOVIIDRIETIIPQSVLDETENQLESEREV
600 610 620 630 640 650
650 660 670 680 690 700
cry1a-105.pe NALFTSTNOLGKTNVTDYHDQVSNLVTYLSDFCLDEKHELSKHKAKLSERNLL
650 660 670 680 690 700
X07082_1 NALFTNDKDALNTGTTDYIDQANLVCEISEELYPKEXMLLDEVKNAKQLSQRNL
660 670 680 690 700 710
710 720 730 740 750 760
cry1a-105.pe QDSNFKDINRPERGWGSGTIGTIQGGDDVFKENYVTLSGTFD---ECPTYLYQKIDES
710 720 730 740 750 760
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X07082_1  QNGDFESATL-----CWTTSNITIQEDDPIFKGHYLHMSGARDIDGTIPTVIFQKIDES
720 730 740 750 760
750 760 770 780 790 800
cry1a-105.pe KLAFTRIYQLRGYIEDSDDEIYSIRYNAKHETV-NVPGT-GSLWPLSAQSPIGKCGEPN
750 760 770 780 790 800
X07082_1 KLAFTRIYVRGFGSSKDEIVLVSRYGEEIDAIMNVVPADINLYPSTFD-----CEGSN
770 780 790 800 810 820
800 810 820 830 840 850
cry1a-105.pe RC---AP-HLEWNPDLDCSCR--DGEK---CAHSHHFSLDIDVGCTDLNEDLGVWVIF
800 810 820 830 840 850
X07082_1 RCETSAPVANTIGNTSDMLYSCQYDTGKKHVVC-QDSHQFSETIDTGALDTNENIGVWVWF
830 840 850 860 870 880
850 860 870 880 890 900
cry1a-105.pe KIXTQDGHARLGNLEFLEKPLVGEALRVKAEKKMKDKREKLEWETINIVYKEAKESVD
850 860 870 880 890 900
X07082_1 KISSPGVASLDNLEVEIEGPIGDEALSRVKHMEKKWQNDQMEAKRSETQOAYDVAKQAID
890 900 910 920 930 940
910 920 930 940 950 960
cry1a-105.pe ALFVNSQYDQLQADNTIAMHRAADKRVHSIREAYLPESLVIPGVNAAIFFEELEGRIFTAF
910 920 930 940 950 960
X07082_1 ALFTNVQDEALQDFTTLAQIQYAEYLVQSIPYVNDWLSDVPGMNWYDIYVELDRAVAQAR
950 960 970 980 990 1000
970 980 990 1000 1010 1020
cry1a-105.pe SLYDANRVTKNGDFNGLSCWNVKGVHDVVEEQNNORSVLVVPWEAEVSCVEVRVCPGRGY
970 980 990 1000 1010 1020
X07082_1 YLVDYTNLIKNGDFTQGVGMGHVHTGNADVQ-QIDGVSVLVLSNWSAGVSNVHLQHNHY
1010 1020 1030 1040 1050 1060
1030 1040 1050 1060 1070 1080
cry1a-105.pe ILRVATYKEGYGEGCVTIEHENTDELKFSNCVEEIIYPNNTVTCNDYTVNQEEYGGAY
1030 1040 1050 1060 1070 1080
X07082_1 VLRVIARKEGPGNGVITLMDCENQEKLTFTSCEE-----
1070 1080 1090
1090 1100 1110 1120 1130 1140
cry1a-105.pe TSNRCYNEAPSVPADYASVYEKSYTDGRNCPCEFNRGYRDYTPLPVGYVTKLEYFP
1090 1100 1110 1120 1130 1140
X07082_1 -----GYITKTVDFVP
-----1100
1150 1160 1170
cry1a-105.pe ETDKVWIEIGETEGTIVDSVELLMEE
1150 1160 1170
X07082_1 DTDVRVIEIGETEGSFYIESIELICMNE
1110 1120 1130 1140
1150 1160 1170
cry1a-105.pe
1150 1160 1170
TXN5:C4AA_BACTI
Accession/ID: P16480
Description: P16480 bacillus thuringiensis (subsp. israelensis). pesticidal
crystal protein
Accession/ID: P16480
ID C4AA_BACTI STANDARD; PRT; 1180 AA.
AC P16480; . . .
Scores Initl: 571 Initn: 1577 Opt: 1088 Z-score: 1194.6 E(): 1.2e-60
>>TXN5:C4AA_BACTI
Initn: 1577 Initl: 571 Opt: 1088 Z-score: 1194.6 expect(): 1.2e-60
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Description: Y00423 Bacillus thuringiensis Bacillus thuringiensis gene for 130 kDa delta-endo.

Accession/ID: Y00423

LOCUS Y00423.1 [BTOXD1]

DEFINITION Bacillus thuringiensis gene for 130 kDa delta-endotoxin; . . .

SCORES Init1: 570 Initn: 1551 Opt: 1076 Z-score: 1181.4 E(): 6.8e-60
>TXN5.Y00423.1
initn: 1551 Init1: 570 opt: 1076 Z-score: 1181.4 expect(): 6.8e-60
Smith-Waterman score: 1725; 33.3% identity in 1213 aa overlap
(40-1177:70-1180)

cry1a-105.pe CIPYNGLSNPEVGLGRIETGYTPIDISLSLQFLSEFVPGAGV--LGLVDIIMG-
Y00423_1 QSTNYKDWLNWCQNOQYGGDFETFDISGELSAVTIVGVLTGFGFTPLGLALIGFT
40 50 60 70 80 90

cry1a-105.pe ---IFGPGQ-----WDAFLVQIEQLINQRIEFARNQAISELGLSLNLYQIYAESFREWE
Y00423_1 LIPVLFPAGQDSNTWSDFITQTKNIIRKELASTYISNANKILARSFNVISYVHNLKTWE
100 110 120 130 140 150

cry1a-105.pe ADPTNPALEEMRIQFMDNSALTTPAIPFA-----VQNYQVPLSVVVOAANLHL
Y00423_1 NNP-NPQNTQDVRTQIQLVHYHFQNVPELVNSCPPNPSPDCDYNNILVLSVAQANLHL
160 170 180 190 200 210

cry1a-105.pe SVLRDVSVP---GQRMGFDA---ATINSRYNDLTRIGNYTDHVRWYNTGLERVWG-
Y00423_1 TVLNQAVFEAYLNKRNQFDYLEPLTAIDYVPLTKAIEDYNYCVITYKGLNLKTT
220 230 240 250 260 270

cry1a-105.pe PDSR-----DMIRYNQFRRELTITVLIDVSLFPAYDSRTYPIETVSQLTREIYNPVLN
Y00423_1 PDSNLDGINWNTYRTKMTTAVLDVVVLPFNVDVGKPIGVQSELREIYQ--VL-N
280 290 300 310 320 330

cry1a-105.pe FDGS-FRG-SAQGLEGI-RSPHMDILNSITIIDAHRG-EYYWGHQIMASPVGFSGP
Y00423_1 FEESPKYVDYQYQEDSLTRRPHLFTWLDLNFYKCAQTPPNFFTSYNNPHYT-LDNI
340 350 360 370 380 390

cry1a-105.pe EFTFPLXGTMNAPQORIQAQCGVYRTLSSTL-----YRPFNIGINQQSLVDGT
Y00423_1 SQKSSVFGNH-NVTDKLSLG-LATNIYIFLLNVLISLDNLYLNDYN-NISKMDFFITNGI
400 410 420 430 440 450

cry1a-105.pe -----EPFAYGTSNLPRAVYKSGTVDSLSDEIIPPONNV--PRQGFSLHSHVSPFSG
Y00423_1 RLLEKELTAG-SQQTIDYDNKNIIFGLPKRRENGQNPFTFPYDNYLSL-----FLKS
460 470 480 490 500 510

cry1a-105.pe FSNSSYSIIRAPMFSWIHRGAEFNNIIASDSITQIPLVKAHTQSGTVVRGPGFTGGDI
440 450 460 470 480 490

Y00423_1 LSPATYKTKQVYTFEAWTHSSVDPKNTIVTLTTLQIPAVKANSGLTASKVVOGPGHTGDDL
510 520 530 540 550 560

cry1a-105.pe LARTSGGPATIVNINGQLPQRYRARIYAS--TTNLR--IYTVVAGERIPAGQFNKTM
Y00423_1 IDPKDH--FKITQHSNFQ--QSYFIRIRYASNGSANTRAVINLSIPGVAGELMALNPTF
570 580 590 600 610 620

cry1a-105.pe DTGCD-PLTFOSFAYATINTAFTF-PMSSQSFVAGADTFSSGNEVYIDREFELIPVTATLE
Y00423_1 SGTDTNLYKXDFQYLFESNEVKFAPNQNI SLVFNRSDDVYNTVTLIDKLELPIRSIR
630 640 650 660 670 680

cry1a-105.pe AEY---NLERAQKAVNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSE
Y00423_1 EDREKQKLETQQIINTFYANPKNTLQSELTVDYIDQAAANLVECISEELYPKEMKLILD
690 700 710 720 730 740

cry1a-105.pe KYKXAKRLSDERNLQDSNFKINRQPECGSGTGITIQGGDDVFEKENVYLSGTFP--
Y00423_1 EVNAKQLSQSRNVLQNGDPESATL-----GWTSDNITIQEDDPIFKGHLHMSGARDID
750 760 770 780 790

cry1a-105.pe -ECYPTLYKIDESKLKAPRYOLRGYIEDSOOLEIYSIRYNAKHETV-NVPGT-GSLW
Y00423_1 GTIFTFYIFKIDESKLKAPRYLVLRGFGVSGSKDVELVRSRYGEEIDA LNNVPADLNVLY
800 810 820 830 840 850

cry1a-105.pe PLSAOSPIGKCGEPNRC-----AP-HLEWNPDDDCSR--DGEK---CAHSHHFSLDIDV
Y00423_1 PSTFD-----CEGSNRCETSAPVANIGNTSDMLYSQQVDYTGKHHVC-QDSHQFSTTIDT
860 870 880 890 900 910

cry1a-105.pe GCTDNLDELGVVVFVKIKTODGCHARLGNLFLEKPLVGEALARVKAERKWRDREKLE
Y00423_1 GALTNNENIGVWVWFKISSPDGVSASLDNLEVEIEGPDIGEALSrvKHEKKNWQDMEAKR
920 930 940 950 960 970

cry1a-105.pe WETNIVYKEAKESVDALFVNSQDQLOADTNMIAMHAAKRVHSIREAYLPELSVIPGVN
Y00423_1 SETQQAAYDVAKAIDALFTNVQDEALQFTTLAQIOVAEVLVQSIPIVYNDLWSLDPVGMN
980 990 1000 1010 1020 1030

cry1a-105.pe AALIFELEGRIPTAFSLYDARNVKNKGNLSCWNVKGVHDVEEQNNQSRSLVLPVEWE
Y00423_1 YDIYVELDARVAQARYLYDIRNIKNKGDFTQGVWGMGHVHTGNADVQ-QIDGVSLVLSNWS
1040 1050 1060 1070 1080 1090

cry1a-105.pe AEYSQSVRVCPGRGYLLRYTAYKEGYGECGVTHIEHNNTDELKFSNCVEEIIYFNNTVT
Y00423_1 AGVSQNVHLQHNHGYLVGLVIAKKEGGNGYVTLMDWEENKEKLTFTTSCIE-----
1100 1110 1120 1130 1140

cry1a-105.pe CNDYTVNQBEYGGAYTSRRNGYNEAPSVADYASVVEEKSYSYDGRRENPCFNRGYDYT
1080 1090 1100 1110 1120 1130

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Smith-Waterman score: 1070; 33.4% identity in 572 aa overlap
(56-607:89-648)

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cryla-105.pe GERIEGYTPIDISLSLTQFLSEFVGAGFVLGVDIIVGIFGSPQDAFLVQAEQLIN
30      40      50      60      70      80
C3CA_BACTK TTDAIQKGISIIIGLLGWGVGFPYGALVSFYTNLLNTIP--GEDPLKAFMQQVEALID
60      70      80      90      100      110

cryla-105.pe ORIEEFARNOAIRLEGLSNLYQIYAESFREWEADP--TNPALREERIQ--FNDMNASALT
90      100      110      120      130      140
C3CA_BACTK OKLADYAKDKATAEIQGLKNVFDYVSALDSWDKTFPLTRDGSQSQRIRIELFESQAESHFR
120      130      140      150      160      170

cryla-105.pe TAPLEAVNQYVPLLSVYQAAHLHLSVLRVDSVFGQMGFDAATINSEYNDLTRLLGN
150      160      170      180      190      200
C3CA_BACTK RSMPSFAVSGYEVLFYTAQAANTHLLLDKDAQIYGTDMGYSFTDLLNEFHTKQKDLTIE
180      190      200      210      220      230

cryla-105.pe YTHDAVRWNTGLERVMPGSDRWIRYNOFRBELFTLVLDIVSLFYNYSRTYPIRTVSO
210      220      230      240      250      260
C3CA_BACTK YTHNCAKWKYAGLKKLRGSIVSEWVAFNREYREMTLVLDLITLFLDYDVRVYTKGVKTE
240      250      260      270      280      290

cryla-105.pe LTRIETNPV--LENFDGSRGAQIEGRISRPHLMDLINSITIYTDHAHGEY-----
270      280      290      300      310
C3CA_BACTK LTRDVLTDPIVANNMNG--YGTFTSNIENYIRKPHLPDYLHATQFHSRLPGQYGYTDSFN
300      310      320      330      340      350

cryla-105.pe YWGHQIMA-SPVPGSGPEFTFLYGTGMNAAPOQIRVIAQGGQVIRTLSS--TLVRRFPFN
320      330      340      350      360      370
C3CA_BACTK YWGNVYSTRSIG-SDEIIRSPFYGNKSTLDVQN--LEFNKGKVFRAVANGLAIVPVG
360      370      380      390      400      410

cryla-105.pe IGINNQLSVLDGTEFAVGTSNN-LPSAVY--RKSGTV--DSLDEIPPONNVPPQGF
380      390      400      410      420
C3CA_BACTK TGGTKLHSGVTKVQSPQSNDEKVEVTQYIDSKRNVGIVFDSIDQLPPIITDESLEKAY
420      430      440      450      460      470

cryla-105.pe SHKLSHVSFRSGFNSNSVIRIAPMFSIHRSAEFNIIASDISITQIPLVKAFHLOSQT
430      440      450      460      470      480
C3CA_BACTK SHQLNIVRCF--LLQGGRGII--PVFTWTHKSVDFNTLDSKIKIPIFFVKAFILVNST
480      490      500      510      520      530

cryla-105.pe TVVRGFGFTGDIILRTSG--GPAYIIVINNGQLPQRYRIRIYASTTNLRIYVTVAGER
490      500      510      520      530      540
C3CA_BACTK SVVAGPFGTGGDIIDKKTNGSGGLTYVTPAPDLTYTSKTIKIRIYASTSVRFEGIDLSGYT
530      540      550      560      570      580

cryla-105.pe IFAGQFNKMTMDGDLPTLQFSFVATNTAFTPMSSQFTVGADTFSSGNEVYIDREFLI
550      560      570      580      590      600
C3CA_BACTK HSISYFDKIMDKGNLTLYNFNLSSVSRPIEIS--GKNKIGVSGGIGSGDEVIDYIDKIEFI
590      600      610      620      630      640

cryla-105.pe PVATLAEAYNLERAKRAVNALETSTNQLGLKNTVVDHIDQVSNLVTVLVSDFECLDKR
610      620      630      640      650      660
```


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```

AF122897_1 -----YVTKLEIFPDTE
                               1130

cry1a-105.pe 1160 1170
:::|||||:::
AF122897_1 QIRIEGTEGTFVDSVLLMEE
1140 1150 1160
:::|||||:::

cry1a-105.pep
TXN5:QQA_A_BACTF

Description: Q9X597 bacillus thuringiensis (subsp. finitimus). pesticidal
crystal protein cr
Accession/ID: Q9X597
=====General comments=====
ID QQA_BACTF STANDARD; PRT; 1163 AA.
AC Q9X597;

SCORES Initl: 640 Initn: 1878 Opt: 686 z-score: 751.1 E(): 6.3e-36
>>TXN5:QQA_BACTF
Initl: 1878 Initn: 640 opt: 686 Z-score: 751.1 expect(): 6.3e-36
Smith-Waterman score: 2081; 34.7% identity in 1194 aa overlap
(36-1176:68-1162)

cry1a-105.pe NINECIFNYCLNPEVEVLGGERIETGVTPIDISLSLTFLLSEF-VPGAGFVLGVLDII
10 20 30 40 50 60
:::|||||:::
QQA_A_BACTF FCADDFLQSYGEFNMDFGESEPFIDASGAINAAIGVTGTVLGLGVPPAGALTTFYQKL
40 50 60 70 80 90
:::|||||:::

cry1a-105.pe WGIFGS-----QWDAFLVQEQLINQRINIEFARNQIRSLGSLNLYIYAESPREWAD
70 80 90 100 110 120
:::|||||:::
QQA_A_BACTF FGLFPPNNNTQKEEFKQVEALIDEKISDAVNKAISELQGLVNNITLYTEALEEWLEN
100 110 120 130 140 150
:::|||||:::

cry1a-105.pe PTPALRREMRIQFNDWNNSALTTATPLFAVQNYQVPLSVVQANHLHSLVRDVSVFGQ
130 140 150 160 170 180
:::|||||:::
QQA_A_BACTF KENPAVDRLVQRWRILDFEFGQMPFAVNGEVLVVVTQANHLHSLVRDAYIYGA
160 170 180 190 200 210
:::|||||:::

cry1a-105.pe RWGFDAAATINRKYNDLFRILGNYTDHVAWYNTGLRVEWGPDSDMIRYNQPRRLITV
190 200 210 220 230 240
:::|||||:::
QQA_A_BACTF EWGLTPTNIDQWHLRLHSAEYTDHCVMYNTGLKQLENSDAKSMFQYNRFRREMTLSV
220 230 240 250 260 270
:::|||||:::

cry1a-105.pe LDIVSLFPNYDSRTPYPIRVQSOLREIYTPV-----LENFPGSRGA---QGIGGS-IR
250 260 270 280 290
:::|||||:::
QQA_A_BACTF LDVIALFPAYDKMYPPIPTNFQLTREVTVIGKIGRNDSDHWTYANAFSFNLESTLIIR
280 290 300 310 320 330
:::|||||:::

cry1a-105.pe SPHLMILNSITIV--TDHARGEY----YMSGHOIMASPGVGSPEFTPLPYGTMGNDAP
300 310 320 330 340
:::|||||:::
QQA_A_BACTF TPHPVDYIKKIKFVATVDYGIYGRSKWGH-IITSATNSANTETRN--YGIIVNHS
340 350 360 370 380 390
-350

cry1a-105.pe QQRIVAQCGQVYTLSTLSTYRPPFNIGINNQLQSVLDGTFF--AYGTSNLPSPAVRKS
350 360 370 380 390 400
:::|||||:::

```

[illegible]

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[illegible]

~~Product Characterization Center~~

```

>>>X:CUBA_BACUH
Description: 086170 Bacillus thuringiensis (subsp. higo) . pesticial crystal
protein cryIAbA
Accession/ID: 086170
=====
>>>G:Comments:=====
ID CUBA_BACUH STANDARD, PRT: 882 AA.
AC 086170; . . .

SCORES Init1: 157 Initn: 237 Opt: 633 z-score: 695.0 E(): 8.4e-33
>>>X:CUBA_BACUH
Initn: 237 Init1: 157 opt: 632 z-score: 695.0 expect(): 8.4e-33
Smith-Waterman score: 638; 26.2% identity and 59 aa overlap
(51-628:79-658)

```

CRYLA-105.pe VEVILGRIETGYTPIDISLSTQFLLSFFVPSAGWLG-INVINGLFGSQ-WDEL
CUBA BACUH NMCEEASYSASSPSQLFKVGGISVAILGNIDVGPCLSNWMLSLFPWTTIEKNTWEDMS

50 60 70 80 90 100 110 120 130 140 150

```

110  KIVAVLWKLWVLEINQALNLR  120  130  140  150  160
CJBA_BACU

170  180  190  200  210  220
CRY1A_105.pe  NSALTTAIPL-FAVQNYQVPLLSVYVOANLHLSVLRDVSVFGQRMFGDAATINSRYNDL
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
HILFTROIQSDTSLSGYETVLLPSPYASANLHLLLRVATVYKGLGYSTDSVFEYNEQ
170  180  190  200  210  220
CJBA_BACU

```

```

cry1a-105.pe TELIGNYTDHAEWVNTGLERWVGDSRWIRYFRBELTTLTVDLIVSLFNYDSRTYP
                200      210      220      230      240      250
                : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CJBA_BACUH KYYTEKYSNVCNTYKSGLE--SKKQIGWSDFNRYRREMTLSVLDIVLFLPYDTGLYP
                230      240      250      260      270      280

```

[illegible]

```
cry-la-105.pe AHGEYVWSGHQIMASFGSPFETPLXYGT-MGNAAPQORIVAQJGGQSVRTLSSTL-  
      :   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |  
.CJBA_BACUH SINSWTFSLSGGENRYFLTBGETIYNQFF.GDTEYCGTSSVIDISNNNSIYNLTWKYE  
      310       360       370       380       390       400
```

```

370      380      390      400      410      420
cryia-105.pe YRPPN--IGNNQOVSVDGT---EFAVTS-NLPsAVRKSCTVDSLDETPPQNNV
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
WIYPWTDVPWTKINSITDNNSSSIYGAERNKPTVRTDFNFLNRAGNGFTTYND-
CUBA BACUH 410      420      430      440      450      460

```

```

cyla-105_pe PPQGFSLRHLSGVMSFGSFGSSNYSVIRAPMFSWTHRAEFPNNIIASDSITQIPUKAH 430 440 450 460 470 480
-----YNNILSYMLINGETFGOKR-----HGVSFAFTHSSVDYNTIVPDKLIVQIPAVKTN 470 480 490 500 510
CJBA_BACUH

```

cryla-105.pe TLQSGTTVVVRGPGFTGCDILRRTSGGPFAYTIVININGQLPQRYRARIRVASTTNLRITYVT 540

[illegible]

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U82518_1 R V V Y T D P I V - M A G G - R T A I P G F T R M E N L V N S A S R V S F L N Q N N I Y T S Y F R P H N I P Y Y W
300 310 320 330 340 350

cryla-105.pe S H Q I M A S P - - - - - V G F - S G P E F T P L Y G T M G N A P Q O R I V A Q L O G G Y R T L S T L Y R R P
320 330 340 350 360 370
U82518_1 S G N Q N F L S G T S N L Y G R S D G R T T F N V S N I - - - - - D I F R V N N T H I G - G A F T D Y R G L H R A E
360 370 380 390 400

cryla-105.pe F N I G I N - - - - - N Q O L S V L D G T E F A Y G T S S N L P S A V Y R - K S G T V D S L D E I P Q N N V P P R Q G F
380 390 400 410 420
U82518_1 F - I G A N T Q N N O R T S L L Y S V E - - - - - I P S S H F R F E N H T V - - - - - F L P G S G L E P N E R N Y
410 420 430 440 450

cryla-105.pe S H R L S H V M F R S G F S N S V S I I R A P M F S W I H R S A E F N N I I A S D S I T Q I P L V K A H T L Q S G T
430 440 450 460 470 480
U82518_1 T H R L F Q M N N E V S V N P N A R G R V F - - - - - L H A W T H R S L R R T N G L R S D Q I L Q I P A V K T I S N G D R
460 470 480 490 500 510

cryla-105.pe T V V R C P G T G D I L R T S G P F A Y T I V N I N G Q L P O R V A R I Y A S T N L R I Y V T V A G E R I
490 500 510 520 530 540
U82518_1 A V L N Y G E N I M K L D N L T T G L S Y K L T A V D S E A S - N T R F I V R V Y A S M N N K L N L V I N G A Q I
520 530 540 550 560

cryla-105.pe F A G O N K T M D T G P L T - - - - - F O S F S Y A T I N T A F T P M S Q S S F T V G A D T F S S G N E V I D R P E
550 560 570 580 590 600
U82518_1 A S L N V E H T V O R G S L D L O Y G N F K Y A T P - - - - - A G N F K M G S Q S I - L G I F K E I P N I D F V L D K I E
570 580 590 600 610 620

cryla-105.pe L I P V T - - - - - A T L E A E Y N L E R A Q K A V N A L F T S T N Q L G L K T N V T D H I D Q V S N L Y T L S D E F C L
610 620 630 640 650 660
U82518_1 L I P S N F M S S L E Q T Q N Y N T Y N Q D T I Y T H N Q G Y D T Y D Q N S S G M Y H Q S Y N N Y D N M D T T Y Q P S
630 640 650 660 670 680

cryla-105.pep
TXN5:CKAA_BACUF

Description: O32321 bacillus thuringiensis (subsp. fukuokaensis). pesticidal
crystal protein
Accession/ID: O32321
ID CKAA_BACUF
AC O32321,
=====General comments=====

SCORES Initl: 158 Initn: 410 Opt: 625 z-score: 686.6 E(): 2.5e-32
>TXN5:CKAA_BACUF
Initn: 410 Initl: 158 Opt: 625 z-score: 686.6 expect(): 2.5e-32
Smith-Waterman score: 635; 28.7% identity in 658 aa overlap
(2-616:18-641)

cryla-105.pe M D N P N I N E C I P Y N C L S N P E V U L G G E R I E T G Y T P I D I S L T Q
10 20 30 40
CKAA_BACUF M N P Y O N D E I V D P E N Y D N L N R - - - - - Y E Y A N D P N V A M Q N T Y N K D W M G Y E E I N F S - S I T A
10 20 30 40 50

cryla-105.pe F L - - - - - L S E F V P G A G F V L G - - - - - L V D I I W G I G F - - - - - P S Q W D A F L V Q I E Q L I N Q R I E F A
50 60 70 80 90

CKAA_BACUF I L A S I G I L N R V I A L T G - V L G N T Q E V I S I I Q A D A G F T R N G T G N E L L I H V E Q L I Q O T L A T Q Y
60 70 80 90 100 110

cryla-105.pe R N Q A I S R L E G S L N L Y Q I Y A E S F R E W E A D P T N P A L R E E M R I Q F N D M N S A L T A I - P L F A V -
100 110 120 130 140 150
CKAA_BACUF R S A A T G A I Y G T S R S Y N L M F F R O W E R N T R E N - G Q O V E S A F T I N T I L C I N A L A P O A S L S
120 130 140 150 160 170

cryla-105.pe Q N Y Q V P L L S Y V Q A A N L H L S V L R D V S V F G O R W G F D A - A T I N S R Y N D L T R L I G N Y T H A V
160 170 180 190 200
CKAA_BACUF R G F F T L L P N Y A A N F H L L R D A V L Y R N Q M L S N S I S T A N V N L I R A A I N E Y I I T H C T
180 190 200 210 220 230

cryla-105.pe R W Y N T G L E R V M G P D S R - - - - - D W I R Y N Q F R R E L T L V L D I V S L F P N Y D S R T Y P I R T V S O L T
210 220 230 240 250 260
CKAA_BACUF R W Y O D G L N R - F D R S S A N W N E R F N A Y R D M T L S V L D F A T V F P T Y D P V L P F A A T N V E L T
240 250 260 270 280 290

cryla-105.pe R E I Y N P V L N F N G S P R G S A Q G - - - - - I E G S I R S P H L M D I L N S I I Y T D - - - - - A H R - G E Y W
270 280 290 300 310
CKAA_BACUF R V Y Y T D P I V - M A G G - R T A I P G F T R M E N L V N S A S R V S F L N Q N N I Y T S Y F R P H N I P Y Y W
300 310 320 330 340 350

cryla-105.pe S C H O I M A S P - - - - - V G F - S G P E F T P L Y G T M G N A P Q O R I V A Q L O G G Y R T L S T L Y R R P
320 330 340 350 360 370
CKAA_BACUF S G N Q N F L S G T S N L Y G R S D G R T T F N V S N I - - - - - D I F R V N N T H I G - G A F T D Y R G L H R A E
360 370 380 390 400

cryla-105.pe F N I G I N - - - - - N Q O L S V L D G T E F A Y G T S S N L P S A V Y R - K S G T V D S L D E I P Q N N V P P R Q G F
380 390 400 410 420
CKAA_BACUF F - I G A N T Q N N O R T S L L Y S V E - - - - - I P S S H F R F E N H T V - - - - - F L P G S G L E P N E R N Y
410 420 430 440 450

cryla-105.pe S H R L S H V M F R S G F S N S V S I I R A P M F S W I H R S A E F N N I I A S D S I T Q I P L V K A H T L Q S G T
430 440 450 460 470 480
CKAA_BACUF T H R L F Q M N N E V S V N P N A R G R V F - - - - - L H A W T H R S L R R T N G L R S D Q I L Q I P A V K T I S N G D R
460 470 480 490 500 510

cryla-105.pe T V V R C P G T G D I L R T S G P F A Y T I V N I N G Q L P O R V A R I Y A S T N L R I Y V T V A G E R I
490 500 510 520 530 540
CKAA_BACUF A V L N Y G E N I M K L D N L T T G L S Y K L T A V D S E A S - N T R F I V R V Y A S M N N K L N L V I N G A Q I
520 530 540 550 560

cryla-105.pe F A G O N K T M D T G P L T - - - - - F O S F S Y A T I N T A F T P M S Q S S F T V G A D T F S S G N E V I D R P E
550 560 570 580 590 600
CKAA_BACUF A S L N V E H T V O R G S L D L O Y G N F K Y A T P - - - - - A G N F K M G S Q S I - L G I F K E I P N I D F V L D K I E
570 580 590 600 610 620

cryla-105.pe L I P V T - - - - - A T L E A E Y N L E R A Q K A V N A L F T S T N Q L G L K T N V T D H I D Q V S N L Y T L S D E F C L
610 620 630 640 650 660
CKAA_BACUF L I P S N F M S S L E Q T Q N Y N T Y N Q D T I Y T H N Q G Y D T Y D Q N S S G M Y H Q S Y N N Y D N M D T T Y Q P S
630 640 650 660 670 680

cryla-105.pep

© 07
15603

ID Q95603
 Description: Q95603 bacillus thuringiensis. delta-endotoxin (fragment). 6/2001
 Accession ID: Q95603
 General comment: =====
 PRELIMINARY PRT: 645 AA.

SCORES Init1: 413 Initn: 998 Opt: 0 z-score: 663.3 E(): 4.9e-31
 >>TXN5:Q9SG03
 inchn: 998 init1: 413 opt: 603 z-score: 663.3 expect(): 4.9e-31
 Smith-Waterman score: 1103; 33.7% identity in 317 aa overlap
 (16-600:42-645)

cryla-105.pe

MDNNPNEICIPYNCLSNEPVEVLGGKTIETGYTIDISLTLQF

YPLTDDBNAGLQNNYKEYLQTVGGDGYTDPLINPNSVSGSNVIOVGINLGRLLSFFGE

```
cryla-105.pe -LLSEFVPGAGVLGLVDIIWGIFGPSQWDAFLVQIEQLINQRIBEFARNOISRLESLS  
      :|::|||:|:~::~|||:|:~::~|||:|:~::~|||:|:~::~|||:|:~::~|||:|:~::~|||:|:  
PSSOWTVTYTILL--NSLWPDDENSVDAMERVEELIDOKISEAVKGRADODDNGLO
```

[illegible][illegible][illegible]

```

cryla-105.pe -----FDGSRFG--SAQGIQS--IRSPHLMDLNSITITYTDAHRGEYYWSG-----
                                280      290      300      310
                                : : : : : : : : : : : : : : : : : : : : : :
                                : : : : : : : : : : : : : : : : : : : : : :
                                TTQLCRSWYNPAFNFHLNPFVLENSLRPHLPFLRLSNLQILVNVTQNGSARGRSVRY
Q9S603

```

```
cryla-105.pe HQIMASPVGFSGPFTFLYGTMGNAAPQ--RIVAQLGGGVRTLSSTLVRRPFFNIGIN  
| : | : | : | : | : ||::|| ::  
HYLHSSIIOEKSYGLISDPGANINVQNNDIYIIISOVS-N-PASPVGSSYSVMWDTNFILS
```

[illegible]

440 450 460 470 480 490
cya-105 pe R-SGFSNSSVSTIRA--PMFSWIHRSAEFNNIIASDSITQIPLVKAHTIQSGTTVVRSPG

Q9S603
RFQATQSSPSTVSANLPTCVWTHRDVLDNITANQITQLPLVKAYELSSGATVVKPGP
480 490 500 510 520 530

```

          500      510      520      530      540
cayla-105.pe FTGSDLRRTSGGFPAVTINQGPYRIRARFYASTNRLRVVAGSERIFAFGNFK
|||||::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |::: |:::
FTCGDVRINTNGFGAIRVSVGTGLTORYIRFRYASTIDDFEFVTTGGTYINNRFTR
          540      550      560      570      580      590
Q9S603

```

```

560      570      580      590      600      610
crryla-105.pe TMTGDLPLTFQSFVATINTAFTFPMSSQSFVQADFTFSSGVEVYIDRFLPILPTALEA
|||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
TMRGQSFVESYRVEFTFPTFNFQTSQDIIRTSFQGLSGNGEVYLD
Q9S603

```

620 630 640 650 660 670
civ1a-105.pe EYNLERAKAVNAUFTSTNQLCKLTNVTYDHIDQVSNLVTYLSDEFCLDEKRELSKVKH

cry1a-105.pap
TXN5:AF042733.1

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

Accession/ID: AF042733

~~=====General commercial~~

~~LOCUS AF042733_1 [AF042733] Bacillus thuringiensis delta-endotoxin gene, partial cds.~~

SCSSES Initl: 413 Inttn: 998 Opt: 603 z-score: 663.3 E(): 4.9e-31
 SPSXMS: 4504733.1
 Initn: 998 Opt: 603 z-score: 663.3 expect(): 4.9e-31
 Smith-Waterman score: 1103% 33.7% identity in 617 aa overlap
 (18-608; 42-645)

AF042733.1 YPLPDRAGLQNNMVFQIOTYGGVETPLNPILSVGKDVQVQINVGRLLSFGF
cry1a-105.pe MDNPNAINCPIYCNLSNPEVILGERTGYTPIDISLSLTFQ

```

cryla-105.pe--LLSEFVPGAGFVDFELV--IINGINGPQWDAFLVUVEDINOREEFARNQAIISLEGLS
AF042733_1  PFSSQWTVTVTYLL--NSNMPDENSVQDQWDFEVEELLKQ--SEAVKGRALDLDLTGLQ

```

[illegible]

```

cryla-105.pe   VYQANUHLSLVDRSVSFGQWGFDAATINSRNDLTRELIGNYDTHAVRYNTGKERPS
                  170      180      190      200      210      220
3E042733.1    VAQRANIHLILMDADITYGARWGINOTIDDFHSROOSLITOTYNHCVTNDSLAALRG
                  170      180      190      200      210      220

```

```
cryla-105.pe PDSRDWIRYQFRRETLVLIVLSFPNTSDSYPIRVSQLTREIYNPV-----LEN-  
:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::  
AF042733_1 TTAESFKNYQRRREMLTAMDVALPYVNLQYDPDGTNQLTRTYITDPIADFLEQP  
250 260 270 280 290 300
```


cry1a-105.pe -----FQSGERG--SAQIEGS--IRSPHLMIDILNITITDARHGEYVWSG-----
310 320 280 290 300 310
AF042733_1 TTOLCRSYWIPAFRNHLNFSVLNLSLRPPLPRLSNLOILVYQVNGSNWGRSVRY
310 320 330 340 350 360
cry1a-105.pe HQIMASPVGSGPEFTPLPYGTMGNAPOQ--RIVAQLGGQVYRTLSSTLYRFRPFGIN
320 330 340 350 360 370
AF042733_1 HYLRSIIQEKSYGLLSDPVGANVQNDYQIIISQVSN--FASPVGSSYSWMDTNFVLS
370 380 390 400 410 420
cry1a-105.pe NQQLSVLDGTEFAIGTSSNLPASVYKSGTVDSLDEIPDNNVPPRQGFSHRLSHVSMF
380 390 400 410 420 430
AF042733_1 SGQVSGISGY-----TOGGIPAVCIQQRNSTDELPSLNPEGDII---RNYSHRLSHITQY
430 440 450 460 470
cry1a-105.pe R-SGFSNSVSIIRA--PMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTTVWRGPG
440 450 460 470 480 490
AF042733_1 RFQATQSGSPSTVSANLPTCVWTHRDVLDNTITANQITOLPLVXAYELSSGATVWKGRG
480 490 500 510 520 530
cry1a-105.pe FTGGDLIRTSGGPFAYTIIVNINGQLPQRYRIRYASTTNLRIYTVVAGERIFAGQFNK
500 510 520 530 540 550
AF042733_1 FTGGDVIRRTTGGFGAIRVSVTGPLTORIRFRYASTIDFDFVTRGGTTINNFRPTR
540 550 560 570 580 590
cry1a-105.pe TMDTGDPITFQSFYATINTAFTFMSQSSFTVGADFFSGNVEYIDRFELIPVATILEA
560 570 580 590 600 610
AF042733_1 TMRQGRYRYSYRTVEFTFPFQSDIIRTSIQGLSNGSEYILD
600 610 620 630 640
cry1a-105.pe EYNLERAQAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLYSDFCLEKRELSEKVKH
620 630 640 650 660 670
cry1a-105.pep
TXNS:Q53431
Description: Q53431 bacillus thuringiensis, delta-endotoxin cry1ab7
(fragment). 6/2001
Accession/ID: Q53431
ID Q53431 PRELIMINARY;
AC Q53431; PRT; 91 AA.
=====General comments=====

SCORES Initl: 589 Initn: 589 Opt: 589 z-score: 660.7 E(): 6.8e-31
>>TXNS:Q53431
Initn: 589 Initl: 589 Opt: 589 z-score: 660.7 expect(): 6.8e-31
Smith-Waterman score: 589; 93.4% identity in 91 aa overlap
(1-91:1-91)

cry1a-105.pe MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
Q53431
MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
AF042733_1 IDLWGFVGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
cry1a-105.pe EYNLERAQAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLYSDFCLEKRELSEKVKH
620 630 640 650 660 670
cry1a-105.pep
TXNS:Q53431
Description: Q53431 bacillus thuringiensis, delta-endotoxin cry1ab7
(fragment). 6/2001
Accession/ID: Q53431
ID Q53431 PRELIMINARY;
AC Q53431; PRT; 91 AA.
=====General comments=====

SCORES Initl: 589 Initn: 589 Opt: 589 z-score: 660.7 E(): 6.8e-31
>>TXNS:Q53431
Initn: 589 Initl: 589 Opt: 589 z-score: 660.7 expect(): 6.8e-31
Smith-Waterman score: 589; 93.4% identity in 91 aa overlap
(1-91:1-91)

cry1a-105.pe MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
Q53431
MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
AF042733_1 IDLWGFVGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
cry1a-105.pe EYNLERAQAVNALFTSTNQLGLKTNVTDYHIDQVSNLTVLYSDFCLEKRELSEKVKH
620 630 640 650 660 670
cry1a-105.pep
TXNS:Q53431
Description: Q53431 bacillus thuringiensis, delta-endotoxin cry1ab7
(fragment). 6/2001
Accession/ID: Q53431
ID Q53431 PRELIMINARY;
AC Q53431; PRT; 91 AA.
=====General comments=====

SCORES Initl: 589 Initn: 589 Opt: 589 z-score: 660.7 E(): 6.8e-31
>>TXNS:Q53431
Initn: 589 Initl: 589 Opt: 589 z-score: 660.7 expect(): 6.8e-31
Smith-Waterman score: 589; 93.4% identity in 91 aa overlap
(1-91:1-91)

Q53431
IDLWGFVGPSQMDAFLVQIEQLISORIEEF
70 80 90
cry1a-105.pe PTPNPALEEMRIQFNDMNSALITTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
cry1a-105.pep
TXNS:S72313_1
Description: S72313 Bacillus thuringiensis cry1ab7=delta-endotoxin Cry1ab7
[Bacillus thuringi
Accession/ID: S72313
=====General comments=====

LOCUS S72313_1 [S72313]
DEFINITION cry1ab7=delta-endotoxin Cry1ab7 [Bacillus thuringiensis, esp.
[Bacillus thuringi
Accession/ID: S72313
=====General comments=====

SCORES Initl: 578 Initn: 578 Opt: 578 z-score: 648.6 E(): 3.2e-30
>>TXNS:S72313_1
Initn: 578 Initl: 578 Opt: 578 z-score: 648.6 expect(): 3.2e-30
Smith-Waterman score: 578; 92.3% identity in 91 aa overlap
(1-91:1-91)

cry1a-105.pe MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
S72313_1
MNNPNINECTPYNCLSNPEVVLGGERIETGYTPIDISLSLTQFLLSFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
S72313_1 IDLWGFVGPSQMDAFLVQIEQLISORIEEF
70 80 90 100 110 120
cry1a-105.pe PTPNPALEEMRIQFNDMNSALITTAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
130 140 150 160 170 180
cry1a-105.pep
TXNS:CGAA_CLOBI
Description: Q45882 clostridium bifermentans, pesticidal crystal-like protein
cry16aa (insec
Accession/ID: Q45882
ID CGAA_CLOBI STANDARD;
AC Q45882; PRT; 613 AA.
=====General comments=====

SCORES Initl: 145 Initn: 392 Opt: 558 z-score: 614.0 E(): 2.7e-28
>>TXNS:CGAA_CLOBI
Initn: 392 Initl: 145 Opt: 558 z-score: 614.0 expect(): 2.7e-28
Smith-Waterman score: 579; 26.6% identity in 561 aa overlap
(56-580:43-579)

cry1a-105.pe GERIETGYTPIDISLSLTQFLLSFVPGAGFVLGLV--DIIMGIFGPSQMDAFLVQIEQ--
30 40 50 60 70 80
CGAA_CLOBI SKGVASVFKVIDTTHNISKNNFNILTDQFIIDTILSIWLE--DFNENEIFFSMWEDGE
20 30 40 50 60 70
cry1a-105.pe -LINQRIIEFARNQAIISRLGSLNLYQIYAESFREWADPTNPALREEMRIQFNDMNSAL

X94146_1 HDIGLRLTAGSKYITINIOQTENNPSLIYDDFKYFNFNELTSSGIDELXLEF
530 540 550 560 570 580

cry1a-105.pe TFGSGNEVIDRFELIPVTATLEAYNLERAKAVNALFTSTNOLGKINVTDYHIDQVS
590 600 610 620 630 640

X94146_1 YYSYTDGNFDEFPKLSIFPTNYSYC
590 600 610

cry1a-105.pep
TXN5:Q9RNE6

Description: Q9rne6 bacillus thuringiensis. endotoxin (fragment). 6/2001

Accession/ID: Q9RNE6

====General comments====

ID Q9RNE6 PRELIMINARY; PRT; 140 AA.

AC Q9RNE6;

DT 01-MAY-2000 (trEMBLrel. 13, Created) . . .

SCORES Initl: 422 Initn: 494 Opt: 511 Z-score: 571.8 E(): 6.1e-26

>TXN5:Q9RNE6

Initn: 494 initl: 422 opt: 511 Z-score: 571.8 expect(): 6.1e-26

Smith-Waterman score: 511; 54.0% identity in 137 aa overlap

(9-143:1-137)

cry1a-105.pe MDNPNINECIPYCNLSNPEVGLGERIETGYTP--IDISLSLTQFLSEFVPGAGFVL
50 20 30 40

Q9RNE6 QCVFNCNLSNPENEIDIESLSRSRQVAEISLGITRELSLPGASGPF
10 20 30 40 50

cry1a-105.pe GLVDIINGIFGSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

Q9RNE6 ALFDIINGVIGPQWNLFLAQIQLIDQRIEAVHRNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

cry1a-105.pe ADPTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVF
120 130 140 150 160 170

Q9RNE6 GSPNNEGLQDVNRNPSNTDNLITGYL
120 130 140

cry1a-105.pep
TXN5:AF182196_1

Description: AF182196 Bacillus thuringiensis Bacillus thuringiensis endotoxin

gene, partial c

Accession/ID: AF182196

====General comments====

LOCUS AF182196.1 [AF182196]

DEFINITION Bacillus thuringiensis endotoxin gene, partial cds. . . .

====General comments====

SCORES Initl: 422 Initn: 494 Opt: 511 Z-score: 571.8 E(): 6.1e-26

>TXN5:AF182196_1

Initn: 494 initl: 422 opt: 511 Z-score: 571.8 expect(): 6.1e-26

Smith-Waterman score: 511; 54.0% identity in 137 aa overlap

(9-143:1-137)

cry1a-105.pe MDNPNINECIPYCNLSNPEVGLGERIETGYTP--IDISLSLTQFLSEFVPGAGFVL
50 20 30 40

Q9RNE6 QCVFNCNLSNPENEIDIESLSRSRQVAEISLGITRELSLPGASGPF
10 20 30 40 50

cry1a-105.pe GLVDIINGIFGSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

Q9RNE6 ALFDIINGVIGPQWNLFLAQIQLIDQRIEAVHRNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

cry1a-105.pe ADPTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVF
120 130 140 150 160 170

Q9RNE6 GSPNNEGLQDVNRNPSNTDNLITGYL
120 130 140

AF182196_1 QCVFNCNLSNPENEIDIESLSRSRQVAEISLGITRELSLPGASGPF
10 20 30 40 50

cry1a-105.pe GLVDIINGIFGSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

AF182196_1 ALFDIINGVIGPQWNLFLAQIQLIDQRIEAVHRNQAIISRLGSLNLYQIYAESFREWE
60 70 80 90 100 110

cry1a-105.pe ADPTNPALREEMRIQFNDMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSVF
120 130 140 150 160 170

AF182196_1 GSPNNEGLQDVNRNPSNTDNLITGYL
120 130 140

cry1a-105.pep

TXN5:CRAA_BACUH

Description: Q9s597 bacillus thuringiensis (subsp. higo). pesticidal crystal

protein cry27aa

Accession/ID: Q9S597

====General comments====

ID CRAA_BACUH STANDARD; PRT; 826 AA.

AC Q9S597; . . .

SCORES Initl: 70 Initn: 159 Opt: 445 Z-score: 487.3 E(): 3.1e-21

>TXN5:CRAA_BACUH

Initn: 159 initl: 70 opt: 445 Z-score: 487.3 expect(): 3.1e-21

Smith-Waterman score: 585; 24.9% identity in 655 aa overlap

(36-633:88-712)

cry1a-105.pe NINECIPYCNLSNPEVGLGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGVDIIL
10 20 30 40 50 60

CRAA_BACUH GLIPPESEFWMTNGTVAALTIVSVIAGILVTPVSVTAGLITVLGAGAAALAGITPLIW
70 80 90 100 110

cry1a-105.pe GIFGFSQWDAFLVQIQLINQRIEFARNQAIISRLGSLNLYQIYAESFREWEADPTNPA
70 80 90 100 110 120

CRAA_BACUH PATTDITFNKIDTATEVLLNKEISEFVRKTKNTKIDSLQOLIYYQVALENWKKNFDSA
120 130 140 150 160 170

cry1a-105.pe LREEMRIQFNDMSALTATPLFAVQNYQVPLLSVYQAAHLHSLVLRDVSFVGQWGF
130 140 150 160 170 180

CRAA_BACUH ARNTVSTRFOIVNAFVEAMFALSMGPEYVQVAGVAYQAANLHILLREGIAYADQWNL
180 190 200 210 220 230

cry1a-105.pe RATINS-----RYNDLTRLLGNVTHAVRWNTGLERWGPDSRDWRVYQ--FRRLTIL
190 200 210 220 230

CRAA_BACUH RDPMHAAGDLHYKEFLDYRNQYINHCSTWYNEG-----QNEANLNKNGILVYQRTMTL
240 250 260 270 280 290

cry1a-105.pe VLDIVSPFNVDSRTY--PIRTVSQLTREIYVTPVLENFDGSRGSAQIEGSRGPHLM
240 250 260 270 280 290

CRAA_BACUH VLDLIAMFSTYDPRLYTPIKT-EILITRTIYT-----DGVNRNEPK-----SIHNPGLF
300 310 320 330

cry1a-105.pe DILANSITIYDAHRGEYVWSHQIMASPVGSGPEFTFFLYGTGMGAAPQORIVAGLQOG
300 310 320 330 340 350


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cryla-105.pep
TXN5:CLAA_BACTU

Description: P56956 bacillus thuringiensis. pesticidal crystal protein
cry21aa (insecticidal
Accession/ID: P56956
=====
ID CLAA_BACTU STANDARD; PRT; 1167 AA.
AC P56956; . . .

SCORES      Initi: 192      Initn: 688      Opt: 423      z-score: 460.8      E(): 9.3e-20
>>TXN5:CLAA_BACTU
initn: 688      Init1: 192      Opt: 423      z-score: 460.8      expect(): 9.3e-20
Smith-Waterman score: 845;      24.7% identity in 1102 aa overlap
(38-1037:70-1105)

                10      20      30      40      50      60      70      80      90
cryla-105.pe  NECIPYCLNSENPEVVLGERIETGYPTIDISLSTQQLSEFVPGAG----FVLGVLDI
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    BEFGKTYMDPLKQHLQIAWDTSONGTVDYLAITKASTISLIGLPGDAVVPFIMFVD
                40      50      60      70      80      90

                100     110     120     130     140     150
cryla-105.pe  IPFKLGRGQQNAQOQFELIIEKVLVDGFDFRFTLNLLNYLDGQHTALSHFQNDV
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

                160     170     180     190     200     210
cryla-105.pe  QIAYESFRE---WEADPT--NPALRE--EMRIQFNDMNSALITAIPLFA----VQNYQV
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    QIAlCOGEQGLMDQDTACTPTTIDHLISVRESFKDARTTETALPHKFNPLMSTNDNT
                160     170     180     190     200     210

                220     230     240     250     260     270
cryla-105.pe  PDNSDVTLLTFLPMYTTGATLNLIHGYITQFAERKMSVYDESFINQTKVDLQRRIQDY
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

                280     290     300     310     320     330
cryla-105.pe  STTVSTTFEK-FKPTLNPSENKSNKTRIVRSMTLQSLDIAATWFLDNLVNPSPNDVIQ
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

                340     350     360     370     380
cryla-105.pe  LDQ---TELVSFDVAGPMEGN---DNITS-NIIDVLTPTNTGI-----GPGES
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

                390     400     410     420     430     440
cryla-105.pe  ASPVGSGPETFPLXGTGMGNAPQQRIVLAQLQGQYRILTSTLYRRPFGNIGINNQQVLSV
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    SDLRKFTVPRIELQSMQFHGVNSKSVCHYSDG---LKLNYKNKTIITAGVSNIDEN
                380     390     400     410     420     430

                440     450     460     470     480     490
cryla-105.pe  LQGTFFATGSSNLP-SAVYRKSQTVGSDEIPQNNVVPFPGQFSHRLSHVSIMFRSFS
                : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
CLAA_BACTU    QNN-KHNTGPIVNSPITDINNVSNSQYLDLNSVNGGQYKQVTCSPSSNGSNNAALP
                440     450     460     470     480     490

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~~Product Characterization Center~~

cryla-105.pe FNSVSIIRAPMF--WHRSAENNIASDSITQIPLVKHAHTQSGTTVVRGPGFTGG
 SSN--ICGGRSSLHAWTHASLDNRNILLDEITQIPATYAEIRGNSSVVAAGPGSTGG
 COAA_BACTJ 490 500 510 520 530 540 550

 cryla-105.pe DILLRTSGGPAYTIVNINIGOLPQRYARIRYASTTNLIYV-----TVAGERIFAGQFN
 DLVMSYHSVWSFKVYC--SEL-KNVRVRIIRVASHGNCQFLMKRWPSTGVAPROWA--RHN
 COAA_BACTJ 550 560 570 580 590 600 610

 cryla-105.pe KTWMDTGDPLTFQSFYSYATINTAFTPFMSQSFVAGDTFSSGNEVYIDRFELIPVAT--
 VOGTFNSMRVEAFKYLDI--FTIPEENNAFTID--LESQGDLEDFIKFIEFVSGSAF
 COAA_BACTJ 600 610 620 630 640 650 660

 cryla-105.pe LEAEYNLERAKAVNALFTSTNQLGKTNVDYHIDQVSNLYLISDFECLDEKRELSE
 EYEGKNIIEKTOKAVNDLFIN
 COAA_BACTJ 660 670

 cryla-105.pep
 TXNS_CHAA_CLOBI
 Description: O05102 clostridium bifementans, pesticidal crystal-like protein
 Accession ID: O05102
 ID: CHAA_CLOBI
 SC 005901
 General comments:=====
 STANDARD; PRF; 618 AA.
 Scores: Init: 215 Initn: 389 Opt: 403 z-score: 442.9 E(): 9.2e-19
 >>TXNS_CHAA_CLOBI init: 389 Opt: 403 z-score: 442.9 expect(): 9.2e-19
 Smith-Waterman score: 515; 24.4% identity in 651 aa overlap
 (3.606:2-616)
 cryla-105.pe MNNPNII--NECPDNYC--SNREVEVLGCEKEGTGTPIDISLTQTLSEFVPGAG
 CHAA_CLOBI 10 20 30 40 50
 MNNKIEQNKIVENSNDIQDQETLHAGL-VPGAT--VSILPLIGTTAVVPGVVG
 10 20 30 40 50
 cryla-105.pe FVLGLV---DIWGFGPSQ---WDMVAQIQELINIAIEEFANQANSRLEGLSNIYQ
 CHAA_CLOBI 60 70 80 90 100
 GVIGIIAALLPVPWPGATSSNLFDAVMDTMMDEKSEVYVNDAMTLESLYNILD
 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280
 cryla-105.pe IYAESFREWADPTNPALREEMRIQFNMDNSALTTAIPETRYQVOTPLSVYQANLH
 CHAA_CLOBI 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280
 IYLSKDFWEKNKDDPLATAELKEFESKLHSQFIESMAYFKEANLEVLIPAYAKAAH
 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280
 cryla-105.pe LSVLRDVSVFQWRGFDAAITRSRYNDLTRIGNYTHAVRWYNTGLRWGPGSDPWE
 CHAA_CLOBI 170 180 190 200 210 220 230 240 250 260 270 280
 LILLREGLLNKVID-NFITEGILHYEEFKTRSTYIAHCSWTYNGLENINKK--TRDFNK
 180 190 200 210 220 230 240 250 260 270 280

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[illegible]


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cryla-105.pe 300 310 320 330 340 350
310 320 330 340 350 360
cryla-105.pe HRGEYVMSGHOIMASPVGSGPEFTPLGTMGN---AAPQRIVAQGGQGVITLSSTL
M12662_1 SRD--ILDPYDIFS-----FIGNQAFTHNDRNIMGAVHGNISQDTSKVF-----PF
360 370 380 390 400
cryla-105.pe YR-RPFN-IGNNQQLSVLDGTEFAYGTSSNLPASAVYKSGTVDSLDGIPQNNNVPRQ
M12662_1 YANKIDKVEIVHREYSIIYEMIFFSN---SEVFRYSSSTIENNYKKTDSYMPKQ
410 420 430 440 450 460
cryla-105.pe G-----FSHRLSHVSMFRSGFSNSVSIIIRAPMFSWTHRSAEFNIIASDSITQIPLVKA
M12662_1 TWKNEYGHTLSYIKT--DNYIFSVVRERRRVAFSWTHSVDPQNTIDIDNITQIHAKA
470 480 490 500 510
cryla-105.pe HTLQSGTTVVRGPGFTGGDLARTSGGPPATIV-NINGQLPORYRARIYASTNIRIY
M12662_1 LKVSDDSKIVGPGHTGGDLVLKSDMDFRVFLKNVSRQ-----YQVRIRYATNAP-KTT
520 530 540 550 560 570
cryla-105.pe VTVAGERIFAGQFNKMTDGTDP---LTFQSFYATINTAF---TPMSQGSFTVGADTF
M12662_1 VLTGIDRISVELSTSRQNPNAOLDIYADFGVTFPRVPNKTPEGEDTLMLTLAGTP
580 590 600 610 620 630
cryla-105.pe SSGNEVYIDREFELIPVTATL---EAEYNLERAQAVNALETSTNQLGKTNVTYDIDQV
M12662_1 NHSYNIYIDKIEFIPITQSVDLYTEKQNIKTQKIVNDLEVN
640 650 660 670
cryla-105.pe SNLVYILSDPELCDEKELSEKVKYHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITI
680 690 700
cryla-105.pep
TXN5:L07026_1
Description: L07026 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (CryA(b)) g
Accession/ID: L07026
LOCUS L07026_1 (BACCRYVAB)
DEFINITION Bacillus thuringiensis delta-endotoxin (CryA(b)) gene, 5' end.
-----General comments-----
SCORES Init1: 186 Initn: 484 Opt: 338 z-score: 366.3 E(): 1.7e-14
>>TXN5:L07026_1
Initn: 484 Init1: 186 Opt: 338 z-score: 366.3 expect(): 1.7e-14
Smith-Waterman score: 725; 23.4% identity in 1263 aa overlap
(6-1105:45-1267)
cryla-105.pe
M12662_1 VLAYTPPSFLPDAGTQATPADLTAYEQLLKNEKINAGTYSKAIADVLKGFIDDTINY
20 30 40 50 60 70
(6-1105:45-1267)
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cryla-105.pe -TPIDISLSLTOFLSE---FVPGAGFVLGLVDIIMGIFGSPQSDAFLVQ---IEQLINQ
L07026_1 QTYVNIIGLSLITLAVPEIGIFTPIGLFFAALNKHDA PPPNAKDIIEAMKPAJOEMIDR
80 90 100 110 120 130
cryla-105.pe RI---EEFARNQAIISRLGLSNLYQIYAESPREWEA-DPTNPALREEMRIQFNMDMSALT
L07026_1 TITADEIGTFLNGEISQLNLAARYQSTMDDIQSHGSGFNKVDISGLIKXFTDEVLSNSFYT
140 150 160 170 180 190
cryla-105.pe TAILPLFAVONY-QVPLSV--YVQAANHLVSLVEDSVFGQW---GFDAATINSRYND
L07026_1 DRLPVFIITDADRTLLGLPYFAYILASWMLMLLDIITKGPWDKINFTDAIDSKFTD
200 210 220 230 240 250
cryla-105.pe LTRLIGNYTDHAVRYWNTGLRWGVP-DSRDWIRYNOFRRELTIVLDIVSLFFNYDSRT
L07026_1 IKNNIKLYSKTIYDVFOQGLASVGTSPDLESFAKKQKVIEMTHCLDFARLFTFPDPL
260 270 280 290 300 310
cryla-105.pe YP-----IRTVSOLT---REIYTN--PVLENFDGSPGSAQGI--
L07026_1 YPTGSGDISLOKTRRIILSPPIRTADGLTLNNTSIDTSNMPNYENGANGAPENPKERILK
320 330 340 350 360 370
cryla-105.pe -----EGSIRSPHL--MDILNSI--TIY-----TDAHRGEYVMS---GHOIM-
L07026_1 QKFLPSWRAAQYGLLQPLYLWAEIVQDSVETRLYGQLPADVDPQAGNIVSIDSNPLIQ
380 390 400 410 420 430
cryla-105.pe -----ASPVGSGPEFTPLYGTMGNAAPQOR---IVAQLGQGVYRTLSST-----
L07026_1 INMDTWKTPPGQASGWNTL-MRGSVSGLSFLQDGTRLSAGMGGGFADTIYSLPATHYL
440 450 460 470 480 490
cryla-105.pe --LYRRPFN-----IGINNQQQLSVLD---GTEFAYGTSSNLPASVYKRS--GT
L07026_1 SYLYGTPYQTSNDYNSGHVAGLVGSTPQEA TLPHIIIGQDPEQGNVSTMGFPPEKASYGTT
500 510 520 530 540 550
cryla-105.pe V-----DSLDEIPQNNNVPRGQFSHRLSHVSMFRSGF--SNSSVSII-----RA
L07026_1 VVKEWLNANAKLSPOQSIGIP-----INVTSGEYQIRCRYASNDNTNVFENVDTGGAN
560 570 580 590 600
cryla-105.pe PMFSWTHRSAEFNIIASDSITQIPLVKAHTLQSGTTVVRGPGFTGGDLIRTSGGPFAY
L07026_1 PIQIQINFASVTNNTGVOGANGVYVVKSIATDNSFTVKIPAKTINVHLTNQSGSDVFL
610 620 630 640 650 660
cryla-105.pe TIYNNQGPQRYRARIYASTT---NLRIYV---TVAGERIFAGQFN---KTMWDGDP
L07026_1 DRIEFYPILESNTVTFNNSYTGGSANLIPALPAWSTSSDKALTSMTSGRTTTPNSDD
670 680 690 700 710 720
```

cry1a-105.pe LTFQSFYATINAFPEPMSSQSF-----VGADTFSSGNEVYIDREFLIP
L07026_1 ALRFEKATQTIIPGSGDQFNTLEIQDIVSIDIFVGGSLGSGSGIKLDFTNNS
cry1a-105.pe VTA-----TAEVNDFAQAVNALFTSTNGGLKTNVTHYHIDQVSLVLYLSDFLD
L07026_1 GSGGPKFQNDLENITFNALTSNTQVLAIVSDHDEEVKLVKVALSDEVFGK
cry1a-105.pe EKRESEKVKHAKELSDERNLQDNFKDINGQPERGCGSGTITGGDDVFEKENVTL
L07026_1 EKTLRFKVNQAKELSKARNLLVGGNEDND-----LWYFRRVNVSVHKLKSDHLL
cry1a-105.pe SGTFDECRYPTLYKIDESKLAFTYQLRGVIEDSDLEIYIRYNAK-PEVNVPEFG
L07026_1 PPP-GLSPSIFQKVEESKLKENTRYTVSGFIAHATDLENVSNLGOELKXVGP-XG
cry1a-105.pe SLWPSAOSPICKGEPNRCAPHLEWNPDLDCSCDGEKAMHSHFSDINGSDLINE
L07026_1 EAPPLTSSGPV-C-----CIPHSTSGNLG-----NPHFFSYSIDVGAISVDI
cry1a-105.pe DLGVWVFIKIKTQGHASLGNLEFLEKPLVGEALARYKAEKKWDKREKLEMETNIVY
L07026_1 NPGLFGLRVNFTGMARVSNLEIRDRPLANEIRQVQVARNWTEYEKERAETSLI
cry1a-105.pe KEAKESVDALFVNSQYD-QLQADTNIAHIA-ADKRVHSTREAYLPESVIPGVNAIFE
L07026_1 QPVNIRGLYNGWNGSIRSDISYONIDAIVLPTPLKLRHMFMSDFSEQG---DIMA
cry1a-105.pe EVRVC---PGRGVILRVTAKEYGEGCVTIHEINN-----TDELKFSNCEVEEIPNNT
L07026_1 TIENFDPEKXQVLF---HSGEGVTLEHGETKYIETHTHFANFTTQO-ROGIT
cry1a-105.pe VTCDNYTVNOEEYGGAYTSRNRGYNEAPSVADYASVYEKSYTDGRKPNCFNRYGHD
L07026_1 FESKNVTVTSSDEGEFLVDNIALVEAP-LPTDDQNSEGNTASSTNSDTSMMNQ
cry1a-105.pe YTPLFVGVTYKELEYFETDKVWIEGETEGTFIVDSVELLMEE
cry1a-105.pep
TXN5:CSAB_BACUD

Description: Q45753 bacillus thuringiensis (subsp. darmstadtensis).
pesticidal crystal prote
Accession/ID: Q45753
ID CSAB_BACUD STANDARD; PR7; 1289 AA.
AC Q45753;
SCORES Init1: 186 Initn: 484 Opt: 338 Z-score: 366.3 E(): 1.7e-14
>TXN5:CSAB_BACUD
Initn: 484 Init1: 186 opt: 338 Z-score: 366.3 expect(): 1.7e-14
Smith-Waterman score: 725; 23.4% identity in 1263 aa overlap
(6-1105:45-1267)
cry1a-105.pe MDNPNINECIPYCNLSNPEVEVLGGERIET--GY
CSAB_BACUD VLAYTPPSFLPDAGTQATPADLTAYEOLLKNEKGINAGTYSKAIADVLKGFIDDTINY
cry1a-105.pe -TPIDISLSLTOFLLE---FVPGAGFVLGVLDIIMGIFGSPQWDAFLVQ---TEQLNQ
CSAB_BACUD QTVVNLGLSLITLAVPSIGTIFPFIFGLFPAALNKHDAPPNPNKADIFEAMKPAIGEMDR
cry1a-105.pe RI---REFARNCAISRLGLESLNLYQIYAESFEWEA-DPTNPALREEMRIQFNDMNSALT
CSAB_BACUD TETADSCOTFINGEISGLQNLAAARYQSTMDIQSHGGFNKVDSGLIKKFTDEVLSINSFYT
cry1a-105.pe TAPLFAVNY-QVPLLSV-VYQAAHLHSLVRDVSFVGQW---GFDAATINSRYND
CSAB_BACUD DRPELTNTATRLTGLPYVAILASMHMLLRDIITKGTMDSKINFPTDAIDSFKTD
cry1a-105.pe LTELISNYTHAVRMYVPSLERVAGP-DSRDWIRYNQFRRELITLVDIVSLFPNYDSRT
CSAB_BACUD IKNNIKDKSKTYDVVFSLASVGTGPSA-ESAKKQKQYIEIMTHICLDFARLFFPDPDL
cry1a-105.pe YP-----IRTSQLT-REIYN--FULENFDGSGFRSGAQI--
CSAB_BACUD YPTGSGDISLOKTRAILSPFPFIPATAGLITLSTLDSNWPNNENGGAFNPKERILK
cry1a-105.pe EGSIKPSHL--MDILNSI--ITY---TDAHGEVMS--GROM-
CSAB_BACUD QFKLYPSWRAAQVGLLOPYLWALEVQDSVETRLYGQSAVSPQAGEVYVSASSNPFIQ
cry1a-105.pe ASVPGSGGPEFTFLYIGTMNAAPQOR-----IVAOLGQVYRTLSST--
CSAB_BACUD INMDTWTKTPQGSAGWNNTNL-MRGSVSGLSFLORDCTRLUSAGMGGGGADTIYSKRNHVL
cry1a-105.pe LYERFPN-----IGINNQOLSVDL---GTEFAYGTSSNLPSPAVYRKS--GT
CSAB_BACUD SYLNGTPTQISDNYSGHVCAUVGVSTPQEATLNIIGQPDQGNVSTMGPPFEKASVGET

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500      410      420      430      440      450
cry1a-105.pe V-----DSLDEIPQNNVPPRQGFHSLSVMSFRSGF--SNSSVSII-----RA
550      560      570      580      590      600
CSAB_BACUD VVKELWGANAMKLSPOOSIGIP-----ITNVTSGEYQIRCRVASNDNTNFFNVDITGGAN
510      460      470      480      490      500      510
cry1a-105.pe PMFSIHSAFNNIIASDSITQIPLVKAHTLQSGTIVVPGPFGTGGDILLRTSGGFPAY
520      610      620      630      640      650      660
CSAB_BACUD PIFQOINFASVDNTGQGVGVVVKSIATDNTSFTVKIPAKTINVLHNTQOSSDVFL
530      520      530      540      550      560
cry1a-105.pe TIVNGOLPORYRIRRYASTT---NLRIYV---TVAGERIFAGQFN---KTMMDTGDGP
570      670      680      690      700      710      720
CSAB_BACUD DRIEFVPILESNTVTIENNSYITGSANLIPALPMWSTSSDKALTGSMISITGRITPNSDD
580      570      580      590      600
cry1a-105.pe LTFQSFYSATINTAFTFPMSSQSF-----VGADTFSSGNEVYIDRFELIP
590      730      740      750      760      770      780
CSAB_BACUD ALLRFKNTYDTQPIPIPGSGKDFITLIEIQDIVSIDIFVSGLHSGDSIKLOFTNNNS
610      620      630      640      650      660
cry1a-105.pe VTA---TLEAEYNLEAQAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDFCLD
670      790      800      810      820      830      840
CSAB_BACUD GSGGSPKFTQNDLENIITQVNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDFCLD
680      670      680      690      700      710      720
cry1a-105.pe EKRELSKVKHAKLSDERNLLQDSNFKDINRQPERGMGSGTITIGQDDVFKENYVTL
690      850      860      870      880      890      900
CSAB_BACUD EKKTLRKFNQAKLSKARNLLVGNFNLID-----AWYGRNVNVSNHLLSKDVL
710      740      750      760      770      780
cry1a-105.pe SGTDFECYPTLYQKIDESKLAFTRYQLRGVIEDSDLEIYSIRNAK-HETVNVFGTG
720      910      920      930      940      950      960
CSAB_BACUD PPP--GLSPSVIFOKVEESKKRNTRYTSGFIAHATDLEIVSVRYGQEKKKVQVP-YG
730      790      800      810      820      830      840
cry1a-105.pe SLWPLSAQSPGKCGEPNRCAPHLENNPDLCSCRDGKCAKHHSHFSLDIDVGGTDLNE
740      970      980      990
CSAB_BACUD EAFPLTSSGPV--C-----CIPHSTSGNLTG-----NPHEFSYIDVGLDVIDT
750      850      860      870      880      890      900
cry1a-105.pe DLGVWVIFKIKTQGHARLGNLEFEEKPLVGEALARKVAEKKKWDEKLEWETNIVY
760      1010      1020      1030      1040      1050      1060
CSAB_BACUD NPGIEFGLRIVNPTGMARVSNLEIREDRPLAANEIRQVRVARNWTEYERAEAVTSLI
770      910      920      930      940      950
cry1a-105.pe KEAKESVRLAFNQCVD--QLQADTNIAIHA-ADKRVHSIREAYLPELSVIPGVNAAIFE
780      1070      1080      1090      1100      1110      1120
CSAB_BACUD QPVINRGLNGDNGNWSIRSISYQNTIDAIVLPTPKLRHMFMDRFSQEG---DIMA
790      960      970      980      990      1000      1010
cry1a-105.pe ELRGFTFAFSLYDARNVKNFGNGLSCMNVKGVHDVBEQNNORSVLPWPEAEVSO
800      1070      1080      1090      1100      1110      1120
CSAB_BACUD KFGQALNRAYAQLEQNTLLHNGHFTKDAANWIVEGDHQAQVLEDEGKRVLRLPDSSVSQ
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1020      1030      1040      1050      1060      1070
cry1a-105.pe EVRVC---PGRGYILRVATKGYGEGCVTTHEIENN---TDELKFSNCVBEIYFNTT
1030      1130      1140      1150      1160      1170      1180
CSAB_BACUD TIEIENFDPDKEYQLVP---HGOGEVTVLEHGETKYIETHHFAFTSQ--RQGLT
1040      1080      1090      1100      1110      1120      1130
cry1a-105.pe VTCNVTYNQEEYGATSNRGYNEARSVADYASVVEKSYTDGRRNCFENRGYRD
1050      1240      1250      1260      1270      1280
CSAB_BACUD FESNKVTVTISSEGEFLVDNIALVEAP-LPTDDQNSEGNATASNTSDTSMNNQ
1060      1140      1150      1160      1170
cry1a-105.pe YTPLPGVGVTKLEYFPTDKWIEIGETGTFIVDSVELLMEE
1070      1190      1200      1210      1220      1230
cry1a-105.pep
TXN5:CSAA_BACUD
Description: Q45760 bacillus thuringiensis (subsp. darmstadtensis).
pesticidal crystal prote
Accession/ID: Q45760
====General comments=====
ID CSAA_BACUD STANDARD; PRT; 1385 AA.
AC Q45760; . . .
SCORES Initl: 169 Initn: 471 Opt: 333 Z-score: 360.3 E(): 3.7e-14
>>TXN5:CSAA_BACUD
Initn: 471 Initl: 169 opt: 333 Z-score: 360.3 expect(): 3.7e-14
Smith-Waterman score: 633; 29.1% identity in 529 aa overlap
(587-1105;879-1363)
cry1a-105.pe TGDPLTFQSFYSATINTAFTFPMSSQSFVGVADTFSSGNEVYIDRFELIPVTATLEAYN
560      570      580      590      600      610
CSAA_BACUD VYSPFDITIQTEADSLLELOPRYGFATVNGTATVKSPNRY-DRSFKLPI-----D
570      620      630      640      650      660      670
cry1a-105.pe LEBAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTLSDEFCLDEKRELSKVKHAKR
580      690      700      710      720      730
CSAA_BACUD LQNIITQVNALFASGTQNMALHNVSDHDIIEEVVLKVDALSDEVGDEKKALFKLVQAKR
590      620      630      640      650      660      670
cry1a-105.pe LSEDERNLLQDSNFKDINRQPERGMGSGTITIGQDDVFKENYVTLGTFDECYPTLYQ
600      680      690      700      710      720      730
CSAA_BACUD LSPARNLLIGSGSFENWD-----AWYGRNVNVTSDEHLFKSDHVLPLPP--GLSPSYIFQ
610      740      750      760      770      780      790
cry1a-105.pe KIDESKLAFTRYQLRGVIEDSDLEIYSIRNAK-HETVNVFGTSLWPLSAQSPGKGC
620      800      810      820      830      840      850
CSAA_BACUD KVSESKLKNTRYIVSGFIAHAKDLEIVSVRYGQEKKKVQVP-YGEAFPLTSSGPV--C
630      860      870      880      890      900      910
cry1a-105.pe GEFNRCAPHLENNPDLCSCRDGKCAKHHSHFSLDIDVGGTDLNEGLVWVIFKIKTQD
640      1070      1080      1090      1100      1110      1120
CSAA_BACUD -----CPRPSTSGNLT-----GDP-----HPFSYSIDVGLDQANPGIEGLRIVNPT
650      860      870      880      890      900      910
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cry1a-105.pe CHARLGNLEFDEPPLAVGEALARVRAEKVRDKREKLEWETNI VYKEAKESVDALFVNS
1129 926 933 940 950 960 970
cry5AA_BACUD GVARVSAEEDREDPLANEIRQVORVARNWRTYEYKERAETVTSIQPVINRINGLYENG
1129 1130 1140 1150 1160 1170
cry1a-105.pe QYD-SLQNTNIAHFAKRVHSEIRYIPELSVIPGVNAAIFEELEGRIFTAFSLYD
926 933 940 950 960 970
cry5AA_BACUD NMGVSRSDSYNDNDIAIVLTLPLKHWFSRPSRQSG--DIMAKFOGALNRAYAQLE
1180 1190 1200 1210 1220 1230
cry1a-105.pe ARNVIKNGDFNNGLSNWNVACHVUEVEQNNQSYLVVPEVKAIVSEVRV--CPGRGYI
980 990 1000 1010 1020 1030
cry5AA_BACUD QSTLLHNGHFTKDAANWITIGEDAHQTLTLDGERVRLPDPSSVSQMLELNFNDKXEYN
1240 1250 1260 1270 1280 1290
cry1a-105.pe LRVTAYPEGVEGCGVTIHEIENN---TDELFKSNVESEYIPNNTVNCNIVNBYQRY
1040 1050 1060 1070 1080
cry5AA_BACUD LVF---HQGGEGVTLEHGEETKYIETHTHFAFFTSSO RQVLFESKATVYLAISSED
1300 1310 1320 1330 1340
cry1a-105.pe GAYTSNRNGYNEAPSPADVASVEKSYTDERENPCFENRGYDYTPNGVTKELL
1090 1100 1110 1120 1130 1140
cry5AA_BACUD GEFVLDNIALVAP-LPTDDQNSEGNFTASSTSMNNQ
1350 1360 1370 1380
cry1a-105.pep
TXNS:L07025_1
Description: L07025 Bacillus thuringiensis Bacillus thuringiensis
delta-endotoxin (CryA(a)) g
Accession/ID: L07025
LOCUS L07025.1 [BACDRVAA]
DEFINITION Bacillus thuringiensis delta-endotoxin (CryA(a)) gene, 5' end
=====General comments=====
SCORES Initi: 169 Initn: 471 Opt: 333 Z-score: 360.3 E(): 3.7e-14
>>TXNS:L07025_1
initn: 471 initi: 169 opt: 333 Z-score: 360.3 expect(): 3.7e-14
Smith-Waterman score: 633; 29.1% identity in 529 aa overlap
(587-1105:879-1363)
cry1a-105.pe TGDPLTFQFSYATINTAFTPMSSQSGFTVGATFSSGNEVVYDRFELIPVTATLEAYNNY
560 570 580 590 600 610
L07025_1 VYSPFDITIQTEADSLLELQPRYGATVNGTATVKSPPNVY--DRSFKLP-----D
850 860 870 880 890 900
cry1a-105.pe LERAKAVNALFTSTNQLGLNTVTDYHIDQVSNLVYLSDEFCLDEKREISEKVKHKKR
620 630 640 650 660 670
L07025_1 LQNTITQVNALFASGCTQNLAHWVSDHIEIPEVLKDALSDSEVFGDEKKALKRLVNOAKRFR
910 920 930 940 950 960
cry1a-105.pe LSDERNLQDSNFKDINROFERGWGSGTITIQGGDDVFKENIVYLSGTFFDECFTYLCVVC
680 690 700 710 720 730
L07025_1 LSRARNLIGGSFNWD-----AMTKGENVVYSDHLEFKSDHVLPLPPF--GLSPSPYIF
960 970 980 990 1000 1010

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cryla-105.pe KIDSKKAFATRYOLRGVIEDSODLEIVSYRYNAK-HETUNYPTGTSWPLSAQSQIGX
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
KVEESKLKNTRYTVSGFATGHKKDLIEIVSYGOEVQKVQP-VGEAFFLITNGPV--C
1020 1030 1040 1050 1060

cryla-105.pe GENRCAPHELNPPDLCSCROGCAHSHFSFLDIDVGCTDLNEDLGWVVPFKIKTGD
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
-----CPPRSTSNGL-----GDP-----HFFSYSIDVAGLDLOANFGIEFGELRIWNPT
1070 1080 1090 1100 1110

cryla-105.pe CHARLENLFEEEXPLVGEALARVKRAEKWRDKREKLEWTINIVTKAKESVDALPVS
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GMARVSLNIREDFPLAANEIROVRVARNRWTEYEKRAEVTLSLIQPIVNIRINGLYENX
1120 1130 1140 1150 1160 1170

cryla-105.pe QYD-QIQAOTNIAMTHA-ADKRVHSJREAYLPESLVIPGVNAAIPPELEGRIFTAFSLYD
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
NWNGSRISDSIQNDIDAIVLTPIPKLRHWFMSSDRFSEGG--DIMAKFOGALNRAYAOLE
1180 1190 1200 1210 1220 1230

cryla-105.pe ARNVYKGFNNGLSCMNWKGVHDVVEEQNNRSVLVVPWEAEVSGEVTV--CPGRGIY
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QSTLLHGHTKDAANWTIEGDAHQTLEDGRRLVLPDMSSSVSQMIEINFNPDKRYN
1240 1250 1260 1270 1280 1290

cryla-105.pe IRYNYKEVGEGCVTHETENN----TDELFNCSEVEEIYPNTVTCNDYTVNOBEYG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
LVF--RHSGQGTVLEHGETEKYIETHIFANFTSQ-RGLTFESNKVTVTISSSED
1300 1310 1320 1330 1340

cryla-105.pe GAYSRGKQKAPSPASVASVYEKSYYTDGRRENCFENRGYRDYPLPGVYKTEL
1090 1100 1110 1120 1130 1140

L07025_1 GELAVDNALVEAP-LPTDDNSMQNSTASSDTSDSMNNNQ
1350 1360 1370 1380

cryla-105.pcp
TXMS:CSAC_BACTU

Description: P56955 bacillus thuringiensis pesticidal crystal protein (insecticidal)
Accession/ID: P56955
=====General comments=====
ID CSAC BACTU PRT; 1220 AA.
AC P56955; . . .

SCORES Initl: 162 Initn: 449 Opt: 325 Z-score: 352.1 E(=)le-13
>>TXMS:CSAC BACTU
Initn: 449 initl: 162 opt: 325 Z-score: 352.3 expect(=)le-13
Smith-Waterman score: 765; 23.8% identity in 1212 aa overlap
(6-1105;45-1198)

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crv1a-105.pe      MDNPNINCEIPYNCLSPVEVILGGERIE--TQ
CSAC_BACTU        VLAYTPSEFPDAGTGATPADLTAYFQLLKLUKNGIAGTYSTAIADVLKGIFDDITNT
                  : ::::: : : : : : : : : : : : : : : : : : : : : : : : : : :
                  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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cry1a-105.pe --VTATLEAY-----NLERAQAVNALFTSNGLKTNVTVDYHIDQVSNLVT
 CSAC_BACTU RGIDCTLCOVENQLPSPFVTLDIRNITSOVGLFAPQGTQRLAQIASHDIEVLVXLVD
 720 730 740 750 760 770
 cry1a-105.pe VLSDFCLDEKELSEKVKHAKRLSDERNILQDSNFKDINQRPQGGSGTITQTGGDD
 660 670 680 690 700 710
 C5AC_BACTU ALSDEIGTNKKALKRLVKNQAKRLSARNLLIGGSFENWD----AWYKGRNVTVSDHE
 780 790 800 810 820
 cry1a-105.pe VFNENYTLTGTFDCYPTIYLQKIDESKLKFTYRLQRGVIEDSDQLEIYSIRNAK-H
 720 730 740 750 760 770
 C5AC_BACTU LFKSDHVLVLP--GLSPSYFQKVESEKLKANTRYTSGVFAHATDLEIVVSRVGOEIK
 830 840 850 860 870 880
 cry1a-105.pe ETNVVPTGSLWPLNSQSPIGKCEPNRCAPHLEWNPLDSCSDGEKCAHSHHFSLDI
 780 790 800 810 820 830
 C5AC_BACTU KVVQVP-YGEAFITSSGPV--C-----CIPHSTSGTLG-----NPHFFSYSI
 890 900 910 920
 cry1a-105.pe DWGCTDLNEDLGVWVIFKTKDGHARLGNLEFLEEXPLGVALARVKAERAKKWRDKREK
 840 850 860 870 880 890
 C5AC_BACTU DWGALDVTNPGTEFCLRLVNPCTGWARVSNLEIRDRPLAANEIRQVRVARNWATEYK
 930 940 950 960 970 980
 cry1a-105.pe LEWETNIVYKEAKESVDALFVNSQYD-QLOADNTIAMIIHA-ADKRVHSIREAXVLPESVI
 900 910 920 930 940 950
 C5AC_BACTU ERAEVTSLIQPVINRINGLYENENWNGSIRSDISYQNIDAIVLPTLPLTHFMFMSDRFSE
 990 1000 1010 1020 1030 1040
 cry1a-105.pe PGVWNAIFEELEGRIETAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEQNQRSLVW
 960 970 980 990 1000 1010
 C5AC_BACTU QS---DIMAFQALNRAYALQESTILLHNGHFTKDAANWIEGDARHQITLEDGRKVLRL
 1050 1060 1070 1080 1090 1100
 cry1a-105.pe PEWEAYESQVRV---CPGRGVILRTAYKEGEGCVTIIHEN---NTDELKFSNCV
 1020 1030 1040 1050 1060
 C5AC_BACTU PWSSSVSOMIEIENENPDKENLVF---HGQEGVTLEHGETKYIETHTHFANFT
 1110 1120 1130 1140 1150
 cry1a-105.pe EEEIYPNNVTICNDYTOEYGGAYTSRRNGYNEAPSVPADYASVYEEKSYTDGSRNP
 1070 1080 1090 1100 1110 1120
 C5AC_BACTU TSO-RQGLTFESKNKVTVTISSEDEGLFVDNIALVEAP-LPTDDQNSGNTAFSTSDTSM
 1160 1170 1180 1190 1200 1210
 cry1a-105.pe CEFNRGRVDYTPVGVYVTKELFPPETDKWIEGTEGTFIVDSVELLMEE
 1130 1140 1150 1160 1170
 C5AC_BACTU NNNQ
 1220
 cry1a-105.pep
 TXN5:CPAA_BACTU
 Description: O87906 bacillus thuringiensis (subsp. jegathesan). pesticidal
 crystal protein c
 Accession/ID: O87906

Description: 087906 bacillus thuringiensis (subsp. jegathesan). pesticidal crystal protein c
Accession/ID: 087906

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Product Characterization Center

CRY1A-105.pe R-YRARIYASTITNRIYVTVAGERIFAGQFNKMTGDPDLPFTQSFYATINTAFTFPM
CPAA_BACTJ DVFRIRIRCASIGVSTISVDNNGSSQVTVASTAASLDTLAYESFQVTSVPGNYFDS
AC 067906: 580 590 600 610 620 630

CRY1A-105.pe SOSSTVAGADTFSSGNEVYIDRFELIPVTATLEAYNL-ERAKVNAALFTSTNQLGLT
CPAA_BACTJ APR-----IILLRQFGRLLVDRIIIPVNF-----FPLSEQENKSVDSLFIN
580 590 600 610 620 630

CRY1A-105.pe NVTYHIDQVSNLYTSLDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINROPER
580 590 600 610 620 630

CRY1A-105.pep
TXN5:CEAA_BACTS
Description: Q45710 bacillus thuringiensis (subsp. sotto). pesticidal crystal
protein cry1Aa
Accession/ID: Q45710
ID CEAA_BACTS STANDARD; PRT; 1186 AA.
AC Q45710: . . .

SCORES Initl: 155 Initn: 558 Opt: 308 z-score: 333.7 E(): 1.1e-12
>>TXN5:CEAA_BACTS
Initn: 558 Initl: 155 Opt: 308 z-score: 333.7 expect(): 1.1e-12
Smith-Waterman score: 775; 24.9% identity in 1144 aa overlap
(461070:75-1134)

CRY1A-105.pe LSNPEVLEKSERIETGYPDISLSTQFLLSEFVPGAGFVLGLVDIIMGIFGSPQ---
CEAA_BACTS SFSLTAQQQFSSQSGANLYTLQSGISLAGSFVPGGFVAPVANNVGNLWPHKNT
580 590 600 610 620 630

CRY1A-105.pe WAF-LVQ-----LEINORREFARNOAISRLGLSNLYQIYAESF--REME--ADPT
CEAA_BACTS ADTENDKLDDEELQKQVWLLDODANNWLFLESIFDTSATVSNNAIDQWGSQVDTT
580 590 600 610 620 630

CRY1A-105.pe N-----PALREEMRI--QFNQNSALAIKFAVQNNQVPLSVVQVQANHLHSLVLRDV
CEAA_BACTS NQOQTETTSYLVNVGKFDSDSSITINENQVNNFVAAEPTVATGATRLSLYSY
580 590 600 610 620 630

CRY1A-105.pe SVFGQW-----GFAATINSRYNDLTL-----IGNVTDAAVRWY--NTGSRVWGPD
CEAA_BACTS IKFCNSWDVGFSTNDANTQKANKLRYKLWRTTNEYTSRQVKKVFKDSAMPTI--STN
580 590 600 610 620 630

CRY1A-105.pe SRDITRNFQRELTTLVLDIVLFPNYSRTYPIRTVSQLTREIYNPV--LENFSQSF
CEAA_BACTS KFSVDANVYVKGMTLAVLDWVAIMSSLYPNNDYTSQTAIEQTRVTFNNVVGQEGTQTL
580 590 600 610 620 630

CRY1A-105.pe RGAQIEGSIKRSPLHM---DILNSTIITVDHARGEYWSGHQIMASPVGFSQPEFTPL
CEAA_BACTS K--IYNTFDSLSYQHSPLPNNVNLISYYTDELQNL-----ELAVYTPKGGSG--YATP-

CRY1A-105.pe EVLGGRIETGYPDIDISLSTQFLLSEFVPGAGFVLGLVDIIMGIFGSPQWDAF---LV
CPAA_BACTJ NECDGTFPSIFGLGLVASIVISTNLNPSISGALNSGI-GEWPKTSFPLSVA
AC 067906: 580 590 600 610 620 630

CRY1A-105.pe QIEQLINQRIEFARNOAISRLGLSNLYQ-IVASSFRFQAD--PTNPA--LEENR
CPAA_BACTJ DVNLEIRALDQNAINRATGKENGIMTYNTVYLNQDMDYDIPANPAGDSREAR
580 590 600 610 620 630

CRY1A-105.pe LFAVQNYQVPLLSVVOAANHLHSLVLRDVSVFGWQSD---AA
CPAA_BACTJ RSLSEIERDRKALAGEFAEAGSQIVLLPIYAQAANIHLILKDAQMFRDGLGLRPPV
580 590 600 610 620 630

CRY1A-105.pe LRLIGNYTDHVRWNTGLRW--GPDSDRWIRYNQFRLTLT
CPAA_BACTJ PITSAEDPPESFLLR--IKKYTDHCISYDDGLAKIRSGDGTWFEKFRRENTLT
580 590 600 610 620 630

CRY1A-105.pe L-MDILNSITIIY---TDHARGEYVWSG-HQIMASPVGSGPEFTFPLYGTWGNAPQOR
CPAA_BACTJ EFNLYNSVQLFASTVSNNGEVLGNLXIM-----FEGGWTSRSGDGVTTGTFPST
580 590 600 610 620 630

CRY1A-105.pe IVAQLGQGVYRTLSLTYRPPNI--GINNQSLVLDGTEF--AYGTSSNLPASVYRKSGTV
CPAA_BACTJ MDWSYGMVYPRKHVAEITRSQALPGLANSIHVIVGIDSPRAIGPGQGDHFTSLPG--
580 590 600 610 620 630

CRY1A-105.pe DLSLEIPQNNVPPROGFHRLSHVSMERSGF---SNSSVSIIRAPM--FSWIHRSAEFN
CPAA_BACTJ DMVDCGKQVINFLEIDYRNSDHSIMMTINOSVQLASNPQTOTAFSAFSLGHHSSAGNR
580 590 600 610 620 630

CRY1A-105.pe NIITASITQPLVKAHTLOSQTTVVRGPGTGGDILRTSGGP--FAYTI--VNINGQLPQ
CPAA_BACTJ NVYDKITQIPATK--TVREHP--MIKGFPGTGGDLADLSSNSDILQYDLRSDYDRLTE
580 590 600 610 620 630

CRY1A-105.pe NIITASITQPLVKAHTLOSQTTVVRGPGTGGDILRTSGGP--FAYTI--VNINGQLPQ
CPAA_BACTJ NVYDKITQIPATK--TVREHP--MIKGFPGTGGDLADLSSNSDILQYDLRSDYDRLTE
580 590 600 610 620 630

CRY1A-105.pe NIITASITQPLVKAHTLOSQTTVVRGPGTGGDILRTSGGP--FAYTI--VNINGQLPQ
CPAA_BACTJ NVYDKITQIPATK--TVREHP--MIKGFPGTGGDLADLSSNSDILQYDLRSDYDRLTE
580 590 600 610 620 630

CRY1A-105.pe NIITASITQPLVKAHTLOSQTTVVRGPGTGGDILRTSGGP--FAYTI--VNINGQLPQ
CPAA_BACTJ NVYDKITQIPATK--TVREHP--MIKGFPGTGGDLADLSSNSDILQYDLRSDYDRLTE
580 590 600 610 620 630

cryIa-105.pe YGTMGNAPOQRIUAQLGGVYRTLSSTLYR--PEN-IGINNQQLSVLDGTEPAYTSS
CEAA_BACTS YGFIILNYAN-----SNKYGDNDPTGKPLNKQDGFQIQINNAATONSKYLDG-ETINGIGA
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe NLP-----SAV-----YRKSGTVDLSLDE-IPPQNN--VPPRQGFSHLSHVSFRRGFS
CEAA_BACTS SLPGYCTTGCSATQEPFSCITSTANSYKASCNPSTNQKINALVFTQINVGSGTKGLVL
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe NSSVSIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAHTLQSGTIVVRGPGFTGSDILR
CEAA_BACTS ASLVYPDLNPKNVFGEIILSDTNVI-----LKGIPAEGYFPNNARPTVVKEMINGASAVP
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe RTSGGPFATYTVINGQLPORVYARLYA---STNRIYVTVAGERIPAGOF-----N
CEAA_BACTS FYSGNLPFWTAINLAT---QYKIRIRANPMSDTQIGVLITONGSQISNMLTYSTTD
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe KTMIDGDLPTQSFYSATINTAFTFPMSSQSFVTGADTF--SSGNE-VYIDRFELIP---
CEAA_BACTS SSMSSNLQNVYVTEGNGNYTLDDLSTNVLTSTGDTILKLTGNGKQIFIDRIEFTMP
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe VTAT-----LEAYNLERAKQAVNALTIST
CEAA_BACTS VPAPTNTNNNGDNGNNPPHHGCAIAGTQOLCGPPKPEQVSDLEKITQVYMLFKSS
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe NQLGLKTVDTYHIDQVSNLVTLSDE-FCLDEKRELSKVKHAKLSDERNLQDSNFK
CEAA_BACTS SYEELALKVSSQINQVALKAWALSDEKFC-EKELRLKLVNKANQLLEARNLLVGNF-
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe DINRQPERGWGGTGITIQGGDDVFKENYVL---SGTFDECPTYLYQKIDESKLRAFT
CEAA_BACTS ---ETTONWVLGTNAVINYDLSFLFNGYLSLQPASGFT-----SVAYQKIDESTLKYPT
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe RYQLRGYLEDSDLEIYSIYNAKHETV-NVPGTGSMLPSAQSPTKCGENRCAPHLE
CEAA_BACTS RYKVGFGICQSNQVELIISRYGREIDKILNVPYAGPL-PITADASI-TC-----CAPEID
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe WNPDLDCSRGDEKCAHSHHFLSDIDVCGCTDLNEDLGVVWFIKIKTOGHARLGNLEFL
CEAA_BACTS -----QCDGQGS-----DSHFFNYSIDVGAHPENLPGIEIGIKLVQSGNYGITYISNLEII
400 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 340 350 360 370 380 390

cryIa-105.pe EEKPLVGEALAPKRAEKWKRRKLEWETNI--VYKEAKESVDALFVNSQYDQLQADT
CEAA_BACTS EERPLTEMEIQAVNRKQKW--KREKLECASVSELQPIINQIDSLFKDANW-----Y

cryIa-105.pe NIAMTHRAADKEVHSIREAYLPEL-----SVIPGVNAAIFEELEGRIETAFSLYDARNVIK
CEAA_BACTS NDILPHVYIQLKNIIVPDLPLKWKWFDHLPFGYHEIEQKKKALKHAFTOLDEKLIH
930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 930 940 950 960 970 980 990 1000

cryIa-105.pe NGDFNNGLSCNVKNGHVDVEEQNNQRSVLVVPWEAEVSEQVRVC---PGRGYILRVYAY
CEAA_BACTS NGHFATNLIDWQVEGDARMKVLNNALALQLSNWDSSVSQSIDILEFDEDKAYKLRY--Y
980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120

cryIa-105.pe KEGYEGCVTTHEENTDELKPSNCVVEEYIPNNTVTCNDIYVNOEEYGAAYTSRNRGY
CEAA_BACTS AQCGST-----IOFGNCEDEAFQFNNTSFVYKEKIIYFDTPTPSINLHIQSEG
1040 1050 1060 1070 1080 1090 1100 1110 1120 1040 1050 1060 1070 1080 1090 1100 1110 1120 1040 1050 1060 1070 1080 1090 1100 1110 1120

cryIa-105.pe NEAPSVADYASVVEEKSYPDGRNCPENRGYRDYTLPLVGVYTKLEYFPETDKWVI
CEAA_BACTS SEFVSSSIDLVLSDDDE
1100 1110 1120 1130 1140 1150 1160 1170 1180 1100 1110 1120 1130 1140 1150 1160 1170 1180

cryIa-105.pe
TXN5:U13955_1
Description: U13955 Bacillus thuringiensis Bacillus thuringiensis sotto
PS80JUL delta endotoxin
Accession/ID: U13955
=====General comments=====

LOCUS U13955_1 [BU13955]
DEFINITION Bacillus thuringiensis sotto PS80JUL delta endotoxin gene, complete
(46-1070:75-1143)

SCORES Init1: 155 Initn: 558 Opt: 308 z-score: 333.7 E(): 1.1e-12
>>TXN5:U13955_1
initn: 558 init1: 155 opt: 308 z-score: 333.7 expect(): 1.1e-12
Smith-Waterman score: 775; 24.9% identity in 1144 aa overlap

cryIa-105.pe LSNPEVILGGERIETGYTPIDISLSLTOFLLSFVPGAGFVLGLVDIITWIGFPGSQ---
U13955_1 SFLSLALQGGFSASQGGAFNYLTLQSGISLAGSFVPGGTFAPIVNMVIGLWLPKHKNT
50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220

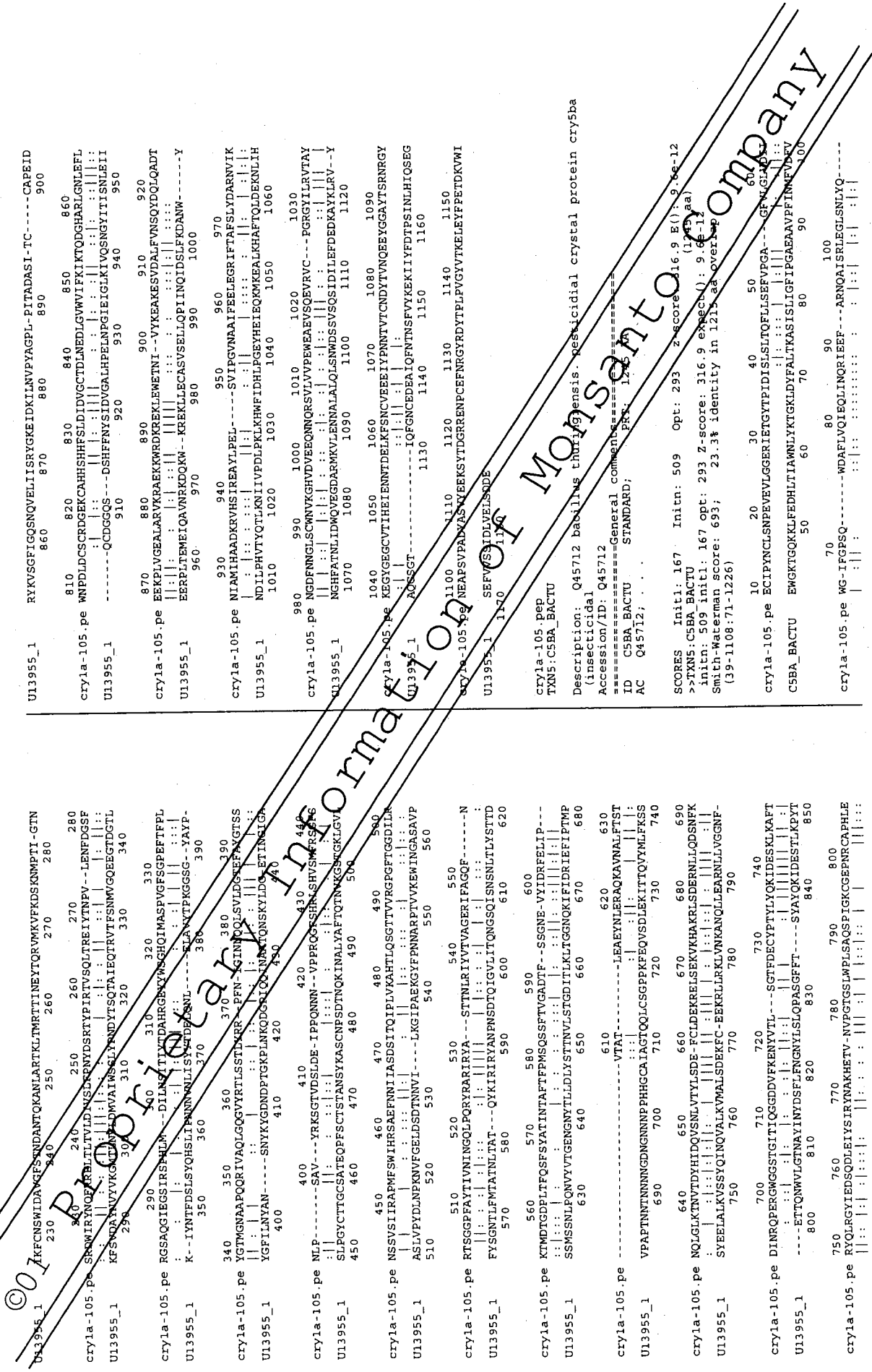
cryIa-105.pe WDAF-LVQ-----TEQLINGRIEFARQAISRLEGLSNLYQIYAESF--REWE--ADPT
U13955_1 ADTENLIKILDEEIQKQNKALLDQDRNNTSFLIESIFDTSATVSNAIDAQMSGTVDTT
110 120 130 140 150 160 170 180 190 200 210 220 110 120 130 140 150 160 170 180 190 200 210 220

cryIa-105.pe N-----PALREEMRI--QFNDMSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLRDV
U13955_1 NRQOKTPTTSDYLVNVGKFDSDADSSLIITNENQIMNGNFDVAAPYFVIGATLRLSLYQSY
170 180 190 200 210 220 170 180 190 200 210 220 170 180 190 200 210 220 170 180 190 200 210 220

cryIa-105.pe SVFGQRW-----GFDAATINGRYNDLTRL-----IGNYTDHVRVY--NTGLERVWGPD
180 190 200 210 220 180 190 200 210 220 180 190 200 210 220 180 190 200 210 220 180 190 200 210 220

U13955_1 AKFCNSWIDAGFSNDANTQKANKARTKLTWRTTINEYTORUMKVPKDSKNMPTI-GTN
230 240 250 260 270 280
cry1a-105.pe SRWIRYNOPRELLTLVLDNSLSNYSRTYPIRTVSQUTRIYINPV--LENFDSF
280 290 300 310 320 330 340
U13955_1 KFSNDYANVYVKGCLMADWVAISLILYNDYTSQTAIEQTRVTFNSMVGQEEGTDL
290 300 310 320 330 340
cry1a-105.pe RGSAGIEGSIKSPHM--DILASITITVDARHGVSWSHQIMASPCFSGPFTPL
340 350 360 370 380 390
U13955_1 K--RYNTFDSLSYQHSILPNNNULISYVDFSNL-----ELAWTPKGGSG--YAYP-
350 360 370 380 390
cry1a-105.pe YGTLNLAN-----SNKYGNDPTGKPLNKQDGRLOSNATONSKYLDS--ETINGIG
400 410 420 430 440
cry1a-105.pe NLP-----SAV---YRKSQTVDLSDE--TPQNNN--VPRQGSRSRSHVSNWRSFSS
440 450 460 470 480 490 500 510
U13955_1 SLPGYCTTGCSATEQPFSTANSYKASCPNPSDTQKINALYAFQTQTNKSGSKLGV
450 460 470 480 490 500 510
cry1a-105.pe NSSVSIIRAMPFSWHRSAEFNNIADSITQIPLVKAHTLOSQTTVRGPGTGGDIL
510 520 530 540 550 560
U13955_1 ASLVYDLNPKVFGELSDTNVLI---LKGIPAKGFPNNRPTVKEWINGASAVP
510 520 530 540 550 560
cry1a-105.pe RTSGGPAYTIIVNINQLPQRYRIRYA--STTNIRIYTVVAGERIFAGQF-----N
560 570 580 590 600 610 620
U13955_1 FVSGNTLFMTNLATAT---QYKIRIRYANPNSDTQIGVLITONGSQSLSNLTSTTD
570 580 590 600 610 620
cry1a-105.pe KTMIDGDLTFQSFYSATINTAFTFMSQSFVGDTP--SSGNE-VYIDREFLIP---
620 630 640 650 660 670 680
U13955_1 SSMSSNLPQNVYVTGNGNYTLDDLYSTTNVLSTGDTITLKTGGNOKIFIDRIEFTMP
630 640 650 660 670 680
cry1a-105.pe VTAT-----LEAYNLEAQAQVNAFTST
680 690 700 710 720 730 740
U13955_1 VPAPNTNNNGDNGNNPPHGCAIAGTQOLCSGPPFEQVSDELEKITTVYMLFKS
690 700 710 720 730 740
cry1a-105.pe NQLGKTNVTDYHIDQVSNLTVLSDE--FCILDERELSEKVKHAKLSDERNLQDSNFK
740 750 760 770 780 790
U13955_1 SYEELAKVSSYQINQVALKVMAISDEKFC--EKKLRKLKLVANKALLLEARNLLVGGNF-
750 760 770 780 790
cry1a-105.pe DINRQPGWGGSTGITQGGDDVFNKYNVL-----STTFECPTTYLQKIDSKLXFT
800 810 820 830 840 850
U13955_1 -----ETTONWVLGNVAYINDYDFLNGNLYLSLOPASGFT-----SVAYQKIDESTLKPYT
800 810 820 830 840 850
cry1a-105.pe RYQLRGYEDSQDLEIYSIRYNAKHETV--NVPGTGSLWPLSAQSPGKCGENRCAPHLE
850 860 870 880 890 900

U13955_1 RYKVGFIGSQSNQVELIISRYGKEIDKILNVFYAGPL-PITADASI-TC-----CAPEID
860 870 880 890 900
cry1a-105.pe WNPDLCSRDGECAHSHHFSLDIDVCGCTDLNEDLGWVWIFKIKTODGHARLGNLEFL
810 820 830 840 850 860
U13955_1 -----QCDGQS---DSHFYNSIDVGLALPELNPGLIEGLKIVSGNGYITINLEII
910 920 930 940 950
cry1a-105.pe EEKPLVGEALARKVKAERKWKREKLEWETNI--VYKEAKESVDALFVNSQYDQLOADT
870 880 890 900 910 920
U13955_1 EERPLEMEIQAVNRKQDKW--KEKLECASVSELLOPIINQIDSLFKDANW-----Y
960 970 980 990 1000
cry1a-105.pe NIAMIHAADKRVKIREAYLPDL-----SVIPGVNRAIFEELEGRIETAFSLYDARNVTK
930 940 950 960 970
U13955_1 NDILPHVTVYQTLKNIIVPDLPLKHWFIHLPGVEHEIEQMKREALKHAFPTQDEKNLIH
1010 1020 1030 1040 1050 1060
cry1a-105.pe NGDENNGELSCWNVKGVHVDVEQNNORSVLVVPWEAEVQEVVVC---PGRGYILRVATY
980 990 1000 1010 1020 1030
U13955_1 NGHFATNLIDWQEGDARKVLENNALALQLSNWDSSVSQSIDILEDEDKAYKLAV--Y
1070 1080 1090 1100 1110 1120
cry1a-105.pe KEGVGEQCVTIHEIENNTDELKFCNVEEIEIYPNNTVTCNDYVNOEEYGGAYTSNRGY
1040 1050 1060 1070 1080 1090
U13955_1 AQSSGT-----IQFGNCEDEAIQFNNTSFVYKEKIIYFDTPSINLHIQSEB
1130 1140 1150 1160
cry1a-105.pe NEAFSVPAIVASVIEKSTIDGRNCPNCFNRGRDYTPLPVGYVYKELEYFPETDKVMI
1110 1120 1130 1140 1150
U13955_1 SEFVQSIDLVELSDE
1170 1180
cry1a-105.pe TXN5:CSBA_BACTU
Description: Q45712 bacillus thuringiensis, pesticidal crystal protein cry5ba
(insecticidal)
Accession/ID: Q45712
ID: CSBA_BACTU
AC: Q45712; . . .
General comment: PR: 126
SMITH-WATERMAN SCORE: 693; 23.3% identity in 1215 aa overlap
(39-1108:71-1226)
INITIALS: 167 Initn: 509 Opt: 293 Z-score: 16.9 E(1): 9.6e-12
CRY1A-105.pe ECIPYNCLSNPEVEVLGGERIEGTVPIDISLISLTOFLSEFVPGA---GFVGLAAS
10 20 30 40 50 60 70 80 90 100
CRY1A-105.pe WG-IFGPSQ-----WDAFLVQIEQLINQRIEF---ANQAISELEGLSNLYQ-----
70 80 90 100



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CSBA_BACTU WPKLFGANTGKQDLFNAIMDAVNWQNDKFLSNLSTLNTKTIIEGLQNLGLFNAIQV 110 120 130 140 150 160

cry1a-105.pe -IYAESFRE---WEADPTNPAL--REEM-RI--OFNDMNSALITTAIFL-----A 110 120 130 140

CSBA_BACTU AICQSGTDERVNFQDCTPCPNQPCCKDLDEVASREDTANSQTOHLEFKNPNSDENS 170 180 190 200 210 220

cry1a-105.pe VQNYQ---VPL-LSYVQAAHLVLRDVSFVGQMGF-DAATINSRYNDLTRIGNYT 150 160 170 180 190 200

CSBA_BACTU TQEFKTSVELTLPMTYITVATLHLLYEGYIEFTKMFNEQVYLNKLVELQQLIHYS 230 240 250 260 270 280

cry1a-105.pe DHAVRWNTGLERWGPDSRDWIRYQFRELTLVILVLSFNVDSRTYPIRTVSOLT 210 220 230 240 250 260

CSBA_BACTU ETVRTSFLQFLTLNRSKSVNAYRYVRNVMVNCULDIAATWPTFDTHYHQQGLDLT 290 300 310 320 330 340

cry1a-105.pe RELVTN---PVLENDSFGRSGAGIEGSIKSPH-LMDILNSITITDHRGEYVWSG-- 270 280 290 300 310

CSBA_BACTU RIILSDTAGPIEYITGD---KTSGREHNSITPNILDTSPPTQHSFVSVDISIVSRKE 350 360 370 380 390

cry1a-105.pe -HQIMASPVGSGPFTFPLVGTMGNAAPQQRIVAQLGQGYRILSTL-----YRRPNI 320 330 340 350 360 370

CSBA_BACTU LQQLDIATYSTNNSNCHP-YGLRLSYDGSYDYGDPQPTFTSNNYCHNSYAPITL 400 410 420 430 440 450

cry1a-105.pe GINNQOLSVLDCTEFAYCTSNLPSAVYKSGTV--DS-LDEI--PPON--NNVPRGFS 380 390 400 410 420

CSBA_BACTU -VVARHLYNAKGS--LQNVESLVSTVSGSGSCICDAWYILPPTQTSKNESRDPQKIN 460 470 480 490 500 510

cry1a-105.pe HRLSHVSMFRGFSNNSVSIIRAPMFSWIRHSAEFNNIIAS-DSITQIPLVKAHTL---- 430 440 450 460 470 480

CSBA_BACTU -VLYPITETVWKGTCGNLGVISA-----YVPMELVPENVIGDWNADTKLPLTLQKGFPEK 520 530 540 550 560

cry1a-105.pe -----QSGTIVVRGPTGTDILRTSGSPFAYIVVINGQLQYRARIKRYASTNLR 490 500 510 520 530

CSBA_BACTU YGSEYNNRGLSLVR-EWINGNNAVLKSNQSOSVGIQITN---QTKQYRCRYASKGNN 570 580 590 600 610 620

cry1a-105.pe IYVTV-A-GERIFAG--QFNKMTMDTDLPLTFQSFVATINTAFTFPMSSQSFVTGADTFSS 540 550 560 570 580 590

CSBA_BACTU VYFNVDLSENFPNRSISFGSTESSWGQCGKXIL-LKSITTVIEPAGSFYVHI--TWGG 630 640 650 660 670 680

cry1a-105.pe GNEVYIDRFELIP-----VATILEAEYN----- 600 610

CSBA_BACTU SSDLFLDRIEFVKIQFQCDNNLHCDNPNVDTDCTFCVCCTSLDCCDNNPRGLDCT 690 700 710 720 730 740

cry1a-105.pe -----LERACKAVNALFTSTNQLGKLTNTVDYHIDQVSNLTYLSDEF 620 630 640 650

CSBA_BACTU LCCQVENQLPSPVTLTDLQNTTQVNVALVASEHDTLATDVSDEIEEVVVKVDALSCEV 750 760 770 780 790 800

cry1a-105.pe CLDEKREISEKVKHAKLSLSDSNFQKIDINRQPERGWSGTGITIQGGDDVFKENY 660 670 680 690 700 710

CSBA_BACTU FGKEKALKRLVNHHTKRLSKARNLLIGGNFDNL-----AWYGRNVNVNSDHELFKSDH 810 820 830 840 850

cry1a-105.pe VTLSGTFDECYPTLYQKIDESKLFKFTYQLRGVIEDSQLEIYSIRNAK-HETVNP 720 730 740 750 760 770

CSBA_BACTU VLLPPP--TLYSSYMFQKVEESKLANTRYTVSGFIAHAEDEIVVSRYGQEVKKVQVP 860 870 880 890 900 910

cry1a-105.pe GTCSLWPLSAQSPGKCGEPNRCAPHLENNPDLDCSCHRGEKCAHSHHPSLDDIVGCTD 780 790 800 810 820 830

CSBA_BACTU -YGEAFPLISRGAL--C-----CPFR-----STSGKPA--DEHFFSYSLDVGTL 920 930 940 950

cry1a-105.pe LNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKREKLEWETN 840 850 860 870 880 890

CSBA_BACTU VEAMPGTELGLRIVERTCMARVSNLEIREDRPLKKNELNRVQRAARNWRTAYDQERAET 960 970 980 990 1000 1010

cry1a-105.pe IVYKEAKESVDALFVNSQYDQLQADTNIAIMRAADKRVHSIREAYLPEL-----SVI 900 910 920 930 940 950

CSBA_BACTU ALIQPVLNQINALEYNE-----DMNGAIRSGVS--YHDLEAIVLPTLPKLNHMFMSDM 1020 1030 1040 1050 1060

cry1a-105.pe PGVNAATFELEGRIFTAFSLYDARNVKNNGDFNGLSCWNVKGVHVEEQNNQSRVLV 960 970 980 990 1000 1010

CSBA_BACTU LGEQSLAQFOEALDRAYTOLESITLHNGHFTTDAANWTIEGDAHHAILEDGRVLR 1070 1080 1090 1100 1110 1120

cry1a-105.pe PEMEAESVQEVRC--FGRGYILLRVYAYKEGEGCVTIIEINN-----TDELKFSNCV 1020 1030 1040 1050 1060

CSBA_BACTU PDMSSSVQTIETIENFDPDKEYQLVPHAQ---GEGTVSLQHGEGEYVETHPHKSAFT 1130 1140 1150 1160 1170 1180

cry1a-105.pe EEEIYPNNVTCDYTNQOEYGGAYTSNRNGVNEARSPADYASVVEEKSYTDGREN 1070 1080 1090 1100 1110 1120

CSBA_BACTU TSH-RQGVTFETNKVTVEITSEDEGEFLVDHIALVEAP-LPTDDOSSCGNTSTNNTSM 1190 1200 1210 1220 1230 1240

cry1a-105.pe CEFNRGYRDYPLPVGYVTKSELEYFETDKVWIEGTEGTFIVDSVELLMEE 1130 1140 1150 1160 1170

CSBA_BACTU NNNQ

cry1a-105.pep
TXN5:U19725_1
Description: U19725 Bacillus thuringiensis Bacillus thuringiensis PS86Q3 delta
endotoxin gene
Accession/ID: U19725
LOCUS U19725_1 [BtU19725]
=====General comments=====

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U19725_1 TSH-RGVTFETNKVTVETITSEDEGEFLVDHIALVEAP-LPTDQSDGNTTNTSNTSMT
1190 1200 1210 1220 1230 1240

cry1a-105.pe CEFNRGRDYTPLPVGYVTKLEYFETDKVWIEGEGEYFVDSVELLMEE
1130 1140 1150 1160 1170

U19725_1 NNNQ

cry1a-105.pe
TXN5:Q9S6N5

Description: Q9S6N5 bacillus thuringiensis. cry2aa protein. 6/2001
Accession/ID: Q9S6N5
=====General comments=====
ID Q9S6N5 PRELIMINARY; PRI; 633 AA.
AC Q9S6N5;
DT 01-MAY-2000 (T=EMBLrel. 13, Created) . . .

SCORES Initl: 163 Initn: 163 Opt: 284 z-score: 311.4 E(): 1.9e-11
>TXN5:Q9S6N5
Initn: 163 initl: 163 opt: 284 z-score: 311.4 expect(): 1.9e-11
Smith-Waterman score: 285; 21.3% identity in 597 aa overlap
(41-606:56-626)

cry1a-105.pe IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGVLG--LVDIIWGIF
20 30 40 50 60
Q9S6N5 FEHKS LDTIQEKWEMWRRDTHSLYVAPVVGTVSSFLKK---VGLSIGKRIELSELWGII
30 40 50 60 70 80

cry1a-105.pe GPSQ-----WDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESFREMEADPTNP
70 80 90 100 110 120
Q9S6N5 A-PLSITSSVNTMQQLFLNRLPQFOIQGYQLLLPLPFAQANHLHSFIRDVILNADWGI
150 160 170 180 190 200

cry1a-105.pe ALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVVOAANHLHSVLDRVSVFGQWGF
130 140 150 160 170 180
Q9S6N5 A-PLSITSSVNTMQQLFLNRLPQFOIQGYQLLLPLPFAQANHLHSFIRDVILNADWGI
150 160 170 180 190 200

cry1a-105.pe DAAATINSRYNDLTRLGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTTLVD
190 200 210 220 230 240
Q9S6N5 SAATLRTVRYLRYNTRDYNSYNTVQTAFR--GLNTRLHMDL---EPRTYMFLNVFE
210 220 230 240 250

cry1a-105.pe IVSLFPYNDERTPIPTVSQLTREIYNTPNVLENFDSFGSGAQEGISIRSPHLMILNS
250 260 270 280 290 300
Q9S6N5 YVSIWSLFKYQSLMSSGANL-----YASGSGPQQTQSFTAQNWPFYLSLFQVNSNYILSG
260 270 280 290 300 310

cry1a-105.pe IT-----IYDARGEYVWSGHOIMASPGVSGPEFTPLVGTGNGAPOQRVAOLQG
310 320 330 340 350
Q9S6N5 ISGTLRTFTFNGIGGLPGSGTTHSINSARVNSGCVSS-----GLIGATNLNHNENCSST--
320 330 340 350 360

cry1a-105.pe GYVRLSSTLYRRFPNIGINNQLSV-LDGTEFAYGTSSNLPSAVRYSKGTVDLSDEIPP
360 370 380 390 400 410

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Q9S6N5 -VLPPLSTPFVRSWLDSDGTREGVATSTNQTESQTTLISLRCAFSARGNSNYFPDYPI
370 380 390 400 410 420

cry1a-105.pe QN-NNVP--PROGFSRHLSHVSMERSGFSNSSV-SIIRAPMFSWIHR-----SAEENLI
420 430 440 450 460 470 480
Q9S6N5 RNISGVPLVRMEDLTRPLHYNQIRNIESPGTGGARAYLVSVHKKNDKIYAENGTM
430 440 450 460 470 480

cry1a-105.pe ---ASDSITQIPLVKAHTIQ--SGTIVVRGPGFTG-GDILRTSGGPFAYTIVNINGQLP
470 480 490 500 510 520
Q9S6N5 IHLAPEDYTGTFTISPIHATQVNNQTRTFISEKFGNCGSLARFEQSNNTARYTLRNGN--
490 500 510 520 530 540

cry1a-105.pe QRYRARIYASTTNLRIYTVAGRIIFAGQFNKMTDGTPLTFQFSFYATINTAFTFPM
530 540 550 560 570 580
Q9S6N5 -SYNLYLRVSSIGNSTIRVING-RVTVSVNNTTNNQVNDNGARFSDINIGNIVASD
550 560 570 580 590 600

cry1a-105.pe QSSFTVGAD-TFSSGNEVIDRFELIPVTATLEAENLERAOQAVNALFTSTNQLGLKTN
590 600 610 620 630
Q9S6N5 NTNVTLDINVTLSNGTTPPLNMIMFVNPPPLY
600 610 620 630

cry1a-105.pe
TXN5:C2AA_BACTK

Description: P21253 bacillus thuringiensis (subsp. kurstaki) pesticidal
crystal protein cry2
Accession/ID: P21253
=====General comments=====
ID C2AA_BACTK STANDARD; PRI; 633 AA.
AC P21253; OS2764; . . .

SCORES Initl: 166 Initn: 166 Opt: 282 z-score: 309.2 E(): 2.6e-11
>TXN5:C2AA_BACTK
Initn: 166 initl: 166 opt: 282 z-score: 309.2 expect(): 2.6e-11
Smith-Waterman score: 284; 21.6% identity in 597 aa overlap
(41-606:56-626)

cry1a-105.pe IPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGVLG--LVDIIWGIF
20 30 40 50 60
C2AA_BACTK FEHKS LDTIQEKWEMWRRDTHSLYVAPVVGTVSSFLKK---VGLSIGKRIELSELWGII
30 40 50 60 70 80

cry1a-105.pe GPSQ-----WDAFLVQIEQLINQRIEFAFNQALSRLEGLSNLYQIYAESFREMEADPTNP
70 80 90 100 110 120
C2AA_BACTK PFSGSTNMQDILRETEQFLNORLNTDILARVNAELIGLOANIREFNOQVDNF--LNFQIN
90 100 110 120 130 140

cry1a-105.pe ALREEMRIQFNDMNSALTTAIFLFAVQNYQVPLLSVVOAANHLHSVLDRVSVFGQWGF
130 140 150 160 170 180
C2AA_BACTK PVPLSITSSVNTMQQLFLNRLPQFOIQGYQLLLPLPFAQANHLHSFIRDVILNADWGI
150 160 170 180 190 200

cry1a-105.pe DAAATINSRYNDLTRLGNYTDHAVRWYNTGLERVWGPDSR--DWIRYQFRRELTTLVD
180 190 200 210 220 230 240

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CRYA_BACTK SAATLRVYRDYDNTYRDYSNYCINTYOTAFR---GLNTRLHDM---EFTYMLNVEE
CRYA-105.pe IVSAPFNQDRTYRTVTSQSLPRTNPNVLENFGDSRGAQOIEGSRPHLMDILNS
CRYA_BACTK YVSIWLEFYQSLWMSGANL---YAGSGSQOQTOSTAQNWFFLSLVFQVNSNYLISG
CRYA-105.pe IT-----IYTDARCEYVSGHQMAWGFSGPPTPLNG---TWGNAAPQORVAOL
CRYA_BACTK ISGTRLSITFPNIGGLPGSTTHSNGARVNSGG-VSSGLLRNHNHNCSTVLPLP
CRYA-105.pe GQGVRT-LSSTLYRRPFGNINNOQ-----LSMLDGTFFAGSSNLSAIVRM-SGT
CRYA_BACTK STPFVRSLDGTDRSGVATSTNMOTESFOTLLSACGASRGSNSYFFPTIRNLSGV
CRYA-105.pe ---VDSLDIIPP-ONNVPPROGFGHRLSHVSMFRSGNSVSLEA-PMFSWISAE
CRYA_BACTK PLVIRNELLTRPLHYNQIRNIESPSGTPGGARVYLVSVHNRKNNIYAANENGTHLAPL
CRYA-105.pe -FNNIADSITQPLVAKHTLQSGTVVRGFGTGDILRRSGTGGPAYTIVNINQOLP
CRYA_BACTK DYTFG-----TISPATQVNN-QTRTFISEKFG-NOGDSLRFSQNTTARVTLRNGN--
CRYA-105.pe QRYRARIYASTNLRIVTVAGERIFACQFNKMTDGDPLTFQTSFYATINTAFTFMS
CRYA_BACTK -SYNLYLRVSSIGNSTIRVTING-RVYTVSNVNTITNDGVDNGARFSDINIGNIVASD
CRYA-105.pe QSSFTVGAD-TFSSGNEVIDRELPVATLEAEYNLERAQAVNALFTSTNQLGLKTN
CRYA_BACTK NTVNTLDINVTLSGTPFDLMIMFVTLNPLPY
CRYA-105.pep
TXNS:Q9S6N4
Description: Q9S6N4 bacillus thuringiensis. cry2aa protein. 6/2001
Accession/ID: Q9S6N4
ID Q9S6N4 PRELIMINARY; PRT; 633 AA.
AC Q9S6N4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
SCORES Initl: 166 Initn: 166 Opt: 282 z-score: 309.2 E(): 2.6e-11
>TXNS:Q9S6N4
Initn: 166 Initl: 166 Opt: 282 Z-score: 309.2 expect(): 2.6e-11
Smith-Waterman score: 284; 22.3% identity in 602 aa overlap
(41-606:56-626)
CRYA-105.pe IPYNCLSNPEVILGGERIETGYTIDISLSTQFLISEFVPGAVFLG--LVDIINGIFP
CRYA_BACTK

Q9S6N4 FEHKSLLDTQKEMENKTDHSLYVAPVVGTVSSFLKK---VGSILGKRILSELWGII
CRYA-105.pe GPSQ---WDALFVQIEQLINRIEFPARNOAISLEGLSNLYOIAESFREWEDPTNP
Q9S6N4 FFSSTNLMDILRETEQFLNRLNITDITLARVNAELIGLANIREFNQQVDFN- LNPTQN
CRYA-105.pe ALREMIQNDNSALITATPLFAVONQVPLLSVYQAOANLHLSVLDRVSVFGQRWGF
Q9S6N4 PVPISITSSVNTMQQLFNRLPQFOGYQQLLLPLFAOANMHLSTIRVILNADEWGI
CRYA-105.pe DAATINRKYNDLTRLLGNVTDHAWNTGLERWGPDSR--DWIRYNQFRELTLTVLD
Q9S6N4 SAATLRVYRDYDNTYRDYSNYCINTYOTAFR---GLNTRLHDM---EFTYMLNVEE
CRYA-105.pe IVSLEFPNVDSTYPIRTVSOL-----TREIYTN---PVLEN-FDGSFRGSAQIEG-
Q9S6N4 YVSIWLEFYQSLWMSGANLVSAGSGGQOQTOSTAQNWFFLSLVFQVNSNYLISGSGT
CRYA-105.pe SIRSPLMDILNISTITV-DAHRGEYVWGHQIMASPVGFSGPEFTPLYGTMGN-AA
Q9S6N4 PLSITFPNIGGLPGSTTHSLSARVNY--SGG-VSSGLIGATNLNHNFCSTVLPLST
CRYA-105.pe PQORIVAOQLAGVAF---TLLSSTLYRRPFGNINNOQLSVLDGTETPAYTSSNLSAVYR
Q9S6N4 PFVAF--WLPQSTDRSGVATSTNMOTESFOT---TILSRCAFGASRGSNSYFFPTIR
CRYA-105.pe K-SGT---VDSLDIIPP-ONNVPPROGFGHRLSHVSMFRSGNSVSIIIRA-PMFSWI
Q9S6N4 NISGVPLVNEBTRPLDQVNNIESSTPFGARAYLVSVHNRKNNIYAANENGTMII
CRYA-105.pe HRSAE-FNNIADSITQPLVAKHTLQSGTVVRGFGTGDILRRSGTGGPAYTIVNINQOLP
Q9S6N4 HLAPEDYTG-----TISPATQVNN-QTRTFISEKFG-NOGDSLRFSQNTTARVTLRNGN
CRYA-105.pe NGQIPQRYRARIYASTNLRIVTVAGERIFACQFNKMTDGDPLTFQTSFYATINTAFTFMS
Q9S6N4 NGN--SYNLYLRVSSIGNSTIRVTING-RVYTVSNVNTITNDGVDNGARFSDINIGNIVASD
CRYA-105.pe TFPMSQSFTVGAD-TFSSGNEVIDRELPVATLEAEYNLERAQAVNALFTSTNQLGLKTN
Q9S6N4 IVASDNTNVTLDINVTLSGTPFDLMIMFVTLNPLPY
CRYA-105.pe GLKTNVTYDHYDQVSNLVTLSDEFLDEKRELSEKVKHAKLSDERNLLQDSNFKDINR

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cry1a-105.pe 490 500 510
TTVRRGP-----GFT-----GDILRRTSGGPFAYIVVINGQ
: : : ||| : : : : : : : : : : : : : : : : : :
CIBA_PAEPP TMIHQAPNDGTGFTVSPHLASFTHPSEAHIQENYGNSGDSLRLT--GPTAITAYMLSGD
530 540 550 560 570 580 590

cry1a-105.pe 520 530 540 550 560 570 580 590
LPQRYRARIYASITNIRIYTVAGERIFAQNFMTDGDPLT-----PQSESY-ATIN
: : : : : : : : : : : : : : : : : : : : : : : :
CIBA_PAEPP GRTIYKLVLRVSGVIT-RIITAKVRGNSGYLEYINTVNNQGITDNGSKPDQFEFRPTII
590 600 610 620 630 640 650

cry1a-105.pe 580 590 600 610 620 630 640 650
TAFTFPMQSQSTFGVAGDTFGSGNEVYIDRFILPVTATLEAEYNLERAKAVNALETSTN
: : : : : : : : : : : : : : : : : : : : : : : :
CIBA_PAEPP IDAQTVILE-PSATSN-FDLMLNIFIPYDT-PIY
650 660 670

cry1a-105.pe 640 650 660 670 680 690
QLGLKNTVDYHDQVNLNVTYLSDFCLDEKRELSKKVHKRUSDERNLLQDSNFKOI

cry1a-105.pep
TXN5:C2AB_BACTK

Description: P21254 bacillus thuringiensis (subsp. kurstaki). pesticidal
crystal protein cry4
Accession/ID: P21254
=====General comments=====
ID C2AB_BACTK STANDARD; PRI; 633 AA.
AC P21254; . .

SCORES Init1: 128 Initn: 128 Opt: 273 Z-score: 299.2 E(): 9.2e-11
>>TXN5:C2AB_BACTK
Initn: 128 Init1: 128 Opt: 273 Z-score: 299.2 expect(): 9.2e-11
Smith-Waterman score: 281; 21.0% identity in 600 aa overlap
(41-610:56-630)

cry1a-105.pe 20 30 40 50 60 70 80
IPYNCLSNPEVEVLGERIETGVTIDISLSTPLFISEF--VPGAGFVLGLVDIIWGIF
C2AB_BACTK FQHKSLDTVQKEMTEKKNHSLVLPDVGTVASFLPKKVGSLVKRILSELRLPPSG
30 40 50 60 70 80

cry1a-105.pe 70 80 90 100 110 120
GPSQWDAFLVQIQEIQINRIEERFARNOAISRLGSLNLYQIYAESTREWEADPNP---A
: : : : : : : : : : : : : : : : : : : : : : : :
C2AB_BACTK STNLMODILRETEKFLNQLRNTDTLARVNAETGL---QANVEENFQNVQFNLNPNRA
90 100 110 120 130 140 150

cry1a-105.pe 130 140 150 160 170 180 190
LREEMRIQFNDMSALTTAIPFAYNOYVPLISYVQANLHLVLRDVSFGQRGFD
: : : : : : : : : : : : : : : : : : : : : : : :
C2AB_BACTK VPLSTISSTVMQQFLNRLFPQMGIQQLLPLFAGANLHLFIRDIVLNADENGIS
150 160 170 180 190 200 210

cry1a-105.pe 190 200 210 220 230 240
AATINSRYNDLRLIGNYTDHAWVNTGLERVMGPDSS--DMIRYQNFRELTITVLDI
: : : : : : : : : : : : : : : : : : : : : : : :
C2AB_BACTK AATLETYRDYLVKNYTDVSNYCINTYQSAFK--GNTRLHML---EFTYMFVNLVFEY
210 220 230 240 250 260 270

cry1a-105.pe 250 260 270 280 290 300
VSLFNPYDSRTYPIRTVSQLTRILEYTNVPLENFDPSFGSGAQEGESRSPHMDLINSI
: : : : : : : : : : : : : : : : : : : : : : : :

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Monsanto Company

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Product Characterization Center

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CRY2AD_BACTU STNLMEDILRETEKFLNQKINTDTLSRVNAELTGL---QANVEEFNRQVDNFLNPNRRA
cry1a-105.pe LREEIRIQFDMNSALTAIPPLFAVQNVQVPLSVYVQANLHLSVLRDVSFGQWGF
CRY2AD_BACTU VPLSITSSVNTMOQLFLNRLSQFQMOGOLLPLFLFAQANLHLSFIRVILNABEWGIS
cry1a-105.pe AATINERNDLTRILGNYTHAVRWNTGLERVMGPDSE--DMIRYNQFRRELTTVLDI
CRY2AD_BACTU AATLRTYQNHLENTYTRYDSNYCIDTYQTAFR---GLNIRLHDM---EFTYMFLEWVEY
cry1a-105.pe VSLFPNVDSRTYPIRTVSQLTREIYTNP---VLENFDGSGFRSAQGIIEGSIIRSPHLMDI
CRY2AD_BACTU VSWLSFKYQSILSVSSGANLYAS--GSGPQQTQLTSDQWPELYSLF---QVNSNVVLSG
cry1a-105.pe LNSITTYTD-AHRGEYVWSG--HOIWSAPVSGSGPEFTFPLYGTMGNAAPQRIVAQLGQ
CRY2AD_BACTU FSGASLFTFPNIGLPGSITTTQALLAARVNYSGGITS---GSGISGNFNQNFNCNT--
cry1a-105.pe QVYKLSLTYLRPFGNIGNNOQL--SVLDGTEFAYGTSSNLPSSAVRYKSGTVDSLDEIPP
CRY2AD_BACTU ISPLSTFVSRLWSDSGDRQGVNTVWQTESFETSGLRCCGAFTRGNSNYVGYFI
cry1a-105.pe QNNVPRQSGFSLSHVSMRSGFSNSVSI-----IRAPMFESWIRSAEPNNII
CRY2AD_BACTU RNIF--GSLVLRNQLRPLYYNEKNIESPSGTPGGARAYMVS--VHNKK--NNIY
cry1a-105.pe A-SSEITQIPL---VNRHQSQTTVVRGPGF--TGDDILRTSGSPAYTI
CRY2AD_BACTU AVHENGTMHLNEDNTGTSPIHATOVNSQITTFISEKFGNGDSLRFEQNTTARYT
cry1a-105.pe VNINGOLPQRYRARIYATNRIYVTVGTFAGQFMTMGDPLTFQSPSYATIN
CRY2AD_BACTU LAGNEN--SYNLYLRVSSIGNSTIRKING--KVPANVTITNDQNDNGARFSDIN
cry1a-105.pe TAFTPPMQSQSVFTGAD--TFSSGNEVYIDRFELNVTATLEAYNLHLSVLRDVSFGQWGF
CRY2AD_BACTU IGVNVASSNSDVPDLINVTLSNGTQFDLMMILVPTNISLY
cry1a-105.pe NQLGLKNTVTDYHIDQVSNLVLYLSDFCLEKELSEKVKHAKRLSDENLSDSAFQ
CRY2AD_BACTU TXN5:AF200816_1
Description: AF200816 Bacillus thuringiensis Bacillus thuringiensis crystal protein (cry2) ge

CRY2AD_BACTU VSWLSFKYQSILSVSSGANL---YASGSPQQTQSFTSQDMPFLYSLFQVNSNYVINGF
cry1a-105.pe T-----IVDARGEYVWSGQVPLSPVSGSGPEFTFPLYGTMGNAAPQRIVAQLGQ
CRY2AD_BACTU SGAR-SNRPINIVS---STHALLARVNSGGISS---GDLGASPNQWNCST---
cry1a-105.pe VYRTLSLTYLRPFGNIGNNOQL--SVLDGTEFAYGTSSNLPSSAVRYKSGTVDSLDEIPPQ
CRY2AD_BACTU FLPLLTPEVRSWLDSDSGDRQGVNTVWQTESFETSGLRCCGAFTRGNSNYVGYFI
cry1a-105.pe N-NNVP--PROGFSRLSHVSMRSGFSNSV--SIIRAPMFESWIRSAEPNNII
CRY2AD_BACTU NISGVLVVRNEDLRPLHYNEIRNIASPSGTPGGARAYMVS--VHNKK--NNIY
cry1a-105.pe IASDSITQIPLVKAHTLOSCT--TVVRGPGFTGDDILRTSGSPAYTI
CRY2AD_BACTU HLPANDYGTFTISPIHATOVNSQITTFISEKFGNGDSLRFEQNTTARYT
cry1a-105.pe RYRARIYASTTNRIYVTVGTFAGQFMTMGDPLTFQSPSYATIN
CRY2AD_BACTU SYNLYLRVSSIGNSTIRKING--KVPANVTITNDQNDNGARFSDIN
cry1a-105.pe SSFTVGAD--TFSSGNEVYIDRFELNVTATLEAYNLHLSVLRDVSFGQWGF
CRY2AD_BACTU SDVPLDINVTLSNGTQFDLMMILVPTNISLY
cry1a-105.pe IPYCNLSNPEVILGGERIETGVTPIDISLSLTOFLISEF--VPGAGFVLGVDIIWGIF
CRY2AD_BACTU FOHKSLDITQKWEKWKNDHSLYVDPIVGTVASFLKLGSLIGRILSELRLIFPSG
cry1a-105.pe GPSQWDAFLVQIEQLINRIEIEFARNQAISEGLSNLYQIYAESFREWEADPNP---A

Description: Q9rmg3 bacillus thuringiensis. pesticidal crystal protein cry2ad

(insecticidal)

Accession/ID: Q9RMG3

ID CRY2AD_BACTU STANDARD; PRT; 633 AA.

AC Q9RMG3; .

SCORES Init1: 130 Initn: 130 Opt: 270 z-score: 295.9 E(): 1.4e-10
>>TXN5:CRY2AD_BACTU
Initn: 130 Init1: 130 Opt: 270 z-score: 295.9 expect(): 1.4e-10
Smith-Waterman score: 276; 21.7% identity in 609 aa overlap
(41-610:56-630)

CRY2AD_BACTU FOHKSLDITQKWEKWKNDHSLYVDPIVGTVASFLKLGSLIGRILSELRLIFPSG

CRY2AD_BACTU TXN5:AF200816_1
Description: AF200816 Bacillus thuringiensis Bacillus thuringiensis crystal protein (cry2) ge

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Accession/ID: AF200816
=====General comments=====
LOCUS AF200816_1 (AF200816)
DEFINITION Bacillus thuringiensis crystal protein (cry2) gene, complete cds;

SCORES Initl: 130 Initn: 130 Opt: 270 z-score: 295.9 E(): 1.4e-10
>>TXN5:AF200816_1
Initn: 130 Initl: 130 Opt: 270 Z-score: 295.9 expect(): 1.4e-10
Smith-Waterman score: 276; 21.7% identity in 609 aa overlap
(41-610:56-630)

cry1a-105.pe IPYNCLSNPEVEVLGGERIETGTPIDISLSLQFLLSEF--VPGAGFVLGVDIWGIF
AF200816_1 FQKSLDTIQKEMWKKDNHSLYDPIVGTAVASFLKKLGLSKRLSELNLIFFSG
30 40 50 60 70 80

cry1a-105.pe GPSQWDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAESFREWEADPTNP---A
AF200816_1 STNLMEDILRETEKFNQKLNIDTILSRVNAELTGL-----QANVEFNRQVDNFLNRRNA
90 100 110 120 130 140

cry1a-105.pe LREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYQAAHLHLSDVSVFGQWGED
AF200816_1 VPLSITSSVNTMQQLFLNLSQFQMGVQLLLPLFAQAAHLHLSDVSVFGQWGED
150 160 170 180 190 200

cry1a-105.pe AATINSRYNDLRLGNITDHAIRVNTGLERWGPDSR--DWIRYQFRRLTLVLDI
AF200816_1 AATLRTYDNLRYNTRDYSNYCIDTYQAFR---GLNTRLHDMLE--EFTYVFLNVEY
210 220 230 240 250

cry1a-105.pe VSLFPNDSTYPIRTVSQLTREIYTPN---VLENFDGSPFGSAQGIERSPHLMDI
AF200816_1 VSIWLFKYQSLVSSGANLYAS--GSGPQQTQFTSODWPFYLSLF-----QVNSNYVLG
260 270 280 290 300 310

cry1a-105.pe LNSITIVTD-AHRGEYWSG--HQIMASPVGSGPEFTPLLYGTWGNAAPOQRIVAQLGQ
AF200816_1 FSGASLEFTTFNIGGLPGSTTTQALLAARVNSGGITS-----GSIIGSNFNQNCNT--
320 330 340 350 360

cry1a-105.pe GYVRTLSLTYRPFNPGINNQOL--SVLDGTEFAYGTSNLPASVYKSGTVDSLEIPP
AF200816_1 -ISPLSTSFVRWLSGSGDRQGVNTVINWQTESFETISGLRCGAFTRPGNSVNYPGYFI
370 380 390 400 410 420

cry1a-105.pe QNNVPRPQGSFHRLSHVSNFRSGFSNSSVSI-----IRAPMFSWIHRSAEFNNII
AF200816_1 RNIS-----GVSLVRNEDLKRPLYNKRNIESPSPGCGARAYWVS--VNNKK--NNIY
430 440 450 460 470

cry1a-105.pe A-SDSITQIPL-----VXAHTLQSGITWRGPGF--TGGDILRTSGGFFAYTI
AF200816_1 AVHENGTMHILAPEDNTGFTISPIHATQVNNQTRTFISEKFGNQDLSRFGQSNTTARYT
480 490 500 510 520 530
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cry1a-105.pe VNINGQLPQRYRARIRYASVATNTNRIYVTVAGERIFAGQFNKMTMDTGDLPLTFQSFYSVATIN
520 530 540 550 560 570
AF200816_1 LRGNGN---SYNLYRVSIGNSITRTING-RVYASVNTTINNGVNDNGARESDIN
580 590 600 610 620 630

cry1a-105.pe TAITFPMSQSSFTVGAD-TFSGNEVYDFELIPVTATLEAYNLERAKAVNALFTST
580 590 600 610 620 630
AF200816_1 IGVVASSNSDVLIDINVLNSGTQFDLNMIMLVPTNISPPLY
600 610 620 630

cry1a-105.pe NQLGLKTNVTDYHIDQVSNLVTYLSDFCLDEKRELSEKVKHAKELSDERNLLQDSNFKD
640 650 660 670 680 690

cry1a-105.pep
TXN5:Q9RM89

Description: Q9rm89 bacillus thuringiensis. cry2a protein (fragment) . 6/2001
Accession/ID: Q9RM89
=====General comments=====
ID Q9RM89 PRELIMINARY; PRT: 551 AA.
AC Q9RM89;
DT 01-MAY-2000 (TrEMBLrel. 13, Created) . . .

SCORES Initl: 166 Initn: 166 Opt: 267 z-score: 293.5 E(): 1.9e-10
>>TXN5:Q9RM89
Initn: 166 Initl: 166 Opt: 267 Z-score: 293.5 expect(): 1.9e-10
Smith-Waterman score: 267; 25.5% identity in 231 aa overlap
(41-263:56-275)

cry1a-105.pe IPYNCLSNPEVEVLGGERIETGTPIDISLSLQFLLSEFVPGAGFVLG--LVDIWGIF
Q9RM89 FEKSLDTIQKEMWKKRTHSLYAVPVGVTVSFFLLKK---VGLSKRLSELNMGII
30 40 50 60 70 80

cry1a-105.pe GPSQ-----WDAFLVQIEQLINQRIEFARNQAIISLEGLSNLYQIYAESFREWEADPTNP
70 80 90 100 110 120
Q9RM89 PFSSSTNLMQDILRETEQFLNQRLNITDILARVNAELIGLOANIREFNQVDNF-LAPTON
90 100 110 120 130 140

cry1a-105.pe ALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYQAAHLHLSDVSVFGQWGF
130 140 150 160 170 180
Q9RM89 VPLSITSSVNTMQQLFLNLSQFQMGVQLLLPLFAQAAHLHLSDVSVFGQWGF
150 160 170 180 190 200

cry1a-105.pe DRAATINSRYNDLRLGNITDHAIRVNTGLERWGPDSR--DWIRYQFRRLTLVLD
190 200 210 220 230 240
Q9RM89 SAATLRTYDNLRYNTRDYSNYCIDTYQAFR---GLNTRLHDMLE--EFTYVFLNVEY
210 220 230 240 250

cry1a-105.pe IYSLFPNDSTYPIRTVSQLTREIYTPNVLNFDGSPFGSAQGIERSPHLMDILNS
250 260 270 280 290 300
Q9RM89 YYSIMSLFKYQSLVSSGANLYASGGPQQTQSFQANWPFYLSLFOVNSNYVLGSGIT
260 270 280 290 300 310

cry1a-105.pep
TXN5:L07027_1
```

DESCRIPTION: L07027_1 Bacillus thuringiensis Bacillus thuringiensis
delta endotoxin (CryIAb) ge
Accession: L07027_1
LOCUS L07027_1 (1648 bp)
DEFINITION Bacillus thuringiensis delta endotoxin (CryIAb) gene, 5' end.
(29-1053:60-1177)
SCORES Initl: 207 Initl: 664 Opt: 266 Z-score: 287.0 E(): 4.4e-10
>>TXN5:L07027_1
Initl: 664 Initl: 207 Opt: 266 Z-score: 287.0 E(): 4.4e-10
Smith-Waterman score: 715; 23-28 identity in 1169 aa overlap
(29-1053:60-1177)
cry1a-105.pe MNNNNINECIPNCLSNPEVEVLGGEIEG-YTPDISLSLTOFLLSFEVKGAFV
L07027_1 SKYDEMIKAFKKKKKGKGGKGLLDVAVTYITIGLIDRNNKGVLSVLITLIPFGV
cry1a-105.pe LG---LVDIWG-IFG--PSQWDAFLV---QIEQLINQRIEIEFARNQAIISLGLGANY
L07027_1 ASAASTIVSIFWPKIFGDKPNKKNIFELKPOIEALIQDITNYQDAINKKPKSLQKIV
cry1a-105.pe QIYAESFREWEADPTNPALREMRIQFNDMSALTTAIPLFAVQNVPLSVIVQAND
L07027_1 NLYTVAI-----DNNDYVT---AKTQLENLSILTSIDISIFPEGYEGGPIYAMVANA
cry1a-105.pe HUSVRVSVPGQWGFDAATINSRYNDLTGLIGNVYTHAVRYNTGLERVWGDSRDWI
L07027_1 HILLERDAIVNAKGLSPKDEVDTHKKYIKMTIHNHTEAVIKAFGLNGLDKPKSLDVSNY
cry1a-105.pe RYNOFRELTITVLIDIVSLFPNVDSRTPIRTVSLQTLREIYT---NPVLENFDGS----
L07027_1 KKANYIKGTEWVLDAWLPETDPHYQKEVEIEFTRTISSPYQPVKPNQNTSSSIV
cry1a-105.pe FRGSAQGLEGSIRSPH--LMDILNSI--TIYTDHRRGEYVW-----SGHQ
L07027_1 PSDLFHYQDGLVLEFSTRTDNDGLAKIFTGIRNTFYKSPNTHETVHVDPSVNTQSSGNI
cry1a-105.pe PVGSPGETF---PLV-----GTMGNA--AP-----QORI
L07027_1 SRGSSNPIDLNPPILISTCIRNSFYKATAGSSVLVNFKDTQGYAFQAQPTGAWDHSF
cry1a-105.pe VAOLG--QG-----VYRTLSLYRRFPNI-----GINNQOVLSDGTGEAYGTSSNL
L07027_1 IESDGAPEGHKLNLYITSPGDTL-RDFINVYTLISTPTINELSTEKIKGFPKPKYIKN-
cry1a-105.pe PSAVYKSGTVSLDLEIPPNQNNVPPRQGFSLHLSVSMFR-----SGF---SN

L07027_1 -QGIMKYGKPEYINGAQPVNLENQOQLIFEHASKTAQYTIIRIVASTQGTGKGYFLDN
cry1a-105.pe SSVSIRAPMFWIHRSAEFNNI-----IASDSITO--IPLVKAHTLQSGTTVVRGP
L07027_1 QELTLNIPTS---HNGVVTGNIGENVDLYTIGTSITIGTGHHTLQIQHNDKXGWLDRLE
cry1a-105.pe GFTGCDILART--SGGPAY--TIVNINGOLPQRYRARIYASTTNLRIYVTVAG---ERI
L07027_1 -FVPSQLQSPDQSPPEVHESTIIFDKSSPTIWSNKNHSYSHIHLEGSYTSQGSYPHNL
cry1a-105.pe FAGOFNKT-----MDTGDLPTFOSFYATINTAFTFPMSSQSSFTVGADTFSSGNEV
L07027_1 LINLFHTDPNRNHTIHVNGD---MNVYDGKDSVADGLFNKITATIPSDAWYSGTIT
cry1a-105.pe YIDRFE---LIPVTALEAYNLESAQKAVNALFTSTINGLKTNTVDYHIDOVSNLVTV
L07027_1 SMHFNNDNFKITIPKFLSNLENIITQVNALFASQAOTILASNVSDYVLEQVWVKYDA
cry1a-105.pe LSEFCLDEKRELSKVKAHKLSDERNLLQDSNFKDINRQPERGWSGTITIGGGDDV
L07027_1 LSEVFGKEVKALKLVQAKLSKIRNLLGNGFDNLV---AWYMGKDVVKESDHEL
cry1a-105.pe FKNTVTLSC--TDECYTYLYOKIDESKLAFTRIQRYGIEDSQDLEIYSIRYNAX-H
L07027_1 FKSHVYPPPTF--HNSYIFQVKEESKLKPNTRYTISGFIAGHEDVELVVSRYGOEIQ
cry1a-105.pe ETWVPSGSLWPLHLEPIGKCGEMCAPHLEWNPDLDCRDEKCAHSHHFLSDI
L07027_1 KVMQVPEAL-DUTSEK--SS-----CYRMINETLA-----DPHFFSVSI
cry1a-105.pe DVGCTDLNEDLGVVIFKKTQGHARLKTFFLEKPLNGEAFVKAERAKKWRDKREX
L07027_1 DVGSLMEANFGIEFGRIYKVPQWMAWNSLELIDDLATAKEINQVQSAARDWKQVEQ
cry1a-105.pe LEWETNIVYKEAKSVDAFLVNSQ-----VDQADTNIAHAKRVASIRRA
L07027_1 ERTEITAIQPVLAQINAIYENEDWNGSIRSNVSVYHDLQIMPTLLNTEFICNYDHPA
cry1a-105.pe YLPE-----LSVIPQVNAALFELEGRIFTAFSLYDAARNVKNKDFNNS--SCNVKSHV
L07027_1 FLKVVHWFMDRIGEGHTILARFQALORATQVLESNLLHNGHFTTIDANWTTEGDAH
cry1a-105.pe VEEONNORSVLVPEWEAEVSQEVRCF---GRGVILRTAYKEGEGCVTIHEENNT

CICA_PAEPP PYATKRFNELTSLGTA-GVGGFVRSDVFISNDISVCGLGITNYSSGQTFFDYDYIINISATV
440 450 460 470 480 490
cry1a-105.pe SFRSGFNSVSIIIRAPMSWHRSAEENLIASDSITQIPLVKARTLQSGTTVVRGPG
440 450 460 470 480 490
CICA_PAEPP QVNGNTDISPLYGEGRAITSGNVKVIYAKRKNYDDFTNIGRTIVHEAPDTSGF
500 510 520 530 540 550
cry1a-105.pep
TXN5:C2AC_BACTU
Description: Q45743 bacillus thuringiensis. pesticidal crystal protein cry2ac
(insecticidal)
Accession/ID: Q45743
ID C2AC_BACTU STANDARD; PRT; 622 AA.
AC Q45743; .
=====General comments=====

SCORES Init1: 106 Initn: 141 Opt: 244 z-score: 267.3 E(): 5.5e-09
>>TXN5:C2AC_BACTU
Initn: 141 Init1: 106 opt: 244 z-score: 267.3 expect(): 5.5e-09
Smith-Waterman score: 250; 21.4% identity in 552 aa overlap
(81-607:98-611)

cry1a-105.pe VPGAGFVLGLVDITWIGFGPSQWDAFLVQIQLINQRIEERFARNQAIISLEGL-SNLVQI
60 70 80 90 100
C2AC_BACTU LVCKRILSELONLIFPSSGIDLMQELIRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120
cry1a-105.pe --VAESFREWEADPTNPALREEMRIQFNDMSALTATPFAVONQVPLLSVYQAAANL
110 120 130 140 150 160
C2AC_BACTU NRQVDNLFNPNQVPLAIDSV---NTLQQLFLSRPQFQIQGQLLLPLFAQANF
130 140 150 160 170 180
cry1a-105.pe HLVSFLRDSVFGQWGFDAATINSRYNDLTRIGNYTDHVRVYNTGLERVWGPDSR--D
170 180 190 200 210 220
C2AC_BACTU NLSFIRGVILNDEWGISAAATVRYDRHLKRFHRDYSNVCINPYQAFR---GLNHRLPD
190 200 210 220 230 240
cry1a-105.pe WIRYNQFRRELTLTLDIVSLFPNYSRTYPIRTVSQ-----TREIYTN---PVLEN-
230 240 250 260 270
C2AC_BACTU ML---EFRTYMFILNVFEVYSIWSLFKYQSLVSSGANLYASGSGPTQSFTAQNWPFYLSL
250 260 270 280 290
cry1a-105.pe FDGSGFGSAGQIEGSIRSFHMLDINSITIYDA--HRGEYWSGHQVWASPVGSGPEF
280 290 300 310 320 330
C2AC_BACTU FQVNSYVNLGLSGA-RITTFIPNIGLFPVHNSLTHFARINRGV--VSSSRIGQANLNQ
300 310 320 330 340 350
cry1a-105.pe TFLYXTMGNAAPQRIVAQLGGQVRLTSSLYRPERNIGINNQQSLVDGTER-AYGT
340 350 360 370 380 390
C2AC_BACTU NFNI-STLFPNLOTFFIRSLDSDTDREGVAT-----STNWOSGAFETILLRFSISAGN
360 370 380 390 400 410
cry1a-105.pe SSNLPASVYVRK-SGTVDSLDIIPPQNNVPPRQGFSGHRLSHVSMFRGFSNVSIIIRAP
400 410 420 430 440 450
Initn: 141 Init1: 106 opt: 244 z-score: 267.3 expect(): 5.5e-09
Smith-Waterman score: 250; 21.4% identity in 552 aa overlap
(81-607:98-611)

C2AC_BACTU SNFFPDYFIRNIGVGTIS-----NADLA-----RPLHFEHIEDIGTTAVASLVTVH
420 430 440 450
cry1a-105.pe MF-SWHRSAEENLI--ASDSTQIPLVKARTLQSGT---TVVRGPGFTGDIILRTSG
460 470 480 490 500
C2AC_BACTU NRKNYIDHENGWIMHLAINDTGTFTGTPHATQVNNQIIRTFISEKYNGQDSLRPELS
460 470 480 490 500 510
cry1a-105.pe GPFAITVINGQLPQRYRARIYASTTNLRIYTVAGERIFAGQFNKMTDGTPLTFQS
510 520 530 540 550 560
C2AC_BACTU NPRTARYTLRNGN--SYNLYLRVSSIGSSTIRVTING-RVYTANVNTTINN-DGVLDNG
520 530 540 550 560 570
cry1a-105.pe FSATINTAFTFPMSSQSFVVGADTFSSGNEVIDRIFELIPVTATLEAEYNLERAQKAVN
570 580 590 600 610 620
C2AC_BACTU ARFSDINIGNVVASANTNVPDIDQVTFNGNP---QFELANNIMFVPTNIPPLY
580 590 600 610 620
cry1a-105.pe ALFISTNQGLKTNVTDYHIDQVSNLVYLSDEFCLDEKRELSEKVKHAKRLSDERNLQ
630 640 650 660 670 680
cry1a-105.pep
TXN5:X57252_3
Description: X57252 Bacillus thuringiensis B.thuringiensis plasmid DNA for
cryIIc operon and
Accession/ID: X57252
LOCUS X57252_3 [BTCRYIIC]
DEFINITION B.thuringiensis plasmid DNA for cryIIc operon and gene for cryIIc
=====General comments=====

SCORES Init1: 106 Initn: 141 Opt: 244 z-score: 267.3 E(): 5.5e-09
>>TXN5:X57252_3
Initn: 141 Init1: 106 opt: 244 z-score: 267.3 expect(): 5.5e-09
Smith-Waterman score: 250; 21.4% identity in 552 aa overlap
(81-607:98-611)

cry1a-105.pe VPGAGFVLGLVDITWIGFGPSQWDAFLVQIQLINQRIEERFARNQAIISLEGL-SNLVQI
60 70 80 90 100
X57252_3 LVCKRILSELONLIFPSSGIDLMQELIRATEQFINQRLNADTLGRVNAELAGLQANVAEF
70 80 90 100 110 120
cry1a-105.pe --VAESFREWEADPTNPALREEMRIQFNDMSALTATPFAVONQVPLLSVYQAAANL
110 120 130 140 150 160
X57252_3 NRQVDNLFNPNQVPLAIDSV---NTLQQLFLSRPQFQIQGQLLLPLFAQANF
130 140 150 160 170 180
cry1a-105.pe HLVSFLRDSVFGQWGFDAATINSRYNDLTRIGNYTDHVRVYNTGLERVWGPDSR--D
170 180 190 200 210 220
X57252_3 NLSFIRGVILNDEWGISAAATVRYDRHLKRFHRDYSNVCINPYQAFR---GLNHRLPD
190 200 210 220 230 240
cry1a-105.pe WIRYNQFRRELTLTLDIVSLFPNYSRTYPIRTVSQ-----TREIYTN---PVLEN-
230 240 250 260 270
X57252_3 ML---EFRTYMFILNVFEVYSIWSLFKYQSLVSSGANLYASGSGPTQSFTAQNWPFYLSL
250 260 270 280 290

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CRY1A-105.pe FDGFRGAGGESSIRPHLMIDLSITITIDA--HRGEYVWGHQIMASPVGSGPEF
X57252_3 FOUNSAVLNLSGA-RYNTFNNIGLGVHNSLTHFARINYRGG-VSSSRIGQANLQ
CRY1A-105.pe TFLYNGNAPPOPAVADGQGVYDSSIVRRPNIGNNQSLVDGTET-AYGT
X57252_3 NFNT-STLFNPOTTPAIRSWDSGTREGVAT--SNWOGAFETITLRFISFARGN
CRY1A-105.pe SSNLPASVYRK-SGTVDSLDE-RPNNVPHLOGESRLSHVSMRSGFSNVSIVIRAP
X57252_3 SNFPDFIRNIGSVVGHIS--NARLA-----RLENEIRIDIGTAVASLTVH
CRY1A-105.pe MF-SWIRHSAEFNNII--ASDSITQIPLVKAHTLQSG--TWVRGPGFTGDIILRTG
X57252_3 NRKNNIYDTHENGTHILAPNDYTGFTVSPHATQVNNQIRATISKYGNOQSARFOS
CRY1A-105.pe GFATVINGQOPRYRARIYASITNLEIYTVAGERIFAGQFNKMTDSDPLTFOF
X57252_3 NPTARYTLRGNG--SYNLXLRVSSIGSSTIRVING-RVTIANVNTITN-DGVLSNG
CRY1A-105.pe FSVATINTAFTPMOSOSFTVGADTFSSGNEVYIDREFLIPVTATLEAYNLEAQAVERN
X57252_3 ARFSDINGNVVASANTVPLDIQVTFNGNF---QPELMNIMFVPTNLPPLY
CRY1A-105.pe ALFTSTNGLKNTVDYHIDQVSNLVTVLSDFCLDEKRELSKVHAKRLSDERNLLQ
CRY1A-105.pep
TXN5:CBBA_BACTJ
Description: Q45730 bacillus thuringiensis (subsp. jegathesan). pesticial
crystal protein c
Accession/ID: Q45730
ID CBBA_BACTJ STANDARD; PRT; 724 AA.
AC Q45730;
=====General comments=====

SCORES Initl: 60 Initn: 86 Opt: 178 z-score: 193.5 E(): 7.2e-05
>>TXN5:CBBA_BACTJ
Initn: 86 Initl: 60 Opt: 178 z-score: 193.5 expect(): 7.2e-05
Smith-Waterman score: 199; 18.0% identity in 655 aa overlap
(1-605:1-633)

CRY1A-105.pe MNNPNINECIPNCLNSPEVEVLGGERIETGYTPIDISLS-LTQFV---LSEFVPGAGF
CBBA_BACTJ MNN-NFNTTEINNNINFP--MYNG-RLEPSLAFLIAVAPIAKVLATALAKVAKQGF
CRY1A-105.pe VLGVLVDIINGIFGQSDAFVLOEQLINQRIEERFARNQALSRLEGSLNLYQIYAESRE
TXN5:X86902_1

CBBA_BACTJ AKLKSEIFFPNT-PATMDKVRIVETULLDQRLQDDRVRKILEGEYKGIIDVSKVFTDYVNO
CRY1A-105.pe WEADPTNPALREEMRIQDNWNSALTATPLFAVQNYQVPLLSVYVQAANLHLSVLRDVS
CBBA_BACTJ SKPE-TGTANR-----LFFDTSNQLISRLPQFEIAGYEGVISLFTOMCTFPHGLLKGCI
CRY1A-105.pe VFCQRMGDAATINSRYNDLRLGLNVTGHAHVNTGLERVWGPDSRDMIRYNQPRREL
CBBA_BACTJ LAGSDMGFAPADKDALICQNRFFVNEVTELVLYSKFEGSLAKNLNEALNFRNMSLY
CRY1A-105.pe TLTVLDIVSLFPNYSRTPIRTVSQLTREIYTNPVLENFDSGFRGAQIEGSIKSPHL
CBBA_BACTJ VFPFSEAWSLRYEGTKLENTLSLWNFVGESINNI SPNDWKALYKLLMGAPNQ----RL
CRY1A-105.pe MDILNSTIITIDA--HRGEYV-----WSHQIMASPVG---FSGPEFTFLYGTMGNA
CBBA_BACTJ MNVKFNYSYFSDTOATHRENIHGVLPYNGGPTIITGWNIGRFGSG--LSFPCSNELEIT
CRY1A-105.pe APQQRIVAOLGQGVYRTLSSTLYRR-----PF-NIGINNOQLS--VLDGTET
CBBA_BACTJ KMEIETVNDKGNFNSIVPAATREILATVPTSDAPFFKTADINWKYFSPGLYSGWNI
CRY1A-105.pe AYTSSNLPASVYRK-SGTVDSLDEIPQNNVPPRO---GFSH--RLSHVSMRSGFS
CBBA_BACTJ KTFDTPVKKSVPSLPSNLIKADYDIYIRAVSACPKGVSLAYNHDFLTITYNKLEYDAPT
CRY1A-105.pe NSSVETNAPMFSWIRPEFNNIKASGITOIPLVKAHTLQSGTIVVRGPG-FTGGDIL
CBBA_BACTJ TONIIVGSPONTKSFYRSHYLSITDDAVYDALQFSTVSDRSELEDTDQATDGSIK
CRY1A-105.pe RRTS--GGPFAYTI-VNINQDQRYRPAATNLRVTVNAGERIFAGQFNKMTDT
CBBA_BACTJ FDTVLGNEAKYSIRLATGNTATRYRILIRFIRFARAAAGIRVNSQN--SGN-NKLLG-
CRY1A-105.pe GDPILTFQGSFVATINTAFTTP---MSQSS---TVGADTFSSGNEVYIDREFLIPVTAT
CBBA_BACTJ GIFVEGNSGWDIYITDSFTFDLIGITTSNTAFPSIDSDVNSQOWYTESLTYKESST
CRY1A-105.pe LEAYNLEAQAQVNAALFTSTNGLKNTVDYHIDQVSNLVTVLSDFCLDEKRELSK
CBBA_BACTJ TTOIPLKPVIVVRCPDITFFVSNNSSTSYGQYNNYNNQSSMDQGYNNVSNPNASGTC
CRY1A-105.pep
TXN5:X86902_1

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VW-GVRYSHGGS-----YTKGMA-----PPNTNAYAPPE-FKYPGKYLHSVSAY--
      520      530      540      550

cry1a-105.pe GFNSGSVIIIRAPMSW--IHRSAEFNNIIASDSITQIPL-VKAHTLQSGTIVVRGPGFT
      440      450      460      470      480      490
cry1a-105.pe GTSKAP-DTADSVNMGFRPVLLLENANQLL--TDTALQIIPAEIGITDVVPAPFGRTEEP-IN-
      560      570      580      590      600      610
cry1a-105.pe GSDIL-----RRTSGGPAYTIIVNNGQIPQRYRARIYASTNLR---IYTVVAGERIFA
      500      510      520      530      540
cry1a-105.pe GQDAIIHWESFTSGFGFTVDS-----PQPKYKIYRIANNLSASTVSLTYNNQTFIT
      620      630      640      650      660
cry1a-105.pe GQFNKTMGTGPILTFOFSFVSATINTAFTFPMSSOSFTVGADTF---SSGNEVIDIDRFELI
      550      560      570      580      590      600
cry1a-105.pe DILNISLDP-NGVRGNVGSITLVGG-----PIIE--FSQGNIFKLRSKOGFAIDSIIFS
      670      680      690      700      710      720
cry1a-105.pe PVTATLEAEYNLERAQKAVNALFTSTNQLGLKTNVTYDIDQVSNLVTLSDFECLDEKR
      610      620      630      640      650      660
cry1a-105.pe PVS
      670
cry1a-105.pep
      680
TXNS:CBBB_BACTV
      690
Description: Q9zius bacillus thuringiensis (subsp. medellin). pesticidal
crystal protein cry
Accession/ID: Q9ZIU5
ID CB8B_BACTV STANDARD; PRT; 750 AA.
AC Q9ZIU5; .
General comments:=====
SCORES Init1: 65 Initn: 65 Opt: 163 z-score: 176.7 E(): 0.00062
TXNS:CB8B_BACTV (750 aa)
initn: 65 initl: 65 opt: 163 z-score: 176.7 expect(): 0.00062
Smith-Waterman score: 182; 19.0% identity in 662 aa overlap
(13-605:6-633)
cry1a-105.pe MDNPNINECIPYNCLSNPEVEV--LGGREITGYTPIDISL-LTQFLSEFYPVGAGFV
      10      20      30      40      50
CB8B_BACTV MNNFSNVLANNMNSFPLFNSKIEPSIALIYAVPTAKYALATALAKA-LK
      10      20      30      40      50
cry1a-105.pe LGVLDVIINGIFGSPQNDAFI----VQIEQLINQRIEIEFARNQAIISRLGSLNLYQIYAES
      60      70      80      90      100      110
CB8B_BACTV QGFALIXSEIF-PGNETATNMEKVRLEVTQIILNOTLDTRVATLKAEYEGFHLGKVFYTD
      60      70      80      90      100      110
cry1a-105.pe FREWEADPTNPALREEMRIQFNMDNSALTATPIFLAVONYVPLLSVTVQAANLHLSVLR
      120      130      140      150      160      170
CB8B_BACTV VSOSITPTATA-----KTHFLMNSNLLIQLPQFEIAGVEGVSILFTQCTILGLLXK
      120      130      140      150      160
cry1a-105.pe DVSVFQQRWGF---DAATINSRYNDL-----TRLIGNYT-----DHAVRWYNTG
      180      190      200

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Accession/ID: D01049
=====General comments=====
D01049_1 [SYN25BT]
DEFINITION Cloning vector pACRP25.Bt protoxin gene and polyhedrin promoter
--TXN5:D01049_1
Initn: 92 Initn: 92 Opt: 92 z-score: 125.5 E(): 0.44
(12 aa)
Smith-Waterman score: 92; 100.0% identity in 12 aa overlap
(1-12;1-12)
crry1a-105.pe MDNNPNINECIPYCNCLSNPEVGLGERIETGYTPIDISLSLTQTLFLLSEFPVGFGVLVLG
|||||
MDNNPNINECIP
10
D01049_1 MDNNPNINECIP
10
Description: Q45755 bacillus thuringiensis. pesticidal crystal protein
cry3aa (insecticidal)
Accession/ID: Q45755
====General comments=====
ID CDA_A_BACTU STANDARD; PRT; 803 AA.
AC Q45755; . . .
SCORES Initl: 60 Initn: 60 Opt: 115 Z-score: 123.3 E(): 0.58
--TXN5:CDA_A_BACTU
initn: 60 initl: 60 opt: 115 Z-score: 123.3 expect(): 0.58
Smith-Waterman score: 228; 21.6% identity in 626 aa overlap
(47-607;92-691)
crry1a-105.pe SNPEVGLGERIETGYTPIDISLSLTQFLSEFPVGFGVLGVDFIMGIGTGP--SSOW
20 30 40 50 60 70
CDA_A_BACTU ALEKGFDAAGGSFDYLGLVOAGLGLVTGLGAAPGVSAVPLISMVLGVFWPKTKNQ
70 80 90 100 110 120
crry1a-105.pe DAFLVEQLINRIEEFARNQAISRLEGSLNYQIYAESFREWADPT---NPALR--
130 140 150 160 170 180
CDA_A_BACTU ENLITVIDEVQRILDEKLSDLIKKNADLNFAFTDLVTRLEEVIIDATFENHKPVLQVS
130 140 150 160 170 180
crry1a-105.pe ---FDAATNSRYND--LTRL-----IGNYTDHVRWYNTGLERWPGDSRDIMRYNQ
190 200 210 220 230
CDA_A_BACTU KSNVMKVDSAYSTGGILLTGMSDFDTIVYSKLTLPPLVLGTAKMKLSAHHSYIQGNITWL
190 200 210 220 230 240
crry1a-105.pe NKVYDLSDEGKTMSQALARAKQHMRQDIAFYTSQLAMFTGNLPSP--SSNKYAINDVNV
250 260 270 280 290 300
CDA_A_BACTU
240 250 260 270 280
crry1a-105.pe FRRELTLVDIVSLFFPNYDSRTYPRTIKVSQTREIYNPV--LENPDGSRGSAQGIEG
310 320 330 340 350
CDA_A_BACTU YTRAMVLINGLDIVATWPTLYPPDDYSSQIKLEKTRVIFSDVMVGQSESRRGSGV--TIKNIFD
310 320 330 340 350
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! source="GENBANK_PROT" hypochemical ... 54 54 181 202.0 0.0059
SW.8928023 Begin: 1 End: 633
! description="PESTICIDIAL CRYSTAL PR... 60 86 178 198.0 0.0098
NRAA:971147 Begin: 1 End: 633
! source="GENBANK_PROT" mosquitoideal... 60 86 178 198.0 0.0098
NRAA:66805043 Begin: 91 End: 296
! source="GENBANK_PROT" hypochemical ... 50 50 175 195.5 0.013
NRAA:21685428 Begin: 25 End: 633
! source="GENBANK_PROT" pestidicial c... 119 119 175 195.4 0.014
SW.117327 Begin: 25 End: 633
! description="PESTICIDIAL CRYSTAL PR... 119 119 175 195.4 0.014
NRAA:9798640 Begin: 149 End: 723
! source="GENBANK_PROT" 81-kDa leukem... 99 99 166 184.4 0.056
NRAA:8928042 Begin: 6 End: 633
! source="GENBANK_PROT" Pesticidial c... 65 65 163 180.7 0.09
SW.8928042 Begin: 6 End: 633
! description="PESTICIDIAL CRYSTAL PR... 65 65 163 180.7 0.09
NRAA:68348789 Begin: 7 End: 143
! source="GENBANK_PROT" cry4A insecti... 77 109 151 177.8 0.13
NRAA:75812162 Begin: 97 End: 362
! source="GENBANK_PROT" hypochemical ... 99 99 155 176.1 0.16
NRAA:75812164 Begin: 116 End: 381
! source="GENBANK_PROT" hypochemical ... 99 99 154 174.7 0.2
NRAA:37543234 Begin: 168 End: 741
! source="GENBANK_PROT" 83-kDa crysta... 99 99 156 172.9 0.25
NRAA:75812158 Begin: 116 End: 381
! source="GENBANK_PROT" hypochemical ... 98 98 152 172.4 0.26
NRAA:75812160 Begin: 116 End: 381
! source="GENBANK_PROT" hypochemical ... 99 99 150 170.1 0.35
NRAA:45655920 Begin: 86 End: 295
! source="GENBANK_PROT" DNA gyrase su... 64 64 143 157.3 1.8
SW.14195066 Begin: 335 End: 687
! description="PROBABLE OUTER MEMBRAN... 46 46 137 149.8 4.8
NRAA:15835979 Begin: 335 End: 687
! source="GENBANK_PROT" polymorphic O... 46 46 137 149.8 4.8
NRAA:15618361 Begin: 335 End: 687
! source="GENBANK_PROT" Polymorphic O... 46 46 137 149.8 4.8

cryla-105.pep
NRAA:37048803
37048803 source="GENBANK_PROT" cryia toxin [Bacillus thuringiensis]

SCORES Initl: 7248 Initn: 7248 Opt: 7248 z-score: 8230.2 E(): 0
>>NRAA:37048803
Initn: 7248 opt: 7248 z-score: 8230.2 expect(): 0
Smith-Waterman score: 7248; 92.1% identity in 1177 aa overlap
(1-1177:1-1177)

10 20 30 40 50 60
cryla-105.pe MNNNPNINPCNLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEFVPAGFVLGL
|||||
37048803 MNNNPNINPCNLSNPEVEVLGGRIETGYTPIDISLSLTQFLSEFVPAGFVLGL
10 20 30 40 50 60

70 80 90 100 110 120
cryla-105.pe VDIWIGFSPQWDAFLVQIEQLINORIEEFARNOALSRLEGLSNLYQIYAESFREWAD
|||||
37048803 VDIWIGFSPQWDAFLVQIEQLINORIEEFARNOALSRLEGLSNLYQIYAESFREWAD
70 80 90 100 110 120

130 140 150 160 170 180
cryla-105.pe PTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
|||||
37048803 PTNPALREEMRIQFNDMNSALTITAIPLFAVQNYQVPLLSVYVQAANHLSLVLRDVSFVGQ
|||||
```

```
cryla-105.pe RMGFPDAATINSRYNDLTRIGNYTDHVRVWNTGLERVWGPDSRWIRYVQFRELTLTV
37048803 RMGFPDAATINSRYNDLTRIGNYTDHVRVWNTGLERVWGPDSRWIRYVQFRELTLTV
250 260 270 280 290 300
cryla-105.pe LDIVSLFPNDYDRTYPIRTVSQLTREIYTNVLENFDFGFRGSAQIGSIRSPLMDIL
37048803 LDIVSLFPNDYDRTYPIRTVSQLTREIYTNVLENFDFGFRGSAQIGSIRSPLMDIL
310 320 330 340 350 360
cryla-105.pe NSITTYTDAHRGEYVMSGHQIMASVPGSGPEFTFPLYGTMGNAAPQORIQAQLGQGVYR
37048803 SSITTYTDAHRGEYVMSGHQIMASVPGSGPEFTFPLYGTMGNAAPQORIQAQLGQGVYR
370 380 390 400 410 420
cryla-105.pe TLLSSTLYRRPPIGINNOQLSVLDGTEFAYGCTSSNLPSAVYKSGTVDSLSLEIIPPQNNV
37048803 TLLSSTLYRRPPIGINNOQLSVLDGTEFAYGCTSSNLPSAVYKSGTVDSLSLEIIPPQNNV
430 440 450 460 470 480
cryla-105.pe PPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFWSIHRSAEFNNIIASDSITQIPLVKAH
37048803 PPRQGFSHRLSHVSMFRSGFSNSSVSIIRAPMFWSIHRSAEFNNIIASDSITQIPLVKAH
490 500 510 520 530 540
cryla-105.pe TLQSTTVVRPGPTGGDILRLRTSGGPPAYTIVNINQQLDQRYRARIYASTTNLRIYVT
37048803 NLGSGTSYVGVGPTGGDILRLRTSGGPPAYTIVNINQQLDQRYRARIYASTTNLRIYVT
550 560 570 580 590 600
cryla-105.pe VAGERIFAGQFNKTMGTGDLTQFSFSYATINTAFTFPMSSQSFVTGADTFSSGNEVYID
37048803 IDGRFINGQFNKTMGTGDLTQFSFSYATINTAFTFPMSSQSFVTGADTFSSGNEVYID
610 620 630 640 650 660
cryla-105.pe RFELIPVATIAEYNAELRAQKAVNALFTSNQGLKNTVTDYHIDQVSNLVYLSDEF
37048803 RIEFVPAEVTFEAEYDLERAQKAVNELFTSNQGLKNTVTDYHIDQVSNLVYLSDEF
670 680 690 700 710 720
cryla-105.pe LDEKELSELKVKHAKRLSDERNLQDSNFKDINQPERGMSGSTGITTCGGDVFKENYV
37048803 LDEKQEVSEKVKHAKRLSDERNLQDSNFKDINQPERGMSGSTGITTCGGDVFKENYV
730 740 750 760 770 780
cryla-105.pe TLLSGTDFDCYTYLYOKIDESKLKAFTRVQLRGVIEDSOLEIYSIRYNKAKHETVNVPGT
37048803 TLPCTFDCYTYLYOKIDESKLKAFTRVQLRGVIEDSOLEIYSIRYNKAKHETVNVPGT
790 800 810 820 830 840
cryla-105.pe GSIWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVCGTDLN
37048803 GSIWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVCGTDLN
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```
cryla-105.pe 780 790 800 810 820 830
NYPGTGSLWPLSAGSPGKGFNRCAPHLEWNPDLDCSCRGKCAHSHHFLSDIDVG
117547 NYPGTGSLWPLSAGSPGKGFNRCAPHLEWNPDLDCSCRGKCAHSHHFLSDIDVG
780 790 800 810 820 830

cryla-105.pe 840 850 860 870 880 890
CTDLNEDLGVWVIFKIKTQGHARLGNLEFLEEKPLVGEALARKVRAKKVRDKREKLEW
117547 CTDLNEDLGVWVIFKIKTQGHARLGNLEFLEEKPLVGEALARKVRAKKVRDKREKLEW
840 850 860 870 880 890

cryla-105.pe 900 910 920 930 940 950
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPESLVPQVNA
117547 ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPESLVPQVNA
900 910 920 930 940 950

cryla-105.pe 960 970 980 990 1000 1010
AFPELEGRIETAFSLDARNVKNKNGDFNGLSCWNVKGVHVDVEENORSVLVVPEWEA
117547 AFPELEGRIETAFSLDARNVKNKNGDFNGLSCWNVKGVHVDVEENORSVLVVPEWEA
960 970 980 990 1000 1010

cryla-105.pe 1020 1030 1040 1050 1060 1070
EVSQEVRCPCRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCVEEIEIYNNVTVC
117547 EVSQEVRCPCRGYILRVYAYKEGYEGECVTIHEIENNTDELKFSNCVEEIEIYNNVTVC
1020 1030 1040 1050 1060 1070

cryla-105.pe 1080 1090 1100 1110 1120 1130
NDYTVNQBEYGGATSRNRCYNEAPSVADYASVEKSYTDGGRNCPENRGRDYTP
117547 NDYTVNQBEYGGATSRNRCYNEAPSVADYASVEKSYTDGGRNCPENRGRDYTP
1080 1090 1100 1110 1120 1130

cryla-105.pe 1140 1150 1160 1170
LPVGVTKELEYFETDKWIEIGETGTFIVDSVELLMEE
117547 LPVGVTKELEYFETDKWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170

cryla-105.pep
NRAA:2584729
2584729 sources="GENBANK_PROT" insecticidal crystal protein [Bacillus
thuringiensis]gi|29293657|gb|AA072077.1| CryIAC [Bacillus
thuringiensis]gi|117547|sp|P05068|CRLAC_BACTK_Pesticidal crystal protein cryIAC
(Insecticidal delta-endotoxin CryIa (c))_Crystaline entomocidal protoxin (133
kDa crystal protein)gi|1842095|gb|AAC4841.1| crystal protein [Bacillus
thuringiensis serovar kurstaki]gi|1888559|gb|AAB49768.1| CryIAC delta-endotoxin
```

```
SCORES Init1: 3919 Initn: 7211 Opt: 7222 z-score: 8200.6 E(): 0
>NRAA:2584729
initn: 7211 init1: 3919 opt: 7222 z-score: 8200.6 expect(): 0
Smith-Waterman score: 7222; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)

cryla-105.pe 10 20 30 40 50 60
MDNNPINEICPYNCLSNPEVLOGRIETGYTPIDISLSLTQFLSFEVPGAGFVLGL
2584729 MDNNPINEICPYNCLSNPEVLOGRIETGYTPIDISLSLTQFLSFEVPGAGFVLGL
10 20 30 40 50 60
```

```
cryla-105.pe 70 80 90 100 110 120
VDIIWGIFGSPQWDAFLVQIEQLINQRIEERFARNOAISRLGSLNLIQIYAESFREWEAD
2584729 VDIIWGIFGSPQWDAFLVQIEQLINQRIEERFARNOAISRLGSLNLIQIYAESFREWEAD
70 80 90 100 110 120

cryla-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQYQVPLLSVYQAAHLHSLVRDVSFVGQ
2584729 PTNPALREEMRIQFNDMNSALTTAIPFAVQYQVPLLSVYQAAHLHSLVRDVSFVGQ
130 140 150 160 170 180

cryla-105.pe 190 200 210 220 230 240
RMGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV
2584729 RMGFDAATINSRYNDLTRLIGNYTDHVRWYNTGLERVWGPDSRDWIRYNQFRRELTLTV
190 200 210 220 230 240

cryla-105.pe 250 260 270 280 290 300
LDIVSLFNYDSRYPIRTVYSQLTREIYTNVPLENFDGSPRGSAGIEGSIIRSHPLMDIL
2584729 LDIVSLFNYDSRYPIRTVYSQLTREIYTNVPLENFDGSPRGSAGIEGSIIRSHPLMDIL
250 260 270 280 290 300

cryla-105.pe 310 320 330 340 350 360
NSITVYTDHARGEYMSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYR
2584729 NSITVYTDHARGEYMSGHQIMASPVGFGSGPEFTFPLYGTMGNAAPQORIVAQLGQGVYR
310 320 330 340 350 360

cryla-105.pe 370 380 390 400 410 420
TLSSLYRRPFIINQQQLSVLDGTFAYGTSSNLPSAVYRKSGTVOSLDELIPQNNVY
2584729 TLSSLYRRPFIINQQQLSVLDGTFAYGTSSNLPSAVYRKSGTVOSLDELIPQNNVY
370 380 390 400 410 420

cryla-105.pe 430 440 450 460 470 480
PRQGFSHRLSHVSMFSGFSNSSLIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGN
2584729 PRQGFSHRLSHVSMFSGFSNSSLIIIRAPMFSWIHRSAEFNIIASDSITQIPAVKGN
430 440 450 460 470 480

cryla-105.pe 490 500 510 520 530
TLQSGTVVRGPGFTGCDILRRTSGGPFAYT--IVNINGQLPQ--RYRARIRYASTTNL
2584729 FLFNGS-VISGPGFTGCDVLRLNSSGNIIQRGVIEVPHFPSTSTRYRVRVYASVTPI
490 500 510 520 530

cryla-105.pe 540 550 560 570 580 590
RIYTVVAGERIFACQFNKMTDGLPDTTQSFYSIATINTATFFPMSQSSFTVADTFSSGN
2584729 HLNVMGNSIFSNVTVPATATSLDNLQSSDFGYFESANFTSLGN--IVGVNRFSGTA
540 550 560 570 580 590

cryla-105.pe 600 610 620 630 640 650
EUVIDRFELIPVTATLEAYNLERAKAVNALFTSTNOLGLKTNVTDVHIDOVSNLVTYL
2584729 GVIIIDRFELIPVTATLEAYNLERAKAVNALFTSTNOLGLKTNVTDVHIDOVSNLVTYL
600 610 620 630 640 650

cryla-105.pe 660 670 680 690 700 710
SDEFCLDKRELSEKVKHAKRLSDERNLLQSNFKDINRQPERGWGSGTGIIOGGDDVF
2584729 SDEFCLDKRELSEKVKHAKRLSDERNLLQSNFKDINRQPERGWGSGTGIIOGGDDVF
660 670 680 690 700 710
```

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cry1a-105.pe 720 730 740 750 760 770
KENYVAFQPECPYVLYOKIDSKAFTRVQLRGVYSDSODLEIKSIRYNAKHETV
2584729 KENYVAFQPECPYVLYOKIDSKAFTRVQLRGVYSDSODLEIKSIRYNAKHETV
720 730 740 750 760 770

cry1a-105.pe 780 790 800 810 820 830
NVPQTGLMFLSGSPGKCEFNRCAPHLENPDLDCSRRDGKCAHSHHSDIDVG
2584729 NVPQTGLMFLSGSPGKCEFNRCAPHLENPDLDCSRRDGKCAHSHHSDIDVG
780 790 800 810 820 830

cry1a-105.pe 840 850 860 870 880 890
CTDNLGVMVIFKIKTODGHARLGNLEFEPKPLVGENLAHYNRAEKKAKREKLEW
2584729 CTDNLGVMVIFKIKTODGHARLGNLEFEPKPLVGENLAHYNRAEKKAKREKLEW
840 850 860 870 880 890

cry1a-105.pe 900 910 920 930 940 950
ETNIVYKEAKESVDALFVNSQYDQLOADTNIAHHAADKRVHSREAYDESLAFGVNA
2584729 ETNIVYKEAKESVDALFVNSQYDQLOADTNIAHHAADKRVHSREAYDESLAFGVNA
900 910 920 930 940 950

cry1a-105.pe 960 970 980 990 1000 1010
AIFELEGRIFTAFSLYDARNVKNKGDFNGLSCWNKGVHDVVEONNORSVIANPEKA
2584729 AIFELEGRIFTAFSLYDARNVKNKGDFNGLSCWNKGVHDVVEONNORSVIANPEKA
960 970 980 990 1000 1010

cry1a-105.pe 1020 1030 1040 1050 1060 1070
EVSQEVRCPCRGVILRVATYKEGEGECVTIHEIENNTDELKFSNCVEEELIYNNVTVC
2584729 EVSQEVRCPCRGVILRVATYKEGEGECVTIHEIENNTDELKFSNCVEEELIYNNVTVC
1020 1030 1040 1050 1060 1070

cry1a-105.pe 1080 1090 1100 1110 1120 1130
NDYTVNQEEYGAVTSNRNGYNEAPSPADYASVVEKSYTDGRRENPCFNRGRDYTP
2584729 NDYTVNQEEYGAVTSNRNGYNEAPSPADYASVVEKSYTDGRRENPCFNRGRDYTP
1080 1090 1100 1110 1120 1130

cry1a-105.pe 1140 1150 1160 1170
LPVGVTKELEYFPETDKWIEIGETGTFVDSVELLMEE
2584729 LPVGVTKELEYFPETDKWIEIGETGTFVDSVELLMEE
1140 1150 1160 1170

cry1a-105.pe
NPAA: 52783575
52783575 source="GENBANK_PROT" Cry1AC [Bacillus thuringiensis]

SCORES Initl: 3914 Initn: 7206 Opt: 7217 z-score: 8194.9 E(): 0
>NPAA: 52783575
Initn: 7206 Initl: 3914 Opt: 7217 z-score: 8194.9 expect(): 0
Smith-Waterman score: 7217; 92.0% identity in 1182 aa overlap
(1-1177:1-1178)

cry1a-105.pe 10 20 30 40 50 60
MDNNPNINECIPNCLSNPEVEVLGGRIETGTPIDISLTQFLSEFVPGAGVGLG
25783575 MDNNPNINECIPNCLSNPEVEVLGGRIETGTPIDISLTQFLSEFVPGAGVGLG
10 20 30 40 50 60

cry1a-105.pe 70 80 90 100 110 120
VDIINGIFGSPQDAFLVQIQIOLINQRIEFARNQAIISRLGSLNLYQIYAESFREWAD
52783575 VDIINGIFGSPQDAFLVQIQIOLINQRIEFARNQAIISRLGSLNLYQIYAESFREWAD
70 80 90 100 110 120

cry1a-105.pe 130 140 150 160 170 180
PTNPALEENRQFNDMMNSALTTPILFAVONYQVPLLSVYVQAANHLHLSVLDSVFGQ
52783575 PTNPALEENRQFNDMMNSALTTPILFAVONYQVPLLSVYVQAANHLHLSVLDSVFGQ
130 140 150 160 170 180

cry1a-105.pe 190 200 210 220 230 240
RMGFDAATINSRNDLTRIGNYTHAVRWYNTGLERWGPDSRDWIRYNOFRRELTIV
52783575 RMGFDAATINSRNDLTRIGNYTHAVRWYNTGLERWGPDSRDWIRYNOFRRELTIV
190 200 210 220 230 240

cry1a-105.pe 250 260 270 280 290 300
LDIVSLFENYDSRTYPIRTVSQLTREIYTNPVLNFDFGSRGSAQIGSIRSPLMDIL
52783575 LDIVSLFENYDSRTYPIRTVSQLTREIYTNPVLNFDFGSRGSAQIGSIRSPLMDIL
250 260 270 280 290 300

cry1a-105.pe 310 320 330 340 350 360
NSITITTDHARGEYVWSGHIWASPVGSGPEFTFPLGYTMGNAAPQORIYAQLGQGVYR
52783575 NSITITTDHARGEYVWSGHIWASPVGSGPEFTFPLGYTMGNAAPQORIYAQLGQGVYR
310 320 330 340 350 360

cry1a-105.pe 370 380 390 400 410 420
TUSSTLYSPNIGINNOQLSVLDGTEYAGTSSNLPSAVYRKSQVTSLSDEIIPPQNNV
52783575 TUSSTLYSPNIGINNOQLSVLDGTEYAGTSSNLPSAVYRKSQVTSLSDEIIPPQNNV
370 380 390 400 410 420

cry1a-105.pe 430 440 450 460 470 480
PPOQSHRLSHVSNVSGFSNSVSLIRAPMFWIHRSAEFNNIIASDSITQIPLVKAH
52783575 PPOQSHRLSHVSNVSGFSNSVSLIRAPMFWIHRSAEFNNIIASDSITQIPLVKAH
430 440 450 460 470 480

cry1a-105.pe 490 500 510 520 530
TLOSQGVTVVRGPGTGGSLDRTSGGPAVY IVNINQDRO---RYBARIRYASTTNL
52783575 TLOSQGVTVVRGPGTGGSLDRTSGGPAVY IVNINQDRO---RYBARIRYASTTNL
490 500 510 520 530

cry1a-105.pe 540 550 560 570 580 590
RIYTVAGERIEFAGQFNKMTDGTDLTFOSFNAATNTAFIPMSQSSFTVGRATFSGN
52783575 RIYTVAGERIEFAGQFNKMTDGTDLTFOSFNAATNTAFIPMSQSSFTVGRATFSGN
540 550 560 570 580 590

cry1a-105.pe 600 610 620 630 640 650
EVIYDRELFIPVATLEAEYNLRAQAKVNAFTSTNOIGLTKTVTDHIDQNSNLYL
52783575 EVIYDRELFIPVATLEAEYNLRAQAKVNAFTSTNOIGLTKTVTDHIDQNSNLYL
600 610 620 630 640 650

cry1a-105.pe 660 670 680 690 700 710
SDEFCLDEKEUSEKVKYAKRLSDERNLQDSNFKDINQPERGCGSGSTGITIQGGDDVF
52783575 SDEFCLDEKEUSEKVKYAKRLSDERNLQDSNFKDINQPERGCGSGSTGITIQGGDDVF
660 670 680 690 700 710

	660	670	680	690	700	710	
cry1a-105.pe	720	730	740	750	760	770	
52783575	KENVYVLSGTFDECYTYLYOKIDESKLKAFTRYQYLRGVIEDSOILEYSTRYNAKHETV						
	720	730	740	750	760	770	
	KENVYVLSGTFDECYTYLYOKIDESKLKAFTRYQYLRGVIEDSOILEYSTRYNAKHETV						
cry1a-105.pe	780	790	800	810	820	830	
52783575	NYPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVG						
	780	790	800	810	820	830	
	NYPGTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVG						
cry1a-105.pe	840	850	860	870	880	890	
52783575	CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEW						
	840	850	860	870	880	890	
	CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARVRAEKWRDKREKLEW						
cry1a-105.pe	900	910	920	930	940	950	
52783575	ETNIVYKEAKESVDALFVNSQVDQLQADTNIAHHAADKVHSIREAYLPELSVPICGNA						
	900	910	920	930	940	950	
	ETNIVYKEAKESVDALFVNSQVDQLQADTNIAHHAADKVHSIREAYLPELSVPICGNA						
cry1a-105.pe	960	970	980	990	1000	1010	
52783575	AIFEELEGRIFTAFSLYDARNYIKNGDFNGLSCWNYKGVHVDVEEQNNQRSLVVPWEA						
	960	970	980	990	1000	1010	
	AIFEELEGRIFTAFSLYDARNYIKNGDFNGLSCWNYKGVHVDVEEQNNQRSLVVPWEA						
cry1a-105.pe	1020	1030	1040	1050	1060	1070	
52783575	EVSQVRVCPGRGHILRVYAYKEGEGCVTHIEINNVDLKFNCVBEIEIYNNVTIC						
	1020	1030	1040	1050	1060	1070	
	EVSQVRVCPGRGHILRVYAYKEGEGCVTHIEINNVDLKFNCVBEIEIYNNVTIC						
cry1a-105.pe	1080	1090	1100	1110	1120	1130	
52783575	NDYTVNOEYGGAYTSRNGYNEAPSVPADYASVYEKSYTDGRNPFCEFNRCYRDYTP						
	1080	1090	1100	1110	1120	1130	
	NDYTVNOEYGGAYTSRNGYNEAPSVPADYASVYEKSYTDGRNPFCEFNRCYRDYTP						
cry1a-105.pe	1140	1150	1160	1170			
52783575	LPVGVTKELEYFETDKVWIEIGETGTFIVDSVLLMEE						
	1140	1150	1160	1170			
	LPVGVTKELEYFETDKVWIEIGETGTFIVDSVLLMEE						
cry1a-105.pep							
NRAA:143126							
143126 source="GENBANK_PROT" [Bacillus thuringiensis gene, complete cds.], gene product							
SCORES Init1: 3919 Initn: 7204 Opt: 7215 Z-score: 8192.7 E(): 0							
>NRAA:143126							
Initn: 7204 Init1: 3919 Opt: 7215 Z-score: 8192.7 expect(): 0							
Smith-Waterman score: 7215: 92.0% identity in 1182 aa overlap							
(1-1177:1-1178)							
cry1a-105.pe	10	20	30	40	50	60	
	MDNNPINECIPYNCLSNPEVVLGGRIETGYTPIDISLSLTQFLSEFVPGAGFVLGL						

143126	MDNNPINECIPYNCLSNPEVVLGGRIETGYTPIDISLSLTQFLSEFVPGAGFVLGL	10	20	30	40	50	60	
cry1a-105.pe	VDIIWIGIFGSDQDAFLVQIEQLINQRIEFARNOAISREGLSNLYQIYAESFREWEAD	70	80	90	100	110	120	
143126	VDIIWIGIFGSDQDAFLVQIEQLINQRIEFARNOAISREGLSNLYQIYAESFREWEAD	70	80	90	100	110	120	
cry1a-105.pe	PTNPALREEMRIQFNDMNSALTTAIPFAVONQVPLLSVYVQAAHLHSLVRDVSFVGQ	130	140	150	160	170	180	
143126	PTNPALREEMRIQFNDMNSALTTAIPFAVONQVPLLSVYVQAAHLHSLVRDVSFVGQ	130	140	150	160	170	180	
cry1a-105.pe	RMGFDAATINSRYNDLTRIGNYTHAVRWNTGLERVMPGSDRWIRYNQFRRELTLTV	190	200	210	220	230	240	
143126	RMGFDAATINSRYNDLTRIGNYTHAVRWNTGLERVMPGSDRWIRYNQFRRELTLTV	190	200	210	220	230	240	
cry1a-105.pe	LDIVSLFENYDSRTYRTVSQLTREIYNPVENFDGSGRGAQIEGSIERSPHLMDIL	250	260	270	280	290	300	
143126	LDIVSLFENYDSRTYRTVSQLTREIYNPVENFDGSGRGAQIEGSIERSPHLMDIL	250	260	270	280	290	300	
cry1a-105.pe	NSITITVDHARGYYWSHQIMASVPVGFSGPEFTFPLYGTMGNAAPQORIQAOLGQGVYR	310	320	330	340	350	360	
143126	NSITITVDHARGYYWSHQIMASVPVGFSGPEFTFPLYGTMGNAAPQORIQAOLGQGVYR	310	320	330	340	350	360	
cry1a-105.pe	TLSSSTLYRRPNIGNNQSLVDGTETAYCTSNLPSAVYKSGTVDSLDEIPQNNVY	370	380	390	400	410	420	
143126	TLSSSTLYRRPNIGNNQSLVDGTETAYCTSNLPSAVYKSGTVDSLDEIPQNNVY	370	380	390	400	410	420	
cry1a-105.pe	PPROGFSHRLSHVSMFSGFSNSVSIIRAPMFSWIHRAEFNNIIASDSITQIPVKAH	430	440	450	460	470	480	
143126	PPROGFSHRLSHVSMFSGFSNSVSIIRAPMFSWIHRAEFNNIIASDSITQIPVKAH	430	440	450	460	470	480	
cry1a-105.pe	TLQSGTTVVRGPGFTGDIILRRTSGGPEAYT--IVNINGQLPQ--RYRARIRYASTNL	490	500	510	520	530		
143126	FLFNGS-VISGPGFTGDIILRRTSGGPEAYT--IVNINGQLPQ--RYRARIRYASTNL	490	500	510	520	530		
cry1a-105.pe	RIYTVVAGERIFAGQFNKTMDTGDPILTQSPFSYATINTAFTPMQSSFTVGADTFSSGN	540	550	560	570	580	590	
143126	HLNVNMGNSISFNTVTPATSLDNLQSSDFGYPESANFTSLGN--IVGVNRFSGTA	540	550	560	570	580	590	
cry1a-105.pe	EYVIDREFELIVTATLEAEYNLEAKAVNALFTSTNQLGLKNTVTDYHIDQVSNLYTL	600	610	620	630	640	650	
143126	GVIIIDREFELIVTATLEAEYNLEAKAVNALFTSTNQLGLKNTVTDYHIDQVSNLYTL	600	610	620	630	640	650	
cry1a-105.pe	SDEFCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTITIGQDDVF	660	670	680	690	700	710	

143126 SDECLDSEKAKRLSDERNLQDSNFKDINQPERGWGGSTGTTTQGGDDVF
780 790 800 810 820 830
760 770 780 790 800 810 820 830
cry1a-105.pe KENYVSGTDFCYVLYQKIDSKKATRIQOLGYEISQOILEYIRYNAKHETV
143126 KENYVTSSTGTPCEKAKAQQIDSKKATRIQOLGYEISQOILEYIRYNAKHETV
720 730 740 750 760 770
780 790 800 810 820 830
cry1a-105.pe NYPGTSLWPLSAQSPKCKSPNRCALHNMDDLDSCSDQSCCAHSHHFLDIDVG
143126 NYPGTSLWPLSAQSPKCKSPNRCALHNMDDLDSCSDQSCCAHSHHFLDIDVG
780 790 800 810 820 830
cry1a-105.pe CTDLNEGLVWVIFKIKTQGHARLGNLEFLEKPLVGEALGVKAEKWRDKRLEW
143126 CTDLNEGLVWVIFKIKTQGHARLGNLEFLEKPLVGEALGVKAEKWRDKRLEW
840 850 860 870 880 890
900 910 920 930 940 950
cry1a-105.pe ETNIVYKEAKESVDALFVNSVDQLOADNTIAMIHAADKRVHSIREAYLPELSVTPGVNA
143126 ETNIVYKEAKESVDALFVNSVDQLOADNTIAMIHAADKRVHSIREAYLPELSVTPGVNA
900 910 920 930 940 950
cry1a-105.pe AIFEELEGRIFFATSLYDARNVKNKGFDFNGLSCWNVKGVHVEEQNNORSVLVPEWEA
143126 AIFEELEGRIFFATSLYDARNVKNKGFDFNGLSCWNVKGVHVEEQNNORSVLVPEWEA
960 970 980 990 1000 1010
cry1a-105.pe EVSQEVRCPCRGYILRVYAYKEGEGCVTTHELENTDELKFSNCVEEYIPNNVTVC
143126 EVSQEVRCPCRGYILRVYAYKEGEGCVTTHELENTDELKFSNCVEEYIPNNVTVC
1020 1030 1040 1050 1060 1070
cry1a-105.pe NDYVNOEEYGGAYTSNRNGNEAPSPADYASVYEKSYTDGRNCPCEFNRGYRDYTP
143126 NDYVNOEEYGGAYTSNRNGNEAPSPADYASVYEKSYTDGRNCPCEFNRGYRDYTP
1080 1090 1100 1110 1120 1130
cry1a-105.pe LPGVYVTELEVPFETDKVWIEIGETEGTFIVDSVELLMEE
143126 LPGVYVTELEVPFETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pep
NRAA:3979717
3979717 source="GENBANK_PROT" crystal toxin protein [Bacillus thuringiensis]
SCORES Initl: 3919 Initn: 7189 Opt: 7200 z-score: 8175.6 E(): 0
>NRAA:3979717
Initl: 7189 Initn: 3919 Opt: 7200 z-score: 8175.6 expect(): 0
Smith-Waterman score: 7200; 91.8% identity in 1182 aa overlap
(1-1177:1-1178)

cry1a-105.pe MNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLISEFVPGAGFVLGL
3979717 MNNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLISEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIWIFGFSQMDAFLVOIEQLINORIEEFARNQAIISREGLSNLYQIYAESFREWAD
3979717 VDIWIFGFSQMDAFLVOIEQLINORIEEFARNQAIISREGLSNLYQIYAESFREWAD
70 80 90 100 110 120
cry1a-105.pe PTNPALREEMIOFNMDNWSALTALTPAFQVQVYVPLISVYVQAANLHLSVLRDVSFVGQ
3979717 PTNPALREEMIOFNMDNWSALTALTPAFQVQVYVPLISVYVQAANLHLSVLRDVSFVGQ
130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRYNDLTRLIGNVTYAVRWYNTGLERVWGPDSRDWRVYNOFRRELITV
3979717 RWGFDAAATINSRYNDLTRLIGNVTYAVRWYNTGLERVWGPDSRDWRVYNOFRRELITV
190 200 210 220 230 240
cry1a-105.pe LDIVLSLFPNYSRTYPIRTVSQLTREIYINPVLENFDFGSPRGSQAQIEGSIERSPHLMDIL
3979717 LDIVLSLFPNYSRTYPIRTVSQLTREIYINPVLENFDFGSPRGSQAQIEGSIERSPHLMDIL
250 260 270 280 290 300
cry1a-105.pe NSITITDARHGYWGHQIMASPVFGSGPEFTFPLYGTMGNAAPOQRIVAQLQGQVYR
3979717 NSITITDARHGYWGHQIMASPVFGSGPEFTFPLYGTMGNAAPOQRIVAQLQGQVYR
310 320 330 340 350 360
cry1a-105.pe TLSTLRLRPPNIGNCOASVLDGTEFAFGTSSNLPASVYKSGTVDSLDEIPPQNNV
3979717 TLSTLRLRPPNIGNCOASVLDGTEFAFGTSSNLPASVYKSGTVDSLDEIPPQNNV
370 380 390 400 410 420
cry1a-105.pe PPRQGFSHRLSHVSWFRSSNSVSPAPMFHSWFRSSEFNIIIASDSITQIPAVKGN
3979717 PPRQGFSHRLSHVSWFRSSNSVSPAPMFHSWFRSSEFNIIIASDSITQIPAVKGN
430 440 450 460 470 480
cry1a-105.pe TLOSQITVVRGPGFTGGDILRTTSQGPAYT--NNKQOLPO--RYRARIRYASTNL
3979717 TLOSQITVVRGPGFTGGDILRTTSQGPAYT--NNKQOLPO--RYRARIRYASTNL
490 500 510 520 530
cry1a-105.pe RIYVTVAGERIFAGOFNKMTDGTPLTQSFYSATINTATPTPNSQSSFTGATWSSGN
3979717 RIYVTVAGERIFAGOFNKMTDGTPLTQSFYSATINTATPTPNSQSSFTGATWSSGN
540 550 560 570 580 590
cry1a-105.pe EYVIDRFEIIPVATLEAEYNLERAKAVNALTSNQLKTNVTHYHDOVSNNTVTH
3979717 EYVIDRFEIIPVATLEAEYNLERAKAVNALTSNQLKTNVTHYHDOVSNNTVTH
600 610 620 630 640 650
cry1a-105.pe GVIIDRFEIIPVATLEAEYNLERAKAVNALTSNQLKTNVTHYHDOVSNNTVTH
3979717 GVIIDRFEIIPVATLEAEYNLERAKAVNALTSNQLKTNVTHYHDOVSNNTVTH
660 670 680 690 700 710

```
cry1a-105.pe SDFCLDEKSELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWGSGTITIGGGDDVP
3979717 ||||| 660 670 680 690 700 710
SDFCLDEKSELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWGSGTITIGGGDDVP

cry1a-105.pe KENVYVLSGTFDECYTYLYQKIDESKLKAFTRVQLRGYIEDSQDLEIYSIRYNAKHETV
3979717 ||||| 720 730 740 750 760 770
KENVYVLSGTFDECYTYLYQKIDESKLKAFTRVQLRGYIEDSQDLEIYSIRYNAKHETV

cry1a-105.pe NYPGTSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDVG
3979717 ||||| 780 790 800 810 820 830
NYPGTSGLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFFSLDIDVG

cry1a-105.pe CTDANEDLGWVIFPKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLEW
3979717 ||||| 840 850 860 870 880 890
CTDANEDLGWVIFPKIKTODGHARLGNLEFLEKPLVGEALARKVRAEKKWRDKREKLEW

cry1a-105.pe ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSIPGVNA
3979717 ||||| 900 910 920 930 940 950
ETNIVYKEAKESVDALFVNSQYDQLQADTNIAMHAADKRVHSIREAYLPELSIPGVNA

cry1a-105.pe ALFELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHDVVEQNNQSRVLVVPWEA
3979717 ||||| 960 970 980 990 1000 1010
ALFELEGRIFTAFSLYDARNVKNKGDFNGLSCWNVKGVHDVVEQNNQSRVLVVPWEA

cry1a-105.pe EYSQVRVCPGRGYLLRVYAYKEGYEGECVTIHEIENNTDELKFSNCEEIYFNNTVTC
3979717 ||||| 1020 1030 1040 1050 1060 1070
EYSQVRVCPGRGYLLRVYAYKEGYEGECVTIHEIENNTDELKFSNCEEIYFNNTVTC

cry1a-105.pe NDYTVNQEYGGAYTSNRGYNEAPSVADYASVYEKSYTDGRRENPCFNRGYRDTTP
3979717 ||||| 1080 1090 1100 1110 1120 1130
NDYTVNQEYGGAYTSNRGYNEAPSVADYASVYEKSYTDGRRENPCFNRGYRDTTP

cry1a-105.pe LPVGVTKELEYFPETDKWVIEIGETGTFIVDSVELLMEE
3979717 ||||| 1140 1150 1160 1170
LPVGVTKELEYFPETDKWVIEIGETGTFIVDSVELLMEE

cry1a-105.pep
NRAA:23344760
```

23344760 source="GENBANK_PROT" insecticidal crystal protein CryIAC [Bacillus thuringiensis]

SCORES Initl: 6695 Initn: 6695 Opt: 7192 z-score: 8166.5 E(): 0
>>NRAA:23344760
initn: 6695 initl: 6695 opt: 7192 z-score: 8166.5 expect(): 0
Smith-Waterman score: 7192; 91.8% identity in 1182 aa overlap
(1-1177:1-1177)

```
cry1a-105.pe MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL
23344760 ||||| 10 20 30 40 50 60
MDNPNINECIPNCLSNPEVEVLGGERIETGYTPIDISLSLTQFLSEFVPGAGFVLGL

cry1a-105.pe VDIWIGIFGSDMAFLVOIEQLINQRIEFPARNOAISRLGSLNLYOIAESFREWEAD
23344760 ||||| 70 80 90 100 110 120
VDIWIGIFGSDMAFLVOIEQLINQRIEFPARNOAISRLGSLNLYOIAESFREWEAD

cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLHSLVLRDVSFVGQ
23344760 ||||| 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNYQVPLLSVYQAAHLHSLVLRDVSFVGQ

cry1a-105.pe RNFQDAATINSRNDLTRILGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV
23344760 ||||| 190 200 210 220 230 240
RNFQDAATINSRNDLTRILGNYTHAVRWYNTGLERVWGPDSRDWIRYNOFRRELTIV

cry1a-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGRSAQIEGSIKSPHLMIL
23344760 ||||| 250 260 270 280 290 300
LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDFGRSAQIEGSIKSPHLMIL

cry1a-105.pe NSITTYDAHRGYTYSWGHIWASPVGSGPEFTFPLYGTMGNAAPQORIIVAQLGQGVYR
23344760 ||||| 310 320 330 340 350 360
NSITTYDAHRGYTYSWGHIWASPVGSGPEFTFPLYGTMGNAAPQORIIVAQLGQGVYR

cry1a-105.pe TLSSLTLYRPPNIGINNQQSLVDLGTETEFAYGISNLSNPSAVYKSGTVDSLDEIIPPQNNV
23344760 ||||| 370 380 390 400 410 420
TLSSLTLYRPPNIGINNQQSLVDLGTETEFAYGISNLSNPSAVYKSGTVDSLDEIIPPQNNV

cry1a-105.pe PPRQGFSHRLSHVSMFSGFSNVSIIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH
23344760 ||||| 430 440 450 460 470 480
PPRQGFSHRLSHVSMFSGFSNVSIIIRAPMFSWIHRSAEFNIIASDSITQIPLVKAH

cry1a-105.pe FLFNGS-VISGPGFTGDIIVRLNLSGNNIQRGYIEVPIHFPSSTIRVVRVYASVTPI
23344760 ||||| 480 490 500 510 520 530
FLFNGS-VISGPGFTGDIIVRLNLSGNNIQRGYIEVPIHFPSSTIRVVRVYASVTPI

cry1a-105.pe RIYVTVAGERIFAGQFNKMTGDGPIETQFSFYSATINTAFTFPMSSQSFYTGADTFSSGN
23344760 ||||| 540 550 560 570 580 590
RIYVTVAGERIFAGQFNKMTGDGPIETQFSFYSATINTAFTFPMSSQSFYTGADTFSSGN

cry1a-105.pe EYVIDRFELIPTVATLEAEYNLERAKAVNALFTSTNQLGKTNVTDHIDQVSNLVTYL
23344760 ||||| 600 610 620 630 640 650
EYVIDRFELIPTVATLEAEYNLERAKAVNALFTSTNQLGKTNVTDHIDQVSNLVTYL
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cry1a-105.pe 660 670 680 690 700 710
SDPCLDKEKLSKVAHNSLSDERNLLQDSNEKIDINRQPERGWSGTGTTIOGGDDVF
SDPCLDKEKLSKVAHNSLSDERNLLQDSNEKIDINRQPERGWSGTGTTIOGGDDVF
SDPCLDKEKLSKVAHNSLSDERNLLQDSNEKIDINRQPERGWSGTGTTIOGGDDVF

cry1a-105.pe 720 730 740 750 760 770
KENYTLGSGTDEKPTVYKIDSKKAPFVYRGYIEDQDLLEIYSIRYAKHETV
KENYTLGSGTDEKPTVYKIDSKKAPFVYRGYIEDQDLLEIYSIRYAKHETV
KENYTLGSGTDEKPTVYKIDSKKAPFVYRGYIEDQDLLEIYSIRYAKHETV

cry1a-105.pe 780 790 800 810 820 830
NVPGTGSLWPLSAQSPICKGGEFNRCAPHLNNDLQDSRDEKCAHSHNSHSDVVG
NVPGTGSLWPLSAQSPICKGGEFNRCAPHLNNDLQDSRDEKCAHSHNSHSDVVG
NVPGTGSLWPLSAQSPICKGGEFNRCAPHLNNDLQDSRDEKCAHSHNSHSDVVG

cry1a-105.pe 840 850 860 870 880 890
CTDLNEDLGWVYFIKIKTQDGHARLGNLEFLEKPLVGEASARKRAEKNWPKLEW
CTDLNEDLGWVYFIKIKTQDGHARLGNLEFLEKPLVGEASARKRAEKNWPKLEW
CTDLNEDLGWVYFIKIKTQDGHARLGNLEFLEKPLVGEASARKRAEKNWPKLEW

cry1a-105.pe 900 910 920 930 940 950
ETNIVYKEAKESVDALFVNSQYDQLQADNTNIAHIAADKRVHSIRAYLPELSVPGVNA
ETNIVYKEAKESVDALFVNSQYDQLQADNTNIAHIAADKRVHSIRAYLPELSVPGVNA
ETNIVYKEAKESVDALFVNSQYDQLQADNTNIAHIAADKRVHSIRAYLPELSVPGVNA

cry1a-105.pe 960 970 980 990 1000 1010
AIFEELEGRIFFAFSLYDARNVINKGDFNNGLSQWNVKGVHVDVEEQNORSVLVWPEEA
AIFEELEGRIFFAFSLYDARNVINKGDFNNGLSQWNVKGVHVDVEEQNORSVLVWPEEA
AIFEELEGRIFFAFSLYDARNVINKGDFNNGLSQWNVKGVHVDVEEQNORSVLVWPEEA

cry1a-105.pe 1020 1030 1040 1050 1060 1070
EVSQEVRVCPGGRYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYIPNNVTTC
EVSQEVRVCPGGRYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYIPNNVTTC
EVSQEVRVCPGGRYLRTVAYKEGYGEGCVTTHEIENNTDELKFSNCVEEYIPNNVTTC

cry1a-105.pe 1080 1090 1100 1110 1120 1130
NDYTVNOEYGGAYTSRNGYNEAPSVPADYASVVEEKSQYTDGRENPCFNRGYRDTTP
NDYTVNOEYGGAYTSRNGYNEAPSVPADYASVVEEKSQYTDGRENPCFNRGYRDTTP
NDYTVNOEYGGAYTSRNGYNEAPSVPADYASVVEEKSQYTDGRENPCFNRGYRDTTP

cry1a-105.pe 1140 1150 1160 1170
LPVGYVTKLEYFPETDKWIEIGETEGTIFVDSVELLMBEE
LPVGYVTKLEYFPETDKWIEIGETEGTIFVDSVELLMBEE
LPVGYVTKLEYFPETDKWIEIGETEGTIFVDSVELLMBEE

(1-1177:1-1177)

cry1a-105.pe 10 20 30 40 50 60
MDNNPNECIPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLSEFVPAGFVLGL
MDNNPNECIPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLSEFVPAGFVLGL
MDNNPNECIPYNCLSNPEVEVLGERIETGYTPIDISLSLQFLLSEFVPAGFVLGL

cry1a-105.pe 70 80 90 100 110 120
VDIINGIIFGSPQMDAFVQLEQINORIEEFARNQALSRLEGSLNLYQIYAESFREWEAD
VDIINGIIFGSPQMDAFVQLEQINORIEEFARNQALSRLEGSLNLYQIYAESFREWEAD
VDIINGIIFGSPQMDAFVQLEQINORIEEFARNQALSRLEGSLNLYQIYAESFREWEAD

cry1a-105.pe 130 140 150 160 170 180
PTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAAHLSLVLRDVSFVGQ
PTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAAHLSLVLRDVSFVGQ
PTNPALREEMRIQFNDMNSALTTAIPFAVQNVQVPLLSVYVQAAHLSLVLRDVSFVGQ

cry1a-105.pe 190 200 210 220 230 240
RWGFDATINRSYNDLRLGLNVTYHAWYNTGLERWVGPDSDRWIRYNQFRRELITV
RWGFDATINRSYNDLRLGLNVTYHAWYNTGLERWVGPDSDRWIRYNQFRRELITV
RWGFDATINRSYNDLRLGLNVTYHAWYNTGLERWVGPDSDRWIRYNQFRRELITV

cry1a-105.pe 250 260 270 280 290 300
LDIVSLFPNVDSRTYPIRTVSQLTREIYNPVLENFQDSFRGSAQIEGSIIRSPHMDIL
LDIVSLFPNVDSRTYPIRTVSQLTREIYNPVLENFQDSFRGSAQIEGSIIRSPHMDIL
LDIVSLFPNVDSRTYPIRTVSQLTREIYNPVLENFQDSFRGSAQIEGSIIRSPHMDIL

cry1a-105.pe 310 320 330 340 350 360
NSITITTSYHREYFWSHQIMASPVGSGPEFTPLPYGTMGNAAPQQRIVLAQLQGQVYR
NSITITTSYHREYFWSHQIMASPVGSGPEFTPLPYGTMGNAAPQQRIVLAQLQGQVYR
NSITITTSYHREYFWSHQIMASPVGSGPEFTPLPYGTMGNAAPQQRIVLAQLQGQVYR

cry1a-105.pe 370 380 390 400 410 420
TLSSYVRRFPNIGVQDLSVADGNEFAYCTSSNLPSAVYKSGTVDSLDEIPQNNNV
TLSSYVRRFPNIGVQDLSVADGNEFAYCTSSNLPSAVYKSGTVDSLDEIPQNNNV
TLSSYVRRFPNIGVQDLSVADGNEFAYCTSSNLPSAVYKSGTVDSLDEIPQNNNV

cry1a-105.pe 430 440 450 460 470 480
PPRGFSHRLSHVSMFSGFNSSVADPAWFSWHSASNNIIASDSITQIPLVKAH
PPRGFSHRLSHVSMFSGFNSSVADPAWFSWHSASNNIIASDSITQIPLVKAH
PPRGFSHRLSHVSMFSGFNSSVADPAWFSWHSASNNIIASDSITQIPLVKAH

cry1a-105.pe 490 500 510 520 530
TLQSGITVVRGPGFTGGDILRTSGGPFAYTIVNNGQDPQ---RYRIRINASNNL
TLQSGITVVRGPGFTGGDILRTSGGPFAYTIVNNGQDPQ---RYRIRINASNNL
TLQSGITVVRGPGFTGGDILRTSGGPFAYTIVNNGQDPQ---RYRIRINASNNL

cry1a-105.pe 540 550 560 570 580 590
FLNNGS-VISGPGFTGGDILRLNNGSNNIQRNGYIENRHSSTSTIRVRVRYASVSI
FLNNGS-VISGPGFTGGDILRLNNGSNNIQRNGYIENRHSSTSTIRVRVRYASVSI
FLNNGS-VISGPGFTGGDILRLNNGSNNIQRNGYIENRHSSTSTIRVRVRYASVSI

cry1a-105.pe 600 610 620 630 640 650
RIYTVVAGERIPAGQPNKMTDGTPLTFQSFVSATINTAFPPMSQSSFTWADTESGN
RIYTVVAGERIPAGQPNKMTDGTPLTFQSFVSATINTAFPPMSQSSFTWADTESGN
RIYTVVAGERIPAGQPNKMTDGTPLTFQSFVSATINTAFPPMSQSSFTWADTESGN

cry1a-105.pe 660 670 680 690 700 710
EYVIDRFEIIPVTATLEAYNLERAKQAVNALFTSNQGLKTNVTYDHIDQVSNLVTYL
EYVIDRFEIIPVTATLEAYNLERAKQAVNALFTSNQGLKTNVTYDHIDQVSNLVTYL
EYVIDRFEIIPVTATLEAYNLERAKQAVNALFTSNQGLKTNVTYDHIDQVSNLVTYL

SCORES Initl: 6688 Inltn: 6688 Opt: 7185 Z-score: 8158.6 E(): 0
>>NRAA:142742
Inltn: 6688 Inltn: 6688 Opt: 7185 Z-score: 8158.6 expect():
Smith-Waterman score: 7185; 91.7% identity in 1182 aa overlap

Monsanto Company

Final Report

Product Characterization Center

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MSL No. 20351
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```
600      610      620      630      640      650
660      670      680      690      700      710
cry1a-105.pe SDFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGSGTGTIGGGDDVF
142742 SDFCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGSGTGTIGGGDDVF
660      670      680      690      700      710
720      730      740      750      760      770
cry1a-105.pe KENYVTLSGTDECPYLYOKIDSKLKAETRYOLRGYLEDSODLEIYSIRYNAKHETV
142742 KENYVTLSGTDECPYLYOKIDSKLKAETRYOLRGYLEDSODLEIYSIRYNAKHETV
720      730      740      750      760      770
780      790      800      810      820      830
cry1a-105.pe NVFGTGSWLPLSAQSPIGKCGFNRCAPHEWNPDLDCSCRDGCKCAHSHHFFSLDIDVG
142742 NVFGTGSWLPLSAQSPIGKCGFNRCAPHEWNPDLDCSCRDGCKCAHSHHFFSLDIDVG
780      790      800      810      820      830
840      850      860      870      880      890
cry1a-105.pe CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARKVKAERKWRDKREKLEW
142742 CTDLNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARKVKAERKWRDKREKLEW
840      850      860      870      880      890
900      910      920      930      940      950
cry1a-105.pe ETNIVYKEAKESVDALFVNSQVDQLQADNTAMIHAADKRVHSIREAYLPELSVPVGNA
142742 ETNIVYKEAKESVDALFVNSQVDQLQADNTAMIHAADKRVHSIREAYLPELSVPVGNA
900      910      920      930      940      950
960      970      980      990      1000      1010
cry1a-105.pe AFPELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNRSVLVPEWEA
142742 AFPELEGRIFTAFSLYDARNVIKNGDFNGLSCWNVKGVHDVEEQNRSVLVPEWEA
960      970      980      990      1000      1010
1020      1030      1040      1050      1060      1070
cry1a-105.pe EYSQEVRCVPCRGVILRVATYKEGYEGCVTHIEIENNTDELKFSNCVEEELYPNNTVTC
142742 EYSQEVRCVPCRGVILRVATYKEGYEGCVTHIEIENNTDELKFSNCVEEELYPNNTVTC
1020      1030      1040      1050      1060      1070
1080      1090      1100      1110      1120      1130
cry1a-105.pe NDVTYNOEYGGVTSNRNGYNAPSVPADVASVVEKSYTDGRRNCPCFNRGVRDVT
142742 NDVTYNOEYGGVTSNRNGYNAPSVPADVASVVEKSYTDGRRNCPCFNRGVRDVT
1080      1090      1100      1110      1120      1130
1140      1150      1160      1170
cry1a-105.pe LPVGWYTKELFFPETDKWIEIGETGTFIVDSVELLMEE
142742 LPVGWYTKELFFPETDKWIEIGETGTFIVDSVELLMEE
1140      1150      1160      1170
cry1a-105.pe
142740
142740 source="GENBANK_PROT" delta-endotoxin
SCORES Init1: 6670 Initn: 6670 Opt: 7167 z-score: 8138.1 E(): 0
-->NRAA:142740
initn: 6670 init1: 6670 opt: 7167 z-score: 8138.1 expect(): 0
```

```
Smith-Waterman score: 7167; 91.6% identity in 1182 aa overlap
(1-1177:1-1177)
10      20      30      40      50      60
cry1a-105.pe MNNNNINCEIPNCLSNPEVEVLGERIETGYTPIDISLSLQFILLSEFVPGAGFVLGL
142740 MNNNNINCEIPNCLSNPEVEVLGERIETGYTPIDISLSLQFILLSEFVPGAGFVLGL
10      20      30      40      50      60
70      80      90      100      110      120
cry1a-105.pe VDLIMGIFGSDWDAFLVQLEQINQRIEERFARNAQISRLGSLNLYQIYAESFREWEAD
142740 VDLIMGIFGSDWDAFLVQLEQINQRIEERFARNAQISRLGSLNLYQIYAESFREWEAD
70      80      90      100      110      120
130      140      150      160      170      180
cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHSLVLDVSVFGQ
142740 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYQAAHLHSLVLDVSVFGQ
130      140      150      160      170      180
190      200      210      220      230      240
cry1a-105.pe RWGFDAAATINSRYNDLTRLIGNYTHAVRWNTGLERVWGPDSRDMIRYNQFRRELITV
142740 RWGFDAAATINSRYNDLTRLIGNYTHAVRWNTGLERVWGPDSRDMIRYNQFRRELITV
190      200      210      220      230      240
250      260      270      280      290      300
cry1a-105.pe LDIVLSLFNYSRTPYRTVSQLTREIYNPVLNFDSGFRGSAQIEGSIKSHPLMDIL
142740 LDIVLSLFNYSRTPYRTVSQLTREIYNPVLNFDSGFRGSAQIEGSIKSHPLMDIL
250      260      270      280      290      300
310      320      330      340      350      360
cry1a-105.pe NSITTYDAHGEYWGSHGIMASPVGSGPEFTFPLYGTWGNAAQQQRIVAQLQGQVYR
142740 NSITTYDAHGEYWGSHGIMASPVGSGPEFTFPLYGTWGNAAQQQRIVAQLQGQVYR
310      320      330      340      350      360
370      380      390      400      410      420
cry1a-105.pe TLSSTLYRRPNIGINNQQLSVLDTGTEFAYGTSSNLPNAVYKSGTVDSLDEIPQNNNV
142740 TLSSTLYRRPNIGINNQQLSVLDTGTEFAYGTSSNLPNAVYKSGTVDSLDEIPQNNNV
370      380      390      400      410      420
430      440      450      460      470      480
cry1a-105.pe PPRQGSFHLHSHVSMFSGSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
142740 PPRQGSFHLHSHVSMFSGSNSSVSIIRAPMFSWIHRSAEFNNIIASDSITQIPLVKAH
430      440      450      460      470      480
490      500      510      520      530      540
cry1a-105.pe TLOGSTTVVRGPGFTGGDILRRTSGGPAYT--IVNINGQLPQ---RYRARIYASTNNL
142740 TLOGSTTVVRGPGFTGGDILRRTSGGPAYT--IVNINGQLPQ---RYRARIYASTNNL
490      500      510      520      530      540
540      550      560      570      580      590
cry1a-105.pe RIYVTVAGERIPFAGQFNKMTDGLTFFQSFYATINTAFTFFPMSSQSFVGVADTFSSGN
142740 RIYVTVAGERIPFAGQFNKMTDGLTFFQSFYATINTAFTFFPMSSQSFVGVADTFSSGN
540      550      560      570      580      590
600      610      620      630      640      650
cry1a-105.pe EVVIDSFELIPVATLEAEYNLERAKAVNALFTSTNOLKNTVTDYHIDQVSNLTYL
142740 EVVIDSFELIPVATLEAEYNLERAKAVNALFTSTNOLKNTVTDYHIDQVSNLTYL
600      610      620      630      640      650
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142740 GVIIIDFEFIPATLAEAYNLERAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTCL
600 610 620 630 640 650
cry1a-105.pe SDKCLDESEFVYKHAKRSDENLLODSFVDINROPEKSGSTGIIIOGDDVF
660 670 680 690 700 710
142740 SDPFSDEPRESEKVFHAKLSDERNLLOSFNFINRQPERGWSGIGIIOGDDVF
660 670 680 690 700 710
cry1a-105.pe KENVTLSTGTFDECPTVYOKIDKSFTRVYOLRYVINDSOLIEKYSIRYNAKHETV
720 730 740 750 760 770
142740 KENVTLSTGTFDECPTVYOKIDKSFTRVYOLRYVINDSOLIEKYSIRYNAKHETV
720 730 740 750 760 770
cry1a-105.pe NVPGTSLWPLSAQSPIGKCGEPNRCAPHNNTNLDSCRFSEKCAHSHHSLIDVIG
780 790 800 810 820 830
142740 NVPGTSLWPLSAQSPIGKCGEPNRCAPHNNTNLDSCRFSEKCAHSHHSLIDVIG
780 790 800 810 820 830
cry1a-105.pe CTIDNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARYKREKRWOKRAKLEW
840 850 860 870 880 890
142740 CTIDNEDLGWVWIFKIKTQDGHARLGNLEFLEKPLVGEALARYKREKRWOKRAKLEW
840 850 860 870 880 890
cry1a-105.pe ETNIVYKEAKESVDALFVNSQVDQLOADTNIAHIAADKRVHSIREAYLPSELSVPGVNA
900 910 920 930 940 950
142740 ETNIVYKEAKESVDALFVNSQVDQLOADTNIAHIAADKRVHSIREAYLPSELSVPGVNA
900 910 920 930 940 950
cry1a-105.pe AIFEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNVKGVHDVPEONQORSVLVPEWEA
960 970 980 990 1000 1010
142740 AIFEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNVKGVHDVPEONQORSVLVPEWEA
960 970 980 990 1000 1010
cry1a-105.pe EVSOEVRVCPGRGYLLRVYAYKEGYGECVTIHEIENNTDELKFSNCVEEIEVPNNVTVC
1020 1030 1040 1050 1060 1070
142740 EVSOEVRVCPGRGYLLRVYAYKEGYGECVTIHEIENNTDELKFSNCVEEIEVPNNVTVC
1020 1030 1040 1050 1060 1070
cry1a-105.pe NDYTVNOEYGGAYTSRNGVNEAPSPADYASVYEKSYTDGRENPCFNRGYRDYTP
1080 1090 1100 1110 1120 1130
142740 NDYTVNOEYGGAYTSRNGVNEAPSPADYASVYEKSYTDGRENPCFNRGYRDYTP
1080 1090 1100 1110 1120 1130
cry1a-105.pe LPVGXVKELEYFETDKVNIIEIGETGTFIVDSVLLMEE
1140 1150 1160 1170
142740 LPVGXVKELEYFETDKVNIIEIGETGTFIVDSVLLMEE
1140 1150 1160 1170
cry1a-105.pep
NRSA:33321716
33321716 source="GENBANK_PROT" CryIAC [Bacillus thuringiensis]
SCORES Initl: 6651 Initn: 6651 Opt: 7148 z-score: 8116.5 E(): 0
>NRSA:33321716

initn: 6651 initl: 6651 opt: 7148 z-score: 8116.5 expect(): 0
Smith-Waterman score: 7148; 91.4% identity in 1182 aa overlap
(1-1177:1-1177)
cry1a-105.pe MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVFGAGVLGL
10 20 30 40 50 60
33321716 MDNPNINCEIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVFGAGVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGQSDAFLVQIEBOLINORIEEFARNQAIISRLIEGLSNLYQIYAESFREWAD
70 80 90 100 110 120
33321716 VDIIMGIFGQSDAFLVQIEBOLINORIEEFARNQAIISRLIEGLSNLYQIYAESFREWAD
70 80 90 100 110 120
cry1a-105.pe PTNEALREEMRIQFNDMSALITTAIPLFAVQNVQVPLLSVYVQAANHLSLVLDVSFEGQ
130 140 150 160 170 180
33321716 PTNEALREEMRIQFNDMSALITTAIPLFAVQNVQVPLLSVYVQAANHLSLVLDVSFEGQ
130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRINDLTILIGNYTHAVRWYNTGLERVMGPDSDRDWYRINQFRRELTIV
190 200 210 220 230 240
33321716 RWGFDAAATINSRINDLTILIGNYTHAVRWYNTGLERVMGPDSDRDWYRINQFRRELTIV
190 200 210 220 230 240
cry1a-105.pe LDVVALPNYDSRRYPPIRTVSQLTREIYTPVLENFDGSRGSAQGIERSIRSPHMLDIL
250 260 270 280 290 300
33321716 LDVVALPNYDSRRYPPIRTVSQLTREIYTPVLENFDGSRGSAQGIERSIRSPHMLDIL
250 260 270 280 290 300
cry1a-105.pe NSITITIDARGYVMSGHQIMASPVGSGPFEFTFLYCTMGNAAPQORIVAOLOGGVYR
310 320 330 340 350 360
33321716 NSITITIDARGYVMSGHQIMASPVGSGPFEFTFLYCTMGNAAPQORIVAOLOGGVYR
310 320 330 340 350 360
cry1a-105.pe TLSSTLRERRNIGINMOLVLDGTETAYGSSNLPASVYKSGTVDLSDEIPQNNNV
370 380 390 400 410 420
33321716 TLSSTLRERRNIGINMOLVLDGTETAYGSSNLPASVYKSGTVDLSDEIPQNNNV
370 380 390 400 410 420
cry1a-105.pe PPROQFSHRSHVSMRSGFSSSSIRAHKSPVRSANRWLMSDSITQIPLVKAH
430 440 450 460 470 480
33321716 PPROQFSHRSHVSMRSGFSSSSIRAHKSPVRSANRWLMSDSITQIPLVKAH
430 440 450 460 470 480
cry1a-105.pe TLOSTTVVRGPGFTGDLIRRTSGGFAVT--IVNNGLSQO---VYAPASVASTNL
490 500 510 520 530
33321716 TLOSTTVVRGPGFTGDLIRRTSGGFAVT--IVNNGLSQO---VYAPASVASTNL
490 500 510 520 530
cry1a-105.pe RIYTVVAGERIFAGQFNKMTDGDPLTFQSPSYATINATFTFNSQSSFTVGNTPSSGN
540 550 560 570 580 590
33321716 RIYTVVAGERIFAGQFNKMTDGDPLTFQSPSYATINATFTFNSQSSFTVGNTPSSGN
540 550 560 570 580 590
cry1a-105.pe EYVIDRFELIPVATLAEAVNLERAKAVNALFTSTNQLGKTNVDYHIDQVSNLVTYL
600 610 620 630 640 650

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MSL No. 20351

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>>NR001:67089175      10          20          30          40          50          60  
inith: 6603 initl: 6603 opt: 7100 Z-score: 8062.0 expect( ): 0  
Smith-Waterman score: 7100;   91.6% identity in 1169 aa overlap  
(8-1171:1-1164)  
  
cryla-105.pe  MDNPNINECVNCISNPVEVLGGRIETGYTIDISLSLTFLLSDFVPGAGFVLGL  
|||||  
67089175      NEICIPNCISNPVEVLGGRIETGYTIDISLSLTFLLSDFVPGAGFVLGL  
||| 10 20 30 40 50  
  
cryla-105.pe  VDIIWGIFGSQWDAFLVQLINORIEEFARNQAISRLEGSLNYQIYAESFREWEAD  
||| 70 80 90 100 110 120  
67089175      VDIIWGIFGSQWDAFLVQLINORIEEFARNQAISRLEGSLNYQIYAESFREWEAD  
||| 60 70 80 90 100 110  
  
cryla-105.pe  PTNPALREEMRIFOENMMSALTTPAIPFAVQNVQPLSVYVQAANHLHSLVRDVSVEFGQ  
||| 130 140 150 160 170 180  
67089175      PTNPALREEMRIFOENMMSALTTPAIPFAVQNVQPLSVYVQAANHLHSLVRDVSVEFGQ  
||| 120 130 140 150 160 170  
  
cryla-105.pe  RWGFDAATINSRVNDLTRLIGNYTDHAVRWNTGLERVMGPDSDMTIRYNQFRRELTLTV  
||| 190 200 210 220 230 240  
67089175      RWGFDAATINSRVNDLTRLIGNYTDHAVRWNTGLERVMGPDSDMTIRYNQFRRELTLTV  
||| 180 190 200 210 220 230  
  
cryla-105.pe  LDIVSLFPNDSTRTPIRTVSQLTRREITYTNPLENFDSFRGSAQGIESIRSHPHMLIL  
||| 250 260 270 280 290 300  
67089175      LDIVSLFPNDSTRTPIRTVSQLTRREITYTNPLENFDSFRGSAQGIESIRSHPHMLIL  
||| 240 250 260 270 280 290  
  
cryla-105.pe  NSIIITDARHGYYWSGHQIMASPVGSGPEPTPLGTWGNAAPQORIVAOLGQGVYR  
||| 310 320 330 340 350 360  
67089175      NSIIITDARHGYYWSGHQIMASPVGSGPEPTPLGTWGNAAPQORIVAOLGQGVYR  
||| 300 310 320 330 340 350  
  
cryla-105.pe  TLSSTLYRRPFIINNQQSLVDGTGEFAVTGTSNNLPNAVRYKSGTVDSLDEIPPQNNVV  
||| 370 380 390 400 410 420  
67089175      TLSSTLYRRPFIINNQQSLVDGTGEFAVTGTSNNLPNAVRYKSGTVDSLDEIPPQNNVV  
||| 360 370 380 390 400 410  
  
cryla-105.pe  PPRQGFSHRLSHVSMFRSGFNSSVSIIRAPMFSWTHRSABFNNI IASDSITOIPLVKAH  
||| 430 440 450 460 470 480  
67089175      PPRQGFSHRLSHVSMFRSG--SSSSVSIIRAPMFSWTHRSABFNNI IASDSITOIPAVKGN  
||| 420 430 440 450 460 470  
  
cryla-105.pe  TLQSQTIVRGPGFTGCDILRETSGGPAT--LVNQIQLPQ--PYRARIRFYASTNL  
||| 490 500 510 520 530  
67089175      FLFGS-VISGPGFTGCDILRVLNSGNNIQRMGYEVP IHFFPS*STRIRVRYRYASVTPI  
||| 480 490 500 510 520 530  
  
cryla-105.pe  RIVYTVAGERIFAQGNKTMDGTDLDPQSFQSVATINTAFTPFMSQSSFVVGADTFSSGN  
||| 540 550 560 570 580 590  
67089175      HLNWNWGNSSIFSNTPVATSLDLHLOSSDGFYGFSANAFTSSLGN--LVGRVNFSGTA  
||| 540 550 560 570 580 590
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Product Characterization Center

CRYIA-105.pe EVVIDREFELIPATNAEAENLERAKAVNAFTSTNOLGLKNTVTDVHIDQVSNLVYL
67089175 GVILIDREFELIPATNAEAENLERAKAVNAFTSTNOLGLKNTVTDVHIDQVSNLVYL
CRYIA-105.pe SDEPCLDERELSKVHGRUSDERNLQSNFADINROPEGNGSGTGITIGGGDVF
67089175 SDEPCLDERELSKVHGRUSDERNLQSNFADINROPEGNGSGTGITIGGGDVF
CRYIA-105.pe KENVYLSGTDECYPTLYOKIDSKKAPRYQLRGYIEDSODAEIYSIRYNAXHETV
67089175 KENVYLSGTDECYPTLYOKIDSKKAPRYQLRGYIEDSODAEIYSIRYNAXHETV
CRYIA-105.pe NVPGTGLSWPLSAQSPIGKGEFNRCAHLEWNPDLDCSDRGEKCAHSHAFSLDVG
67089175 NVPGTGLSWPLSAQSPIGKGEFNRCAHLEWNPDLDCSDRGEKCAHSHAFSLDVG
CRYIA-105.pe CTDLNEDLGWVIFIKITQDGHARLGNLFLEKPLVGEALARYKRAEKWMDREKLEW
67089175 CTDLNEDLGWVIFIKITQDGHARLGNLFLEKPLVGEALARYKRAEKWMDREKLEW
CRYIA-105.pe ETNIVVKEAKESVDALFVNSOYDQLOQADTNIAHIAADKRVHSIREAYLPESVIPGVNA
67089175 ETNIVVKEAKESVDALFVNSOYDQLOQADTNIAHIAADKRVHSIREAYLPESVIPGVNA
CRYIA-105.pe AIFEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNVKGVHDVDEQNNQSVLVVPEWEA
67089175 AIFEELEGRIFTAFSLYDARNVIRKNGDFNGLSCWNVKGVHDVDEQNNQSVLVVPEWEA
CRYIA-105.pe EVSQEVRCVCGRGYILRVITAYKEGVGGCVTHIEIENNTDELKFSNCVVEEIPNNVTVC
67089175 EVSQEVRCVCGRGYILRVITAYKEGVGGCVTHIEIENNTDELKFSNCVVEEIPNNVTVC
CRYIA-105.pe NDYTVNOEEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRENPCFNNGYRDYTP
67089175 NDYTVNOEEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRENPCFNNGYRDYTP
CRYIA-105.pe LPVGVTKELEYFPETDKWMEIGETGTFIVDSVLLMEE
67089175 LPVGVTKELEYFPETDKWMEIGETGTFIVDSVLLMEE
CRYIA-105.pe LPVGVTKELEYFPETDKWMEIGETGTFIVDSV
67089175 LPVGVTKELEYFPETDKWMEIGETGTFIVDSV

CRYIA-105.pep
NRAA:8469139
8469139 source="GENBANK PROT" Pesticidal crystal protein cryIaE (insecticidal
delta-endotoxin CryIa(e)) (crystalline entomotoxin) (134 kDa crystal
protein)gi|142875|gb|AAA22410.1| delta-endotoxin

SCORES Initl: 6520 Initn: 6986 Opt: 6987 z-score: 7933.5 E(): 0
>>NRAA:8469139
initn: 6986 initl: 6520 opt: 6987 z-score: 7933.5 expect(): 0
Smith-Waterman score: 6987; 88.3% identity in 1181 aa overlap
(1-1177:1-1181)

CRYIA-105.pe MONNINIECTPYNCLSNPEVVLGERIETGYTPIDISLSLTOFLSEFVGAGFVLGL
8469139 MONNINIECTPYNCLSNPEVVLGERIETGYTPIDISLSLTOFLSEFVGAGFVLGL
CRYIA-105.pe VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNOAISRLGSLNLYQIYAESFREWAD
8469139 VDIIMGIFGSPQMDAFLVQIEQLINORIEEFARNOAISRLGSLNLYQIYAESFREWAD
CRYIA-105.pe PTPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVOAANLHLSVLDRDVSVEGO
8469139 PTPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVVOAANLHLSVLDRDVSVEGO
CRYIA-105.pe RWGFDATINSRYNDLTRLIKNYTDHAWYNTGLERVWGPDSRDWIRYNQFRRELTIV
8469139 RWGFDATINSRYNDLTRLIKNYTDHAWYNTGLERVWGPDSRDWIRYNQFRRELTIV
CRYIA-105.pe LDIVSPNPPYRTPIPIKIVTQITREIYNFVLENGDFSGSAGGIESIRSPLMDIL
8469139 LDIVSPNPPYRTPIPIKIVTQITREIYNFVLENGDFSGSAGGIESIRSPLMDIL
CRYIA-105.pe NSIITVDARHGYYASCHQIMASPGFSGPEFTFLYGTMGNAAPQORIVAOLGQGVYR
8469139 NSIITVDARHGYYASCHQIMASPGFSGPEFTFLYGTMGNAAPQORIVAOLGQGVYR
CRYIA-105.pe TLISSTLYRRFPNIGINNOQVLDGSAFATSTSSNLPSSVIRKSGTVDSLDEIPQNNVY
8469139 TLISSTLYRRFPNIGINNOQVLDGSAFATSTSSNLPSSVIRKSGTVDSLDEIPQNNVY
CRYIA-105.pe PPROQFGRHLSHVMSRSGFSSVSIIRAPMSRSHRSRANNNIISDSITSLPNAKAR
8469139 PPROQFGRHLSHVMSRSGFSSVSIIRAPMSRSHRSRANNNIISDSITSLPNAKAR
CRYIA-105.pe TLQSGTIVRGPGFTGGDILRLRTSGGPFAYTVINNGQLPQRYARLRYASTNLRVYV
8469139 TLQSGTIVRGPGFTGGDILRLRTSGGPFAYTVINNGQLPQRYARLRYASTNLRVYV
CRYIA-105.pe VAGERIFAGQFKMTMDGDLTFQSFVATINTAFTFPMQSSFTVGADTFSSGNEVYID
8469139 VAGERIFAGQFKMTMDGDLTFQSFVATINTAFTFPMQSSFTVGADTFSSGNEVYID

8469139 description="PESTICIDIAL CRYSTAL. PROTEIN CRYIAE (INSECTICIDAL DELTA-ENDOTOXIN CRYIA(E)) (CRYSTALLINE ENTOMOCIDAL PROTOXIN) (134 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar alesti" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 6520 Initn: 6986 Opt: 6987 z-score: 7933.5 E(): 0
>>SW:8469139
initn: 6986 initl: 6520 opt: 6987 z-score: 7933.5 expect(): 0
Smith-Waterman score: 6987; 88.3% identity in 1181 aa overlap
(1-1177:1-1181)

cry1a-105.pe	MDNNPINECIPNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL	10	20	30	40	50	60
8469139	MDNNPKINECIPNCLSNPEVEVLGGERIETGTPIDISLSLTQFLSEFVPGAGFVLGL	10	20	30	40	50	60
cry1a-105.pe	VDIITWIFGFSQWDAFLVQIEQLINQRIEFAFARQAISRLSGLSNLYQIYAESFREWAD	70	80	90	100	110	120
8469139	IDLIWGVGFSQWDAFLVQIEQLISQRIEFAFARQAISRLSGLSNLYQIYAEAFREWAD	70	80	90	100	110	120
cry1a-105.pe	PTNPALREEMRQFNDMNSALTATPLFAVQNVQVPLLSVVQAAHLHSLVLDVSFQGV	130	140	150	160	170	180
8469139	PTNPALREEMRQFNDMNSALTATPLFTVQNVQVPLLSVVQAAHLHSLVLDVSFQGV	130	140	150	160	170	180
cry1a-105.pe	RWGLDVAITNSRYNDLTGLIGNYTHAVRYNTGLERVWGPDSRDWRVYNQFRRLTLTV	190	200	210	220	230	240
8469139	RWGLDVAITNSRYNDLTGLICTYDAVRYNTGLERVWGPDSRDWRVYNQFRRLTLTV	190	200	210	220	230	240
cry1a-105.pe	LDIVSLFPNVDSTYPTIETVSQLTREIYTNVPLENFDGSPRGSAGIEGSIKPHMDIL	250	260	270	280	290	300
8469139	LDIVSLFPNVDSTYPTIETVSQLTREIYTNVPLENFDGSPRGSAGIEGSIKPHMDIL	250	260	270	280	290	300
cry1a-105.pe	NSIITVTDHARGYVWGHQIMASPVGSGPEFTPLVGTMGNAAPQORIVAGLGGVYR	310	320	330	340	350	360
8469139	NSIITVTDHARGYVWGHQIMASPVGSGPEFTPLVGTMGNAAPQORIVAGLGGVYR	310	320	330	340	350	360
cry1a-105.pe	TLSSLTLRFPNIGINNQLSVLDGTEFAYGSSMLPSAVYRKSGTVDLSLDEIPQNNV	370	380	390	400	410	420
8469139	TLSSLTLRFPNIGINNQLSVLDGTEFAYGSSMLPSAVYRKSGTVDLSLDEIPQNNV	370	380	390	400	410	420
cry1a-105.pe	PPROGFSHRLSHVMSFRSGFSNSSLIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH	430	440	450	460	470	480
8469139	PPROGFSHRLSHVMSFRSGFSNSSLIRAPMFSWIHSAEFNNIIASDSITQIPLVKAH	430	440	450	460	470	480
cry1a-105.pe	TLOSGTTVVRGPGFTGGDILRRSTGGPFAYTVINGQLPQRYRIRYASTTNLFYVT	490	500	510	520	530	540
8469139	TLOSGTTVVRGPGFTGGDILRRSTGGPFAYTVINGQLPQRYRIRYASTTNLFYVT	490	500	510	520	530	540

cry1a-105.pe	RFELIPVTATLAEAVNLERAQAVNALFTSTNQLGKNTVDYHIDQVSNLYTSLDSEFC	550	560	570	580	590	600
8469139	RIFEFVAETVFAEYDLERAQAVNALFTSNQIGLKTDYDHYHIDQVSNLYTSLDSEFC	550	560	570	580	590	600
cry1a-105.pe	LDEKRELSKVKHAKRLSDERNLLQDSNEFKDINROPERGWSGTGITIOGGDDVFKENV	670	680	690	700	710	720
8469139	LDEKRELSKVKHAKRLSDERNLLQDNFRGINRQPDGWRGSDTITIOGGDDVFKENV	670	680	690	700	710	720
cry1a-105.pe	TLSGTDECVPTLYLQKIDESKLAFTRYQLRGYIEDSQDLEIYLRINAKHETVNVPGT	730	740	750	760	770	780
8469139	TLPGTDECVPTLYLQKIDESKLAFTRYELRGYIEDSQDLEIYLRINAKHETVNVPGT	730	740	750	760	770	780
cry1a-105.pe	GSLWPLSASDPTGKCGEPNRCAPHLEWNPDLDSCRDGKCAHSHHFSLDIDVGCIDLN	790	800	810	820	830	840
8469139	GSLWPLSFEFSIGKCGEPNRCAPHLEWNPDLDSCRDGKCAHSHHFSLDIDVGCIDLN	790	800	810	820	830	840
cry1a-105.pe	EDLGWVVIKIKITQDGHARLGNLEFLEKPLVGEALARVKAERKWKDKREKLEMETIV	850	860	870	880	890	900
8469139	EDLGWVVIKIKITQDGHARLGNLEFLEKPLVGEALARVKAERKWKDKREKLEMETIV	850	860	870	880	890	900
cry1a-105.pe	YKEAKESVDALFVNSQYDQLQADNTIAMTHAADKRVHIREAYLPELSVTPGVNAIFEE	910	920	930	940	950	960
8469139	YKEAKESVDALFVNSQYDQLQADNTIAMTHADKRVHIREAYLPELSVTPGVNAGIFEE	910	920	930	940	950	960
cry1a-105.pe	LEGRIPTASLDARNVINKGDFNGLSCNVKGVHDVEEQNNORSVLVVPWEAEVSQOE	970	980	990	1000	1010	1020
8469139	LEGRIPTASLDARNVINKGDFNGLSCNVKGVHDVEEQNNHRSVLVVPWEAEVSQOE	970	980	990	1000	1010	1020
cry1a-105.pe	VRVCPGRGYLRTAVYKEGYEGCVTHIEENNTDELAFKNCVVEEYVNNVTGNDYTV	1030	1040	1050	1060	1070	1080
8469139	VRVCPGRGYLRTAVYKEGYEGCVTHIEENNTDELAFKNCVVEEYVNNVTGNEYTA	1030	1040	1050	1060	1070	1080
cry1a-105.pe	NQBEYGAAYTSNRNGYNEAP-----SVPADYASVYEEKSYTDGRENPCENRGYDYTPL	1090	1100	1110	1120	1130	
8469139	NQBEYGAAYTSNRNGYDYGSNYSVPADYASVYEEKSYTDGRENPCENRGYDYTPL	1090	1100	1110	1120	1130	1140
cry1a-105.pe	PVGVTYKELEYFPEDTKVWIEIGETGTFIVDSVELLMEE	1140	1150	1160	1170	1180	
8469139	PAGVTKQLEYFPEDTKVWIEIGETGTFIVDSVELFLMEE	1140	1150	1160	1170	1180	
cry1a-105.pe							
SN: 8469139							

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cry1a-105.pe 550 560 570 580 590 600
VAGERIFQFNKNDIDQPLTFQSFVAINTAFTPPMSQSFVIGADTFSSGVEYID
8469139 IDGRPNQGNATSMSSGNLQSGSFRVGTTFPFNFSNGSSVFTLSRAVFNFSNGVEYID
550 560 570 580 590 600
cry1a-105.pe 610 620 630 640 650 660
RFEPLPVAATPAEYATGAAGVANAIPFNTNGLKNTDTHIDQVNLVYLSDFEC
8469139 RIEFVPAEVTTPAEYTERAEVAALFTSPNQLASVDVTHIDQVNLVYLSDFEC
610 620 630 640 650 660
cry1a-105.pe 670 680 690 700 710 720
LDEKRELSKVKHAKRLSDERNLQNSFKDNPGRGMGSGTITGGDDVFNENYV
8469139 LDEKRELSKVKHAKRLSDERNLQNSFKDNPGRGMGSGTITGGDDVFNENYV
670 680 690 700 710 720
cry1a-105.pe 730 740 750 760 770 780
TLSGTDECYPTLYQKIDSKLKAFTRYQLRGYIEDSDGSIYSRYNKHETVNPVGT
8469139 TLPGTDECYPTLYQKIDSKLKAFTRYQLRGYIEDSDGSIYSRYNKHETVNPVGT
730 740 750 760 770 780
cry1a-105.pe 790 800 810 820 830 840
GSLWPLSASPTGKGEFNRCAPHLEWFDLDCSCDGEKCAHSHHFSLDITGCGDNLN
8469139 GSLWPLSASPTGKGEFNRCAPHLEWFDLDCSCDGEKCAHSHHFSLDITGCGDNLN
790 800 810 820 830 840
cry1a-105.pe 850 860 870 880 890 900
EDLGWVIFKIKTQGHARLGNLEFLEKPLVGEALARVKAERKMDKREKLEMETIV
8469139 EDLGWVIFKIKTQGHARLGNLEFLEKPLVGEALARVKAERKMDKREKLEMETIV
850 860 870 880 890 900
cry1a-105.pe 910 920 930 940 950 960
YKEAKESVDALFVNSQYDQLOADNTNIAHIAADKRVHSIREAYLPESLVIPGVNAIPEE
8469139 YKEAKESVDALFVNSQYDQLOADNTNIAHIAADKRVHSIREAYLPESLVIPGVNAIPEE
910 920 930 940 950 960
cry1a-105.pe 970 980 990 1000 1010 1020
LEGRIFTAFLSDARNVKNGDFNGLSCWNVKGVHVDVEEQNNORSVLVVPPEWAEVSQE
8469139 LEGRIFTAFLSDARNVKNGDFNGLSCWNVKGVHVDVEEQNNORSVLVVPPEWAEVSQE
970 980 990 1000 1010 1020
cry1a-105.pe 1030 1040 1050 1060 1070 1080
VRVCPGRGYILRTVAYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNNVTICNDYTV
8469139 VRVCPGRGYILRTVAYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNNVTICNDYTV
1030 1040 1050 1060 1070 1080
cry1a-105.pe 1090 1100 1110 1120 1130
NOEYGGAYTNRGRNEAP----SVPADYASVYEKSVTDDRNCENRGRVDTPL
8469139 NOEYGGAYTNRGRNEAP----SVPADYASVYEKSVTDDRNCENRGRVDTPL
1090 1100 1110 1120 1130
cry1a-105.pe 1140 1150 1160 1170
PVGUYTKLEFVPEFDKVMIEIGETEGTFIVDSVELLMEE
8469139 PAGUYTKLEFVPEFDKVMIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170

cry1a-105.pep
NRAA:32344731
32344731 source="GENBANK PROT" delta-endotoxin [Bacillus
thuringiensis]gi|216284|dbj|BAA00257.1| unnamed protein product [Bacillus
thuringiensis serovar aizawai]gi|61252379|sp|POA367|CRIA00 BACTA Pesticidal
crystal protein cry1a (insecticidal delta-endotoxin CryIA(a)) (Crystalline
entomocidal protoxin) (133 kDa crystal protein)
SCORES Initl: 4298 Initn: 6551 Opt: 6851 Z-score: 7779.0 E(): 0
>>NRAA:32344731
initn: 6551 initl: 4298 opt: 6851 Z-score: 7779.0 expect(): 0
Smith-Waterman score: 6851; 87.0% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe MDNNPNINECIPYNCCLNPEVEVLGGERIETGYTPIDISLSLTQFLSSEFVFGAGVLGL
32344731 MDNNPNINECIPYNCCLNPEVEVLGGERIETGYTPIDISLSLTQFLSSEFVFGAGVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGFSQMDAFVLQIEQLINRIEIEFARNQAIISRLEGLSNLYQIYAESFREWEAD
32344731 VDIIMGIFGFSQMDAFVLQIEQLINRIEIEFARNQAIISRLEGLSNLYQIYAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTNPLREEMRIQFNDMNSALTATPLFAVQNVQVPLSVVQVAAHLVSLRDVSVFQ
32344731 PTNPLREEMRIQFNDMNSALTATPLFAVQNVQVPLSVVQVAAHLVSLRDVSVFQ
130 140 150 160 170 180
cry1a-105.pe RWGFDATINRYNLTALIGNYTDHAVRYNTGLERVMGPDSDRDWRYNQFRELTLTV
32344731 RWGFDATINRYNLTALIGNYTDHAVRYNTGLERVMGPDSDRDWRYNQFRELTLTV
190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNDSTYPIPIVAGGQPREIYTNVDFNFDGSPFGSAGGIESIRSPHMDIL
32344731 LDIVSLFPNDSTYPIPIVAGGQPREIYTNVDFNFDGSPFGSAGGIESIRSPHMDIL
250 260 270 280 290 300
cry1a-105.pe NSITIYDHRGVNWSGHQITASVFGSPDEAFPLFCAGAPPV--NSLNGLIER
32344731 NSITIYDHRGVNWSGHQITASVFGSPDEAFPLFCAGAPPV--NSLNGLIER
310 320 330 340 350 360
cry1a-105.pe TILSSTLYRRP-FNIGINNQQSLVDLGTFAYGT-SSNLPSAVYKSGVTSLSLSTPPQNN
32344731 TILSSTLYRRP-FNIGINNQQSLVDLGTFAYGT-SSNLPSAVYKSGVTSLSLSTPPQNN
360 370 380 390 400 410
cry1a-105.pe NVYPFQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFWHSIRSAEENNIASDITGSPDK
32344731 NVYPFQGFSHRLSHVSMFRSGFSNNSVSIIRAPMFWHSIRSAEENNIASDITGSPDK
420 430 440 450 460 470
cry1a-105.pe SVYPFAGFSHRLSHVSMFRSGFSNNSVSIIRAPMFWHSIRSAEENNIASDITGSPDK
32344731 SVYPFAGFSHRLSHVSMFRSGFSNNSVSIIRAPMFWHSIRSAEENNIASDITGSPDK
420 430 440 450 460 470
cry1a-105.pe SVYPFAGFSHRLSHVSMFRSGFSNNSVSIIRAPMFWHSIRSAEENNIASDITGSPDK
480 490 500 510 520 530

Study No. 06-01-62-04

MSL No. 20351

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cry1a-105.pe GYVTKLEVPETDKWVIEIGETEGTGFIVDSVELLMEE
32344731 GYVTKLEVPETDKWVIEIGETEGTGFIVDSVELLMEE
1140 1150 1160 1170

cry1a-105.pep
SW:117540

117540 description="135 KD CRYSTAL PROTEIN (DELTA ENDOXIN) (CRYSTALINE
ENTOMOCIDAL PROTOXIN)." library="NA species="Bacillus thuringiensis serovar
aizawai" source="swissprot_prot" version="NA type="PRT

SCORES Initl: 4298 Initn: 6551 Opt: 6851 Z-score: 7779.0 E(): 0
>>SW:117540
Initn: 6551 Initl: 4298 opt: 6851 Z-score: 7779.0 expect(): 0
Smith-Waterman score: 6851; 87.0% identity in 1179 aa overlap
(1-1177:1-1176)

cry1a-105.pe MDNNPNINECIPYNCLSNPEVEVLGGRIETGYTIDISLSLTOQLLSFEVPGAGVLGL
117540 MDNNPNINECIPYNCLSNPEVEVLGGRIETGYTIDISLSLTOQLLSFEVPGAGVLGL
117540 MDNNPNINECIPYNCLSNPEVEVLGGRIETGYTIDISLSLTOQLLSFEVPGAGVLGL

cry1a-105.pe VDIIWGIFGQSQMDAFLVQIQLINQRIIEFFARNQAISRLEGSLNLYQIYIAESFREMED
117540 VDIIWGIFGQSQMDAFLVQIQLINQRIIEFFARNQAISRLEGSLNLYQIYIAESFREMED
117540 VDIIWGIFGQSQMDAFLVQIQLINQRIIEFFARNQAISRLEGSLNLYQIYIAESFREMED

cry1a-105.pe PTNPALRENRIOFNMDMSALTITAIPLFAVQNVQVPLLSVYVQAANHLISVLRDVSVFQ
117540 PTNPALRENRIOFNMDMSALTITAIPLFAVQNVQVPLLSVYVQAANHLISVLRDVSVFQ
117540 PTNPALRENRIOFNMDMSALTITAIPLFAVQNVQVPLLSVYVQAANHLISVLRDVSVFQ

cry1a-105.pe RMGFDAATINSRINDLTILIGNYTDHARWYNTGLERVWGPDSRDMIRYNQFRRELTITV
117540 RMGFDAATINSRINDLTILIGNYTDHARWYNTGLERVWGPDSRDMIRYNQFRRELTITV
117540 RMGFDAATINSRINDLTILIGNYTDHARWYNTGLERVWGPDSRDMIRYNQFRRELTITV

cry1a-105.pe LDIVSLFPNTDSTYPIRTVSQLTREIYTNPVLENFDSFRGSGAQIGESIRSPHMDIL
117540 LDIVSLFPNTDSTYPIRTVSQLTREIYTNPVLENFDSFRGSGAQIGESIRSPHMDIL
117540 LDIVSLFPNTDSTYPIRTVSQLTREIYTNPVLENFDSFRGSGAQIGESIRSPHMDIL

cry1a-105.pe NSIITIIDHRGEVYWSGHQIMASPVGSGPEFTPLVGTMGNAAPQORVIAQLGQGVYR
117540 NSIITIIDHRGEVYWSGHQIMASPVGSGPEFTPLVGTMGNAAPQORVIAQLGQGVYR
117540 NSIITIIDHRGEVYWSGHQIMASPVGSGPEFTPLVGTMGNAAPQORVIAQLGQGVYR

cry1a-105.pe TLSSTLYRRP-FNIGINNQQSLVDGTGEFAYGT-SNNLPSAVYRKSGTVDLSDEIPPQNN
117540 TLSSTLYRRP-FNIGINNQQSLVDGTGEFAYGT-SNNLPSAVYRKSGTVDLSDEIPPQNN
117540 TLSSTLYRRP-FNIGINNQQSLVDGTGEFAYGT-SNNLPSAVYRKSGTVDLSDEIPPQNN

cry1a-105.pe 420 430 440 450 460 470
SYPPRAGSRHLGSHVMTLSQ--AAGAYTLRAPTSWQHRSAEFNNIPSSQITQIPTLVK
117540 SYPPRAGSRHLGSHVMTLSQ--AAGAYTLRAPTSWQHRSAEFNNIPSSQITQIPTLVK
117540 SYPPRAGSRHLGSHVMTLSQ--AAGAYTLRAPTSWQHRSAEFNNIPSSQITQIPTLVK

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cryla-105.pe 480 490 500 510 520 530
HTLOSSTVYFGFTGSLRTSGGPAYTIVNQLQORVRARIRVASTNRIY
117540 SMLSGTSTVYFGFTGSLRTSGGPAYTIVNQLQORVRARIRVASTNRIY
480 490 500 510 520 530
SMLSGTSTVYFGFTGSLRTSGGPAYTIVNQLQORVRARIRVASTNRIY

cryla-105.pe 540 550 560 570 580 590
VTVAGERIFAGQKNDGDLTFESFATINAFIPMSQSFVTGADTFSSGNEVY
117540 TSIDGRPINQONTSATMSGSLQSGSRFAGVATTFPNSGSLVFLSARFVNSGNEVY
540 550 560 570 580 590
TSIDGRPINQONTSATMSGSLQSGSRFAGVATTFPNSGSLVFLSARFVNSGNEVY

cryla-105.pe 600 610 620 630 640 650
IDRFELIPVATLEAEYNLERAKVNNLFTSTNOLCLNNYTDYHIDONSNTVLSDE
117540 IDRIEFVPAEVEAEYDLERAKAVNELFTSSNOLCLNNYTDYHIDONSNTVLSDE
600 610 620 630 640 650
IDRIEFVPAEVEAEYDLERAKAVNELFTSSNOLCLNNYTDYHIDONSNTVLSDE

cryla-105.pe 660 670 680 690 700 710
FCLDEKRLSKVKHAKRLSDERNLLQDSNFKDINRPERGNGSSTIQQSDVFEV
117540 FCLDEKRLSKVKHAKRLSDERNLLQDSNFKDINRPERGNGSSTIQQSDVFEV
660 670 680 690 700 710
FCLDEKRLSKVKHAKRLSDERNLLQDSNFKDINRPERGNGSSTIQQSDVFEV

cryla-105.pe 720 730 740 750 760 770
VYTLGTFDECYPTLYQKIDSKLKAFTRYOLRGYEDSQDLIYIRYNAKHETVNP
117540 VYTLGTFDECYPTLYQKIDSKLKAFTRYOLRGYEDSQDLIYIRYNAKHETVNP
720 730 740 750 760 770
VYTLGTFDECYPTLYQKIDSKLKAFTRYOLRGYEDSQDLIYIRYNAKHETVNP

cryla-105.pe 780 790 800 810 820 830
GTGSLWPLSASPIGKCGEPNRCAPHEWNPDLDCSCRDCEKCAHSHHFLSDIDVGCTD
117540 GTGSLWPLSASPIGKCGEPNRCAPHEWNPDLDCSCRDCEKCAHSHHFLSDIDVGCTD
780 790 800 810 820 830
GTGSLWPLSASPIGKCGEPNRCAPHEWNPDLDCSCRDCEKCAHSHHFLSDIDVGCTD

cryla-105.pe 840 850 860 870 880 890
LNEGLGVWVIFKIKTOPGHARLGNLEFLEKPLVGEALARKAEKKWRDKRELEWETN
117540 LNEGLGVWVIFKIKTOPGHARLGNLEFLEKPLVGEALARKAEKKWRDKRELEWETN
840 850 860 870 880 890
LNEGLGVWVIFKIKTOPGHARLGNLEFLEKPLVGEALARKAEKKWRDKRELEWETN

cryla-105.pe 900 910 920 930 940 950
IVYKAEKSVDALEFVNSQDQLQADNTNIAHAAKRVHSIRAYLPULSVIPGNAALIF
117540 IVYKAEKSVDALEFVNSQDQLQADNTNIAHAAKRVHSIRAYLPULSVIPGNAALIF
900 910 920 930 940 950
IVYKAEKSVDALEFVNSQDQLQADNTNIAHAAKRVHSIRAYLPULSVIPGNAALIF

cryla-105.pe 960 970 980 990 1000 1010
EELEGRIFTATSLYDARNVINKGDFNNGLSQWNVKGVDDVEEQNNORSVLVVPWEAEVS
117540 EELEGRIFTATSLYDARNVINKGDFNNGLSQWNVKGVDDVEEQNNORSVLVVPWEAEVS
960 970 980 990 1000 1010
EELEGRIFTATSLYDARNVINKGDFNNGLSQWNVKGVDDVEEQNNORSVLVVPWEAEVS

cryla-105.pe 1020 1030 1040 1050 1060 1070
QEVVCPGFGYILRVATYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNNTVTCNDY
117540 QEVVCPGFGYILRVATYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNNTVTCNDY
1020 1030 1040 1050 1060 1070
QEVVCPGFGYILRVATYKEGYGEGCVTHIEENNTDELKFSNCVEEYIPNNTVTCNDY

cryla-105.pe 1080 1090 1100 1110 1120 1130
TVNQEEYGAYTSRNRGNEAPSPADYASVYEKSYTDGRNCPENFRGYDTPLPV
117540 TVNQEEYGAYTSRNRGNEAPSPADYASVYEKSYTDGRNCPENFRGYDTPLPV
1080 1090 1100 1110 1120 1130
TVNQEEYGAYTSRNRGNEAPSPADYASVYEKSYTDGRNCPENFRGYDTPLPV

cryla-105.pe 1140 1150 1160 1170
GVYTKLEYFPETDKWIEIGETGCTFIVDSVELLMEE
117540 GVYTKLEYFPETDKWIEIGETGCTFIVDSVELLMEE
1140 1150 1160 1170
GVYTKLEYFPETDKWIEIGETGCTFIVDSVELLMEE

cryla-105.pe
SW:61252379
61252379 description="Pesticidal crystal protein crylaa (Insecticidal
delta-endotoxin CryIA(a)) (Crystalline entomocidal protoxin) (133 kDa crystal
protein)." library=NA species="Bacillus thuringiensis serovar aizawai"
source="swissprot_prot" version=NA type=PRT

SCORES Init1: 4298 Initn: 6551 Opt: 6851 Z-score: 7779.0 E(): 0
>>SW:61252379
initn: 6551 init1: 4298 opt: 6851 Z-score: 7779.0 expect(): 0
Smith-Waterman score: 6851; 87.0% identity in 1179 aa overlap
(1-1177:1-1176)

cryla-105.pe 10 20 30 40 50 60
MNNPNINECIPYNCLSNPEVEVLGERIETGYPIDISLSLTQFLSEFVPGAGFVLGL
61252379 MNNPNINECIPYNCLSNPEVEVLGERIETGYPIDISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
MNNPNINECIPYNCLSNPEVEVLGERIETGYPIDISLSLTQFLSEFVPGAGFVLGL

cryla-105.pe 70 80 90 100 110 120
VDSITGTFGSPQNDFAVLQEQINRIEERFARQAIISRLGSLNLYQIYAESFREWEAD
61252379 VDSITGTFGSPQNDFAVLQEQINRIEERFARQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
VDSITGTFGSPQNDFAVLQEQINRIEERFARQAIISRLGSLNLYQIYAESFREWEAD

cryla-105.pe 130 140 150 160 170 180
PTNPEERETATQENDNSATTAIPFAVONQVPLLSVYQAAHLVLRDVSFVGQ
61252379 PTNPEERETATQENDNSATTAIPFAVONQVPLLSVYQAAHLVLRDVSFVGQ
130 140 150 160 170 180
PTNPEERETATQENDNSATTAIPFAVONQVPLLSVYQAAHLVLRDVSFVGQ

cryla-105.pe 190 200 210 220 230 240
RMGFDAAATINSNDLRLIGITTHAVRWYNTGLEWNGPDSRDWRYNQFRRELTLTV
61252379 RMGFDAAATINSNDLRLIGITTHAVRWYNTGLEWNGPDSRDWRYNQFRRELTLTV
190 200 210 220 230 240
RMGFDAAATINSNDLRLIGITTHAVRWYNTGLEWNGPDSRDWRYNQFRRELTLTV

cryla-105.pe 250 260 270 280 290 300
LDIVLFPNYSRYPRTVSQTLRETNLENFSTFSAQGISSTNSPILMDIL
61252379 LDIVLFPNYSRYPRTVSQTLRETNLENFSTFSAQGISSTNSPILMDIL
250 260 270 280 290 300
LDIVLFPNYSRYPRTVSQTLRETNLENFSTFSAQGISSTNSPILMDIL

cryla-105.pe 310 320 330 340 350 360
NSITITDVAHRGVYWSGHQIMASPVGSGPEFTFPFLYGTMGARLQORIVADQVYR
61252379 NSITITDVAHRGVYWSGHQIMASPVGSGPEFTFPFLYGTMGARLQORIVADQVYR
310 320 330 340 350 360
NSITITDVAHRGVYWSGHQIMASPVGSGPEFTFPFLYGTMGARLQORIVADQVYR

cryla-105.pe 370 380 390 400 410
TLSSITLYRRP-FNIGINNQQLSLVDGTETAFYGT-SSNLPASVYKSGTVDSDEIPPOON
61252379 TLSSITLYRRP-FNIGINNQQLSLVDGTETAFYGT-SSNLPASVYKSGTVDSDEIPPOON
370 380 390 400 410
TLSSITLYRRP-FNIGINNQQLSLVDGTETAFYGT-SSNLPASVYKSGTVDSDEIPPOON

cry1a-105.pe NPPRQGSRLSHVSMFRSGFSNSVSIIRAPMFSIHRSAFNNIITASDGIQIPLVK
61252379 SVPPRAGFSRLSHVMTLSQ--AAGAVALTRAPTFSSWOHSASAFNNIIPSSQIQIPLTK
cry1a-105.pe AHTLQSGTVVVRGFGTGGDILRRTSGGPFAYTVINQPOLRYRARIIRASTINLRIY
61252379 STNLQSGTSVVKVGFGTGGDILRRTSGGPFAYTVINQPOLRYRARIIRASTINLQFH
cry1a-105.pe VTVAGERIPAGQFNKMTDGTPLTFQSFYATINTATFFPMSSOSTVGCADTFSSGNEVY
61252379 TSIDGRPINQGNFATMSGNSLQSGSFTVGTFTTFNFNGSGSVFTLSAHVFNSSGNEVY
cry1a-105.pe IDRFELIPVATLEAEVNIERAKAVNALFTSTNQLGKTNVTDYHIDOVSNLVTLSDE
61252379 IDRIEFVPAEVTFAEYDLERAKAVNELFTSSNOIGLKIDVDYHIDOVSNLVECLUSDE
cry1a-105.pe FCIDKRELSKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGTIOGGDDVPFKN
61252379 FCIDKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGTIOGGDDVPFKN
cry1a-105.pe YVTLSTTFDECPYLYQKIDESKLFKAFTRVQLRGYIEDSQLEIYSIRYNAKHETVNVP
61252379 YVTLSTTFDECPYLYQKIDESKLFKAFTRVQLRGYIEDSQLEIYSIRYNAKHETVNVP
cry1a-105.pe GTCSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFSLDIDVGCTD
61252379 GTCSLWPLSAQSPGKCGEPNRCAPHLEWNPDLDCSCRDGCKCAHSHHFSLDIDVGCTD
cry1a-105.pe LNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKKLEWETN
61252379 LNEDLGVWVIFKIKTQDGHARLGNLEFLEEKPLVGEALARYKRAEKKWRDKKLEWETN
cry1a-105.pe IVYKAEKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAIIF
61252379 IVYKAEKESVDALFVNSQYDQLQADTNIAHIAADKRVHSIREAYLPESLVIPGVNAIIF
cry1a-105.pe EELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNORSVLVVPWEAEVS
61252379 EELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNORSVLVVPWEAEVS
cry1a-105.pe QEVVPCFGRYTLRVTAAYKEGYEGCVTHIEJENNTDELKFSNCVBEETYPNNTVTCNDY
61252379 QEVVPCFGRYTLRVTAAYKEGYEGCVTHIEJENNTDELKFSNCVBEETYPNNTVTCNDY

cry1a-105.pe TVNOBEYGGATSRNRCYNEAPSPADVASVYEKSYTDGRRNCPENRGVRYDYTPLPV
61252379 TVNOBEYGGATSRNRCYNEAPSPADVASVYEKSYTDGRRNCPENRGVRYDYTPLPV
cry1a-105.pe GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
61252379 GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
cry1a-105.pe
NRAA:226053
226053 source="GENBANK_PROT" 135kd insecticidal protein
SCORES Initl: 4291 Initn: 6544 Opt: 6844 Z-score: 7771.0 E(): 0
>NRAA:226053
Initn: 6544 initl: 4291 opt: 6844 Z-score: 7771.0 expect(): 0
Smith-Waterman score: 6844; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL
226053 MDNPNINICIPYNCLSNPEVEVLGGERIETGYTPTIDISLSLTQFLLSFVFGAGFVLGL
cry1a-105.pe VDIINGIFPSQWDAFLVQLEQLINORIEEFARNOAISRLIEGLSNLYQIYAESFREWAD
226053 VDIINGIFPSQWDAFLVQLEQLINORIEEFARNOAISRLIEGLSNLYQIYAESFREWAD
cry1a-105.pe PTNPALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYQAAHLVSLDRDVSVEGQ
226053 PTNPALREEMRIQFNDWNSALTTAIPFAVQNYQVPLLSVYQAAHLVSLDRDVSVEGQ
cry1a-105.pe RWGFDAAATINSRYNDLRLIGNYTDHAVRWYNTGLERVMGPDSDRWIRYNQFRRELTIV
226053 RWGFDAAATINSRYNDLRLIGNYTDHAVRWYNTGLERVMGPDSDRWIRYNQFRRELTIV
cry1a-105.pe LDIVSLFVNDSTRTYPTIRTSQLTREIYNPVLENFDFGSRGSAQIEGSIIRPHMLDIL
226053 LDIVSLFVNDSTRTYPTIRTSQLTREIYNPVLENFDFGSRGSAQIEGSIIRPHMLDIL
cry1a-105.pe NSITITVDARHGEYVMSHQIMSPVGFSGPEFTFPLXGTMGNAAPQQRIVAQOLGQGVYR
226053 NSITITVDARHGEYVMSHQIMSPVGFSGPEFTFPLXGTMGNAAPQQRIVAQOLGQGVYR
cry1a-105.pe TLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SNNLPASVAVYKSGTVDSDLEIPQNN
226053 TLSSTLYRRP-FNIGINNQQLSVLDGTEFAYGT-SNNLPASVAVYKSGTVDSDLEIPQNN

cryla-105.pe NVPPROQESRLSHVSTFSSNSVSIIAPMFWSHRSAEFNIIASDIQIPLVK 470
226053 SVPRAGFSALSHVLMQ- RAGAVYTLRAPTFESQHRSAEFNIIAPSSQIPIPLTK 470
cryla-105.pe ANTLOSQVNRGKGTGGVAFETSGPFAETIWMGQLQVRARIRVASTNRIY 530
226053 STNLGSGVSVKGFSTGDIIRN-SPQSTLRVNTRAP- SORVRIIRVASTNIQFHF 530
cryla-105.pe VTVAGERIFAGQFNKMTDGTGDLTQSTSVATINCAITFMSQSPFVGNATFSSGNEVY 580
226053 TSIDGRPINQGNFSATMSSGNSLQSGSPRNGFTIPENTSGNSFTLSAWEVNSNEVY 580
cryla-105.pe IDRFELIPVATLEAEYNLERAKAVNALFTSTNQLGKINVTB- RHIDQGNVYLSDE 600
226053 IDRIEFVPAEYTFEAYDLEFRAKAVNELFTSSNQLGKIDVDV- RHIDQGNVYLSDE 600
cryla-105.pe FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINROPERGWSGTITIOGGDDFKEN 710
226053 FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINROPERGWSGTITIOGGDDFKEN 710
cryla-105.pe VYTLGTFDECYPTLYQKIDESKLAFTYQLRGYIEDSODLEIYSRYNAKHETVNP 770
226053 VYTLGTFDECYPTLYQKIDESKLAFTYQLRGYIEDSODLEIYSRYNAKHETVNP 770
cryla-105.pe GTGSLWPLSAQSPITGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD 830
226053 GTGSLWPLSAQSPITGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD 830
cryla-105.pe LNEDLGVWVIFKIKITQDGHARLGNLEFLEKPLVGEALARVKAERKWRDKREKLEWETN 890
226053 LNEDLGVWVIFKIKITQDGHARLGNLEFLEKPLVGEALARVKAERKWRDKREKLEWETN 890
cryla-105.pe IVYKEAESVDAIFVNSQYDQLOQADNTIAMIAADKRVHSIREAYLPELSVIPGVNAAIF 950
226053 IVYKEAESVDAIFVNSQYDQLOQADNTIAMIAADKRVHSIREAYLPELSVIPGVNAAIF 950
cryla-105.pe EELEGRIFTATSLDARNVINGDFNNGLS- CNWVKGHVDEEQNORSVLVPEWEAEVS 1010
226053 EELEGRIFTATSLDARNVINGDFNNGLS- CNWVKGHVDEEQNORSVLVPEWEAEVS 1010
cryla-105.pe QEVVPCPGYILRTVAYKEGYGCGVTHIEENNTDLKFSNCVEEYLPNNTYCNDY 1070
226053 QEVVPCPGYILRTVAYKEGYGCGVTHIEENNTDLKFSNCVEEYLPNNTYCNDY 1070

cryla-105.pe TVNQEEYGGAYTSRNGYNEARSPADYASVYEKSYTGTGRENCEFNCGYRDYTPLPV 1130
226053 TVNQEEYGGAYTSRNGYNEARSPADYASVYEKSYTGTGRENCEFNCGYRDYTPLPV 1130
cryla-105.pe GYVTKLELYPPTDKVWIEIGETEGTFIVDSVELLMEE 1170
226053 GYVTKLELYPPTDKVWIEIGETEGTFIVDSVELLMEE 1170
cryla-105.pep 1170
NRAA:6687073
6687073 source="GENBANK_prot" delta-endotoxin [Bacillus thuringiensis]
SCORES Initl: 4298 Initn: 6544 Opt: 6844 z-score: 7771.0 E(): 0
>>NRAA:6687073
Initn: 6544 Initl: 4298 Opt: 6844 Z-score: 7771.0 expect(): 0
Smith-Waterman score: 6844; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cryla-105.pe MNNPNINECIPYNCNLSNPEVEVLGGERIETGYTPIDISLSLTOFLLSEFVPGAGFVLGL 50
6687073 MNNPNINECIPYNCNLSNPEVEVLGGERIETGYTPIDISLSLTOFLLSEFVPGAGFVLGL 50
cryla-105.pe VDIIMGSGQMDAFVQLQINORIEEFARNOAISRLGSLNLYQIYAESFREWEAD 120
6687073 VDIIMGSGQMDAFVQLQINORIEEFARNOAISRLGSLNLYQIYAESFREWEAD 120
cryla-105.pe FETPALREEMRIORFNMNSALITLIMFAVQNYQVPLSVYQAAHLISVLRDVSVFGQ 180
6687073 FETPALREEMRIORFNMNSALITLIMFAVQNYQVPLSVYQAAHLISVLRDVSVFGQ 180
cryla-105.pe RWGFDAAATINSRYNDLRLNLYTDAALVWNTGLRWGQSRDWIRYNQFRRELTITV 240
6687073 RWGFDAAATINSRYNDLRLNLYTDAALVWNTGLRWGQSRDWIRYNQFRRELTITV 240
cryla-105.pe LDIVLFSNYSRYPRTVTSQLTREIYTNPNLENSQSPASSAQIEGSIPIPSHMDIIL 300
6687073 LDIVLFSNYSRYPRTVTSQLTREIYTNPNLENSQSPASSAQIEGSIPIPSHMDIIL 300
cryla-105.pe NSITIYTDARHGEYWGSHOIMASPVGSGPEFTFLYCTMGNAAPQSLFNLQSGVNR 340
6687073 NSITIYTDARHGEYWGSHOIMASPVGSGPEFTFLYCTMGNAAPQSLFNLQSGVNR 340
cryla-105.pe TLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPASVAVYRKSTVDSLSDEIPPN 410
6687073 TLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPASVAVYRKSTVDSLSDEIPPN 410

	360	370	380	390	400	410	
cry1a-105.pe	420	430	440	450	460	470	
6687073	420	430	440	450	460	470	
	480	490	500	510	520	530	
cry1a-105.pe	480	490	500	510	520	530	
6687073	480	490	500	510	520	530	
	540	550	560	570	580	590	
cry1a-105.pe	540	550	560	570	580	590	
6687073	540	550	560	570	580	590	
	600	610	620	630	640	650	
cry1a-105.pe	600	610	620	630	640	650	
6687073	600	610	620	630	640	650	
	660	670	680	690	700	710	
cry1a-105.pe	660	670	680	690	700	710	
6687073	660	670	680	690	700	710	
	720	730	740	750	760	770	
cry1a-105.pe	720	730	740	750	760	770	
6687073	720	730	740	750	760	770	
	780	790	800	810	820	830	
cry1a-105.pe	780	790	800	810	820	830	
6687073	780	790	800	810	820	830	
	840	850	860	870	880	890	
cry1a-105.pe	840	850	860	870	880	890	
6687073	840	850	860	870	880	890	
	900	910	920	930	940	950	
cry1a-105.pe	900	910	920	930	940	950	
6687073	900	910	920	930	940	950	
	960	970	980	990	1000	1010	
cry1a-105.pe	960	970	980	990	1000	1010	
6687073	960	970	980	990	1000	1010	
	1020	1030	1040	1050	1060	1070	
cry1a-105.pe	1020	1030	1040	1050	1060	1070	
6687073	1020	1030	1040	1050	1060	1070	

	1020	1030	1040	1050	1060	1070	
cry1a-105.pe	1080	1090	1100	1110	1120	1130	
6687073	1080	1090	1100	1110	1120	1130	
	1140	1150	1160	1170			
cry1a-105.pe	1140	1150	1160	1170			
6687073	1140	1150	1160	1170			
	1170	1180	1190	1200	1210	1220	
cry1a-105.pe	1170	1180	1190	1200	1210	1220	
6687073	1170	1180	1190	1200	1210	1220	
	1230	1240	1250	1260	1270	1280	
cry1a-105.pe	1230	1240	1250	1260	1270	1280	
6687073	1230	1240	1250	1260	1270	1280	
	1290	1300	1310	1320	1330	1340	
cry1a-105.pe	1290	1300	1310	1320	1330	1340	
6687073	1290	1300	1310	1320	1330	1340	

117531 description="133 KD CRYSTAL PROTEIN (DELTA ENDOTOXIN) (CRYSTALLINE ENTOMOCIDAL PROTOXIN)." library="NA species="Bacillus thuringiensis serovar entomocidus" source="swissprot_prot" version="NA type=PRT

SCORES Init1: 4298 Initn: 6535 Opt: 6835 z-score: 7760.8 E(): 0
>>SW:117531
initn: 6535 init1: 4298 opt: 6835 z-score: 7760.8 expect(): 0
Smith-Waterman score: 6835; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)

	10	20	30	40	50	60	
cry1a-105.pe	MDNNPINECIPYNCLENPVEVLGGERIETGTPTIDISLSLTQFLSEFPVAGFVLGL						
117531	MDNNPINECIPYNCLENPVEVLGGERIETGTPTIDISLSLTQFLSEFPVAGFVLGL						
	70	80	90	100	110	120	
cry1a-105.pe	VDIINGIFQSDMAFVQIEQLINQRIEFAFNQAIARLEGLSNLYIYAESFREWAD						
117531	VDIINGIFQSDMAFVQIEQLINQRIEFAFNQAIARLEGLSNLYIYAESFREWAD						
	130	140	150	160	170	180	
cry1a-105.pe	PTNPALREEMRIQFNDMNSALTITAIPLFAYQNYQVPLLSVYVQAANHLVLRDVSVEGQ						
117531	PTNPALREEMRIQFNDMNSALTITAIPLFAYQNYQVPLLSVYVQAANHLVLRDVSVEGQ						
	190	200	210	220	230	240	
cry1a-105.pe	RWGFDAATINSRYNDLRLGNVTDHAVRYNTGLERVWGPDSRDWRYNQFRRLTLTV						
117531	RWGFDAATINSRYNDLRLGNVTDHAVRYNTGLERVWGPDSRDWRYNQFRRLTLTV						
	250	260	270	280	290	300	
cry1a-105.pe	LDIVLFSNVDSRRVPRTYQSLTREIYNPVLENFDSFGSAQSGIESIRSPHMDIL						
117531	LDIVLFSNVDSRRVPRTYQSLTREIYNPVLENFDSFGSAQSGIESIRSPHMDIL						
	310	320	330	340	350	360	
cry1a-105.pe	NSITITDAHREYVWSGHQIMASPVGFSGPFTFPPLXYGTMGNAAPQORIVAQLCGGYR						
117531	NSITITDAHREYVWSGHQIMASPVGFSGPFTFPPLXYGTMGNAAPQORIVAQLCGGYR						
	370	380	390	400	410		
cry1a-105.pe	NSITITVHRGFVWSGHQITASPVGFSGPFTFPPLFGNAGNAAPV-LVSLTGLGIFR						
117531	NSITITVHRGFVWSGHQITASPVGFSGPFTFPPLFGNAGNAAPV-LVSLTGLGIFR						

~~Product Characterization Center~~

cry1a-105.pe	1117531	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960	4970	4980	4990</
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cry1a-105.pe QEVYVCPGRGIVLIRVTAIYKEGVEGCVTHIEINNTDELKFSNCVEEELYPNNVTTCNDY
 1020 1030 1040 1050 1060 1070
 1080 1090 1100 1110 1120 1130
 cry1a-105.pe TVNOEYVCGATSNRNGYNAPSPADVASVVEEKS YDGRGNPCPNFNRGYDVTPLPV
 1140 1150 1160 1170
 cry1a-105.pe GYVTKLEYFETDKVWIEIGETEGFFIVDSVELLMEE
 1180 1190 1200 1210 1220 1230
 1240 1250 1260 1270 1280 1290 1300
 cry1a-105.pe GYVTKLEYFETDKVWIEIGETEGFFIVDSVELLMEE
 1310 1320 1330 1340 1350 1360 1370
 cry1a-105.pe GYVTKLEYFETDKVWIEIGETEGFFIVDSVELLMEE
 1380 1390 1400 1410 1420 1430 1440
 cry1a-105.pe TVNOEYVCGATSNRNGYNAPSPADVASVVEEKS YDGRGNPCPNFNRGYDVTPLPV
 1450 1460 1470 1480 1490 1500 1510
 cry1a-105.pe QEVYVCPGRGIVLIRVTAIYKEGVEGCVTHIEINNTDELKFSNCVEEELYPNNVTTCNDY
 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570

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61221640 NSITITVDVHRGNTYWSGHQITASVPVGFSGFEFAFLFLFCNAGNAAPPV-LVSLTGLGIFR
310 320 330 340 350
370 380 390 400 410
cry1a-105.pe TLSTLYRRP-FNIGNNQOLSLVDGTEFAYGT-SSNPSAVKSKTSVDLSLDETPQQN
410
61221640 TLSSPYRLILGSGFNQELFVLDTGTFESFASLTINPITLYRQRTGVDLSVLPQQN
360 370 380 390 400 410
420 430 440 450 460 470
cry1a-105.pe NVPPROGFSHRLSHVSMFRSGFNSSVSIIRAPMFSTHRSAAEFNNIIASDSTIQPLVK
420 430 440 450 460 470
61221640 SVPPRAGFSHRLSHVMTLSQ--AAGA VYTLRAPTFSWQHRSAEFNNIIPSSQITQPLTK
420 430 440 450 460 470
480 490 500 510 520 530
cry1a-105.pe AHTLQSGTIVVRGPGFTGCDILRTSGGPEAYTIVNINQQLPQRYRARIYASTTNLRIY
480 490 500 510 520 530
61221640 STNLGSGTSVVRGPGFTGCDILRTSPGQISTLRVNTAPLSQRYRARIYASTTNLQPH
480 490 500 510 520 530
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQFNKMTDGTPLTFQSFYATINTAFTFPMSSQSTVFGADTFSSGNEVY
540 550 560 570 580 590
61221640 TSIDGRPIHQGFSAATSSGNSLQSGSFRTVGFITPFNFSSGSSVFTLSAHVNSGNEVY
540 550 560 570 580 590
600 610 620 630 640 650
cry1a-105.pe IDREFELIPATILEAEYNLERAQKAVNALFTSNQLGKTNVTDYHIDQVSNVLYLSD
600 610 620 630 640 650
61221640 IDRIEFVPAEVTFEAEYDLERAQKAVNELFTSSNQIGLKTQVTDYHIDQVSNVLECLSD
600 610 620 630 640 650
660 670 680 690 700 710
cry1a-105.pe FCLDEKREUSEKVKHAKLSDERNLQDSNFKDINRQPERGWSGSGTITIQGDDVFKEN
660 670 680 690 700 710
61221640 FCLDEKQELSEKVKHAKLSDERNLQDPNFRGINRQDRGMWGSDTITIQGDDVFKEN
660 670 680 690 700 710
720 730 740 750 760 770
cry1a-105.pe YVTLSGTFDECYPTLYXKIDESKLAFTRYQLRGYIEDSDQLEIYIRYNAKHETVNP
720 730 740 750 760 770
61221640 YVTLGTFDECYPTLYXKIDESKLAFTRYQLRGYIEDSDQLEIYIRYNAKHETVNP
720 730 740 750 760 770
780 790 800 810 820 830
cry1a-105.pe GTGSLWPLSAQSPFGKCGEPNRCAPHLEWNPDLDCSDRGCEKCAHSHHPSLDDVGCCTD
780 790 800 810 820 830
61221640 GTGSLWPLSAQSPFGKCGEPNRCAPHLEWNPDLDCSDRGCEKCAHSHHPSLDDVGCCTD
780 790 800 810 820 830
840 850 860 870 880 890
cry1a-105.pe LNEDLGWVWIFKIKTODGHARLGNLEFLEKPLVGEALARYKRAEKWRDKREKLEWETN
840 850 860 870 880 890
61221640 LNEDLGWVWIFKIKTODGHARLGNLEFLEKPLVGEALARYKRAEKWRDKREKLEWETN
840 850 860 870 880 890
900 910 920 930 940 950
cry1a-105.pe IVYKEAKESVDALFVNSQDQLQADTNIAHAAKRVHSTREAYLPESLVPVGNAAIF
900 910 920 930 940 950
61221640 IVYKEAKESVDALFVNSQDQLQADTNIAHAAKRVHSTREAYLPESLVPVGNAAIF
900 910 920 930 940 950
960 970 980 990 1000 1010
cry1a-105.pe EELEGRIFTAFSLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNQSRSLVWPWEAEVVS
960 970 980 990 1000 1010
```

```
61221640 EELEGRIFTAFSLYDARNVINKGDFNNGLSQWNVKGVHDVEEQNNQSRSLVWPWEAEVVS
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070
cry1a-105.pe QEVRCVCRGGYILRVATYKEGGEGCVTHIEENNTDELKFSNCVBEIYPNNVTICNDY
1020 1030 1040 1050 1060 1070
61221640 QEVRCVCRGGYILRVATYKEGGEGCVTHIEENNTDELKFSNCVBEIYPNNVTICNDY
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
cry1a-105.pe TVNCEEYGGAYTSRNRGNEAPSPADYASVVEEKS YTDGRRNCPCEFNRGYRDYTLPV
1080 1090 1100 1110 1120 1130
61221640 TVNCEEYGGAYTSRNRGNEAPSPADYASVVEEKS YTDGRRNCPCEFNRGYRDYTLPV
1080 1090 1100 1110 1120 1130
1140 1150 1160 1170
cry1a-105.pe GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
61221640 GYVTKLEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pe
NRAA:40267
40267 source="GENBANK_PROT" unnamed protein product [Bacillus
thuringiensis]gi|61221638|sp|P0A366|CRIA_A_BACTK_Pesticidal crystal protein
cry1aA (insecticidal delta-endotoxin CryIA(a)) (Crystalline entomocidal protoxin)
(133 kDa crystal protein)gi|61221640|sp|P0A368|CRIA_A_BACTE_Pesticidal crystal
protein cry1aA (insecticidal delta-endotoxin CryIA(a)) (Crystalline entomocidal
protoxin) (133 kDa crystal protein)
SCORES Initl: 4298 Initn: 6535 Opt: 6835 z-score: 7760.8 E(): 0
>NRAA:40267
Initn: 6535 Initl: 4298 Opt: 6835 z-score: 7760.8 expect(): 0
Smith-Waterman score: 6835; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe MDNPNINECIPYCNCLSNPEVEVLGGERIETGYTIDISLSLTQFLLSEFVPAGFVGL
40267 MDNPNINECIPYCNCLSNPEVEVLGGERIETGYTIDISLSLTQFLLSEFVPAGFVGL
60
cry1a-105.pe VDIIWGIFGFSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIVAESEFWEAD
40267 VDIIWGIFGFSQWDAFLVQIEQLINQRIEFARNQAIISRLGSLNLYQIVAESEFWEAD
120
cry1a-105.pe PTNPALREERNRQFNDMNSALTTPALFVAVQNVQVPLLSVTVQAANHLSLVDVSVFQ
40267 PTNPALREERNRQFNDMNSALTTPALFVAVQNVQVPLLSVTVQAANHLSLVDVSVFQ
180
cry1a-105.pe RWGFDATINSRVNDLTLCIGNYTDHAVRWYNTGLERVWGPDSDRWIRYNQFRELTLTV
40267 RWGFDATINSRVNDLTLCIGNYTDHAVRWYNTGLERVWGPDSDRWIRYNQFRELTLTV
240
cry1a-105.pe LDIVSFPNVDSRTPIETVSQLPREIYNPVLNENFDGSRGSAQIEGSIKSPHLMQIL
40267 LDIVSFPNVDSRTPIETVSQLPREIYNPVLNENFDGSRGSAQIEGSIKSPHLMQIL
300
```

40267 IVYKEAESVDALFVNSQYDQLOADNTNIAHAAKRVHSIREAYLPFELSVPVGNAAIF
900 910 920 930 940 950
cry1a-105.pe EELEGIFAFSLYDARVVKNGDFNGLSCWNVGHVDEEONNOSVLYVPEWEAEVS
960 970 980 990 1000 1010
40267 EELEGIFAFSLYDARVVKNGDFNGLSCWNVGHVDEEONNOSVLYVPEWEAEVS
960 970 980 990 1000 1010
cry1a-105.pe QEVVPCGIGYILRTVATKEGCGGCVTHEENNTDELKESNCVEEIIYPNNTVCNDY
1020 1030 1040 1050 1060 1070
40267 QEVVPCGIGYILRTVATKEGCGGCVTHEENNTDELKESNCVEEIIYPNNTVCNDY
1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNOEYGGAYTSRNGYNEAPSPADYASVVEEKSYYDGRNPNCFNNGYRDYTPPV
1080 1090 1100 1110 1120 1130
40267 TVNOEYGGAYTSRNGYNEAPSPADYASVVEEKSYYDGRNPNCFNNGYRDYTPPV
1080 1090 1100 1110 1120 1130
cry1a-105.pe GYVTKLEYFPETDKVWIEIGETEGTIVDSVELLME
1140 1150 1160 1170
40267 GYVTKLEYFPETDKVWIEIGETEGTIVDSVELLME
1140 1150 1160 1170
cry1a-105.pe
8488967
8488967
DELTA-EMDJOIN CRY1A(1) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (133 KDA CRYSTAL
PROTEIN). Library=NA Species="Bacillus thuringiensis serovar sotto"
source="swissprot prot" version=NA type=PRT
SCORES Init= 4295 Patch: 6536 Opt: 6835 z-score: 7760.8 E(): 0
>>SW:8488967
Init: 6535 Patch: 4298 Opt: 6835 z-score: 7760.8 expect(): 0
Smith-Waterman score: 6835;
(1-1177:1-1176)
cry1a-105.pe MNNPNINECIPYNCISNPEVEVGEFSTGYTPINISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
8488967 MNNPNINECIPYNCISNPEVEVGEFSTGYTPINISLSLTQFLSEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIIMGIFGSDWDAFVQIEQLINQRIEFAANQALSRLESLYQVYALSEFWEAD
70 80 90 100 110 120
8488967 VDIIMGIFGSDWDAFVQIEQLINQRIEFAANQALSRLESLYQVYALSEFWEAD
70 80 90 100 110 120
cry1a-105.pe PTNPALREEMIQDNMSALATTAIPFAVQYVPLLSVYQAANHLSDVDSFV
130 140 150 160 170 180
8488967 PTNPALREEMIQDNMSALATTAIPFAVQYVPLLSVYQAANHLSDVDSFV
130 140 150 160 170 180
cry1a-105.pe RMGFAATINSRYNDLTRILGNYTHAVRYNTGLERWGPDSROWIRNQFRELLITV
190 200 210 220 230 240
8488967 RMGFAATINSRYNDLTRILGNYTHAVRYNTGLERWGPDSROWIRNQFRELLITV
190 200 210 220 230 240

40267 IVYKEAESVDALFVNSQYDQLOADNTNIAHAAKRVHSIREAYLPFELSVPVGNAAIF
280 290 300
cry1a-105.pe NSITITNDARGFNWAGVATSPVGPAGPFAFPLFGNAGNAAPV-LVSLTGLGIFR
310 320 330 340 350
40267 NSITITNDARGFNWAGVATSPVGPAGPFAFPLFGNAGNAAPV-LVSLTGLGIFR
310 320 330 340 350
cry1a-105.pe TLSTLYRRP-FNIGNNQQVSLDSEFST-SNRSVAVKSTVDSLDSEIPPQNN
360 370 380 390 400 410
40267 TLSTLYRRP-FNIGNNQQVSLDSEFST-SNRSVAVKSTVDSLDSEIPPQNN
360 370 380 390 400 410
cry1a-105.pe NVPPROGFSRHLRSHVSMFSGFSSVSIIRPMWHRDAEENKIASDSLTQIPAVK
420 430 440 450 460 470
40267 NVPPROGFSRHLRSHVSMFSGFSSVSIIRPMWHRDAEENKIASDSLTQIPAVK
420 430 440 450 460 470
cry1a-105.pe AHTLQSGTIVRGPGFTGDLRLRTSGGPFAYTIVNNGQLPORYEALIRASTINRY
480 490 500 510 520 530
40267 AHTLQSGTIVRGPGFTGDLRLRTSGGPFAYTIVNNGQLPORYEALIRASTINRY
480 490 500 510 520 530
cry1a-105.pe VIVAGERIFAGQNKMTDGTPLTFQSFYATINTAFTPMSSQSFVGTGTFSSGNEYV
540 550 560 570 580 590
40267 VIVAGERIFAGQNKMTDGTPLTFQSFYATINTAFTPMSSQSFVGTGTFSSGNEYV
540 550 560 570 580 590
cry1a-105.pe IDRFELIPVATLEAEYNLERAKAVNALFTSNQGLKNTVTDVHIDQVSNVTVLSE
600 610 620 630 640 650
40267 IDRFELIPVATLEAEYNLERAKAVNALFTSNQGLKNTVTDVHIDQVSNVTVLSE
600 610 620 630 640 650
cry1a-105.pe FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINQPERGWSGTGITIGGDDVFKEN
660 670 680 690 700 710
40267 FCLDEKRELSKVKHAKRLSDERNLLQDSNFKDINQPERGWSGTGITIGGDDVFKEN
660 670 680 690 700 710
cry1a-105.pe YVTLSTGDFECYTYLYQKIDSKLAFYVQLRGVYEDSQLEIYLSRYNAKHETVNP
720 730 740 750 760 770
40267 YVTLSTGDFECYTYLYQKIDSKLAFYVQLRGVYEDSQLEIYLSRYNAKHETVNP
720 730 740 750 760 770
cry1a-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
40267 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
cry1a-105.pe LNEIDGVWVIFKIQDGHARLGNLEFLEEKPLVGEALAKVRAEKWRDREKLEWETN
840 850 860 870 880 890
40267 LNEIDGVWVIFKIQDGHARLGNLEFLEEKPLVGEALAKVRAEKWRDREKLEWETN
840 850 860 870 880 890
cry1a-105.pe IYVKEAESVDALFVNSQYDQLOADNTNIAHAAKRVHSIREAYLPFELSVPVGNAAIF
900 910 920 930 940 950

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cryIa-105.pe IYVKEAKESVDALFVNSQVDQLQADTNIAIHAAVKRHSIREAYLPSELSVPGVNAALF
8488967
900 910 920 930 940 950
900 910 920 930 940 950
cryIa-105.pe EELEGRIFTAFLSYDARNVYKNGDFNGSLSCWNVKGVHVDVEENQNRQSLVLPVEAEVVS
8488967
960 970 980 990 1000 1010
960 970 980 990 1000 1010
cryIa-105.pe QEYVCPGPGYILRVTAKEGYGEGCVTHIEENNTDELAFSCVVEEIIYPNNTVTCNDY
8488967
1020 1030 1040 1050 1060 1070
1020 1030 1040 1050 1060 1070
cryIa-105.pe TVNQEYGGAYTSRNGYNEAPSPADYASVYEKSYTDGRRENPCFNRCGYRDYTPLPV
8488967
1080 1090 1100 1110 1120 1130
1080 1090 1100 1110 1120 1130
cryIa-105.pe GVVTKLEYEPPETDKVWIEIGETGTFIVDSVELLMEE
8488967
1140 1150 1160 1170
1140 1150 1160 1170
cryIa-105.pep
SW:61221638
61221638 description="Pesticidal crystal protein cryIaA (Insecticidal
delta-endotoxin CryIA(a)) (Crystalline entomocidal protoxin) (113 kDa crystal
protein)." library=NA species="Bacillus thuringiensis serovar kurstaki"
source="swissprot_prot" version=NA type=PRT
SCORES Init1: 4298 Initn: 6535 Opt: 6835 z-score: 7760.8 E(): 0
>>SW:61221638
initn: 6535 init1: 4298 opt: 6835 z-score: 7760.8 expect(): 0
Smith-Waterman score: 6835; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cryIa-105.pe MDNNPNEICIPYCNLSNPEVILGGERETGYTPIDISLSLTOPILSEFVPGAGVLGL
10 20 30 40 50 60
10 20 30 40 50 60
61221638 MDNNPNEICIPYCNLSNPEVILGGERETGYTPIDISLSLTOPILSEFVPGAGVLGL
10 20 30 40 50 60
10 20 30 40 50 60
cryIa-105.pe VDIIGIFGFSQMDAPFLVQIQLINQRIEFARQOASIRLEGLSNLYQIVAESFREWAD
70 80 90 100 110 120
70 80 90 100 110 120
61221638 VDIIGIFGFSQMDAPFLVQIQLINQRIEFARQOASIRLEGLSNLYQIVAESFREWAD
70 80 90 100 110 120
70 80 90 100 110 120
cryIa-105.pe PTNPALRENRIOFNDMNSALTATPILFAVQNYQVPLLSYVQAAHLHSLVRDVSVPQG
130 140 150 160 170 180
130 140 150 160 170 180
61221638 PTNPALRENRIOFNDMNSALTATPILFAVQNYQVPLLSYVQAAHLHSLVRDVSVPQG
130 140 150 160 170 180
130 140 150 160 170 180
cryIa-105.pe PTNPALRENRIOFNDMNSALTATPILFAVQNYQVPLLSYVQAAHLHSLVRDVSVPQG
190 200 210 220 230 240
190 200 210 220 230 240
61221638 PTNPALRENRIOFNDMNSALTATPILFAVQNYQVPLLSYVQAAHLHSLVRDVSVPQG
190 200 210 220 230 240
190 200 210 220 230 240

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cry1a-105.pe LAGGDAATINRNDLRLIGNYTHAVRWNTGLERWGPDSRDWRINQFRRLTLTV
61221638 RRGFDAAARNDLRLIGNYTHAVRWNTGLERWGPDSRDWRINQFRRLTLTV
cry1a-105.pe LDIVSPNNOSRTPYFATVQUTREIINNNFNGSGRGAQIEGSRPHMLDIL
61221638 LDIVSPNNOSRTPYFATVQUTREIINNNFNGSGRGAQIEGSRPHMLDIL
cry1a-105.pe NSITIVTAHRGEVYWGHOINLSPGSGPEPTFPYAGTGMNAPQORIVLAQLGQVYR
61221638 NSITIVTAHRGEVYWGHOINLSPGSGPEPTFPYAGTGMNAPQORIVLAQLGQVYR
cry1a-105.pe TSSSTLYRRP-FNIGINNQLSLVDGTEFAYGT-SNKLPKSVYRKSGTVDSLSSTPPON
61221638 TSSSTLYRRP-FNIGINNQLSLVDGTEFAYGT-SNKLPKSVYRKSGTVDSLSSTPPON
cry1a-105.pe NVPRGESHLSVSWFRSGFNSSVIIRAPMFSTHRSAPFNIIASNTCTPLVK
61221638 NVPRGESHLSVSWFRSGFNSSVIIRAPMFSTHRSAPFNIIASNTCTPLVK
cry1a-105.pe AHFLQSGTVVRGPGFTGGDILARTSGGPFAYTVININGOLPORRYARIRYASTINLRIY
61221638 AHFLQSGTVVRGPGFTGGDILARTSGGPFAYTVININGOLPORRYARIRYASTINLRIY
cry1a-105.pe VTVAGERIFAGQNKMTDGLPTTFOSFIATINTAFTFFMSQSSFTVGADTFSSGNEVY
61221638 VTVAGERIFAGQNKMTDGLPTTFOSFIATINTAFTFFMSQSSFTVGADTFSSGNEVY
cry1a-105.pe IDRFELIPVTATLEAYNLERAOKAVNALFTSTINGLKTINVTDYHIDQVSNLVTLSDE
61221638 IDRFELIPVTATLEAYNLERAOKAVNALFTSTINGLKTINVTDYHIDQVSNLVTLSDE
cry1a-105.pe FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQERGWSGTGTTQGGDDVFKEN
61221638 FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQERGWSGTGTTQGGDDVFKEN
cry1a-105.pe YVTLSTFDECYPTLYOKIDESKLAFTRYQYRGYIEDSODLEIYSIRYNAKHETVNVV
61221638 YVTLSTFDECYPTLYOKIDESKLAFTRYQYRGYIEDSODLEIYSIRYNAKHETVNVV
cry1a-105.pe GTSLWFLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTD
61221638 GTSLWFLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFLSDIDVGCTD

cry1a-105.pe LNEGLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKVKAERKWRDKRELEWETN
61221638 LNEGLGWVWIFKIKTQDGHARLGNLEFLEEKPLVGEALARKVKAERKWRDKRELEWETN
cry1a-105.pe IVVKEAKESVDALFVNSQDQLQADNTAMIAHADKRVHSIRAYLPFLSVIPGVNAAIIF
61221638 IVVKEAKESVDALFVNSQDQLQADNTAMIAHADKRVHSIRAYLPFLSVIPGVNAAIIF
cry1a-105.pe EEELEGRIFTAFSLYDAARNVKNKGDFNNGLSQWNVKGVHDVVEEQNNORSVLVVPWEAEVS
61221638 EEELEGRIFTAFSLYDAARNVKNKGDFNNGLSQWNVKGVHDVVEEQNNORSVLVVPWEAEVS
cry1a-105.pe QEVYVCPGSGYILRVATYKEGEGCGCVTHIEENNTDELKFSNCVEEYIPNNTVTNDY
61221638 QEVYVCPGSGYILRVATYKEGEGCGCVTHIEENNTDELKFSNCVEEYIPNNTVTNDY
cry1a-105.pe TVNQEEYGGAYTSNRNGYNEAPSPADYASVYEEKSVYTDGRRNCPCEFNRGYDYTPLPV
61221638 TVNQEEYGGAYTSNRNGYNEAPSPADYASVYEEKSVYTDGRRNCPCEFNRGYDYTPLPV
cry1a-105.pe GUTTELEFFPETDKVWIEIGETEGTFIVDSVELLMEE
61221638 GUTTELEFFPETDKVWIEIGETEGTFIVDSVELLMEE
cry1a-105.pe MDNPNINECIPYCNLSNPEVVLGGERTCTGTPIDISJSGVFLSSEPNQGVGL
225472 MDNPNINECIPYCNLSNPEVVLGGERTCTGTPIDISJSGVFLSSEPNQGVGL
cry1a-105.pe VDIWIIFGFSQWDAFLVQIBOLINQRIEFARNQAIISRLGELNLSYAESFPAQD
225472 VDIWIIFGFSQWDAFLVQIBOLINQRIEFARNQAIISRLGELNLSYAESFPAQD
cry1a-105.pe PTPNALREMRIOFNDMNSALTITAIPLFVQNVQVPLLSVYQVQANHLISVLRDVSFVG
225472 PTPNALREMRIOFNDMNSALTITAIPLFVQNVQVPLLSVYQVQANHLISVLRDVSFVG

SCORES Init1: 4288 Init2: 6533 Z-score: 7758.5 E(): 0
>>NRAA:225472
initn: 6533 initl: 4288 opt: 6833 Z-score: 7758.5 expect(): 0
Smith-Waterman score: 6833;
(1-1177:1-1176)

Information of Monsanto Company

```
cry1a-105.pe 190 200 210 220 230 240
RMGFDAAIINRYNDLRLIGNYTHAVRYNTGLEEVGSPDRDWIYNQFRRLTLTV
225472 RMGFDAAIINRYNDLRLIGNYTHAVRYNTGLEEVGSPDRDWIYNQFRRLTLTV
190 200 210 220 230 240
250 260 270 280 290 300
cry1a-105.pe LDVSLFPNYSRTYRTVTSQITREIYTNVLENFDFGSPRGAQGIERSRSPHLMIL
LDVSLFPNYSRTYRTVTSQITREIYTNVLENFDFGSPRGAQGIERSRSPHLMIL
225472 LDVSLFPNYSRTYRTVTSQITREIYTNVLENFDFGSPRGAQGIERSRSPHLMIL
250 260 270 280 290 300
310 320 330 340 350 360
cry1a-105.pe NSITTYDAHRGEYMSGHQIMASPVGSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYR
NSITTYDAHRGEYMSGHQIMASPVGSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYR
225472 NSITTYDAHRGEYMSGHQIMASPVGSGPEFTFPLYGTMGNAAPQRIVAQLGQGVYR
310 320 330 340 350 360
370 380 390 400 410
cry1a-105.pe TLSSLTYRPP-FNIGINNQOLSVDGTFAYGT-SSNLPSAVYKSGTVDSLEIPQNN
TLSSLTYRPP-FNIGINNQOLSVDGTFAYGT-SSNLPSAVYKSGTVDSLEIPQNN
225472 TLSSLTYRPP-FNIGINNQOLSVDGTFAYGT-SSNLPSAVYKSGTVDSLEIPQNN
370 380 390 400 410
420 430 440 450 460 470
cry1a-105.pe NVPPRQGFSLHSHVMSFRSGFSNSVSIIRAPMFSIHRSAFNIIASDITQIPLVK
NVPPRQGFSLHSHVMSFRSGFSNSVSIIRAPMFSIHRSAFNIIASDITQIPLVK
225472 NVPPRQGFSLHSHVMSFRSGFSNSVSIIRAPMFSIHRSAFNIIASDITQIPLVK
420 430 440 450 460 470
480 490 500 510 520 530
cry1a-105.pe AHTLQSGTVVRGPGFTGGDILRLRTSGGPFAYTIVNGLQPPQRYRIRVASTNLRIRY
AHTLQSGTVVRGPGFTGGDILRLRTSGGPFAYTIVNGLQPPQRYRIRVASTNLRIRY
225472 AHTLQSGTVVRGPGFTGGDILRLRTSGGPFAYTIVNGLQPPQRYRIRVASTNLRIRY
480 490 500 510 520 530
540 550 560 570 580 590
cry1a-105.pe VTVAGERIFAGQFNKMTDGTDLPTQSFYSYATINTAFTPMGSSFTVGATTFSSGNEVY
VTVAGERIFAGQFNKMTDGTDLPTQSFYSYATINTAFTPMGSSFTVGATTFSSGNEVY
225472 VTVAGERIFAGQFNKMTDGTDLPTQSFYSYATINTAFTPMGSSFTVGATTFSSGNEVY
540 550 560 570 580 590
600 610 620 630 640 650
cry1a-105.pe IDRFELIPVATLEAEYNLERAKAUNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDE
IDRFELIPVATLEAEYNLERAKAUNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDE
225472 IDRFELIPVATLEAEYNLERAKAUNALFTSTNQLGLKTNVTDYHIDQVSNLVYLSDE
600 610 620 630 640 650
660 670 680 690 700 710
cry1a-105.pe FCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINROLDRGARGSTDTITIGGDDVFKEN
FCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINROLDRGARGSTDTITIGGDDVFKEN
225472 FCLDEKRELSKVKHAKRLSDERNLLQDPNFRGINROLDRGARGSTDTITIGGDDVFKEN
660 670 680 690 700 710
720 730 740 750 760 770
cry1a-105.pe VYTLGTDDECYPTLYQKIDESKILKAFTRYQLRGYIEDSODLEIYVIRYNAKHETVNVVP
VYTLGTDDECYPTLYQKIDESKILKAFTRYQLRGYIEDSODLEIYVIRYNAKHETVNVVP
225472 VYTLGTDDECYPTLYQKIDESKILKAFTRYQLRGYIEDSODLEIYVIRYNAKHETVNVVP
720 730 740 750 760 770
780 790 800 810 820 830
cry1a-105.pe GTGSLWPLSAQSPGKCGEFPNCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVGCTD
GTGSLWPLSAQSPGKCGEFPNCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVGCTD
225472 GTGSLWPLSAQSPGKCGEFPNCAPHLEWNPDLDCSCRDEKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
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cry1a-105.pe 840 850 860 870 880 890
INEDIGWVVIKIKIQDQGHARLGNLEFLEEKPLVGEALARYRAEKKWRDREKLEWETN
225472 INEDIGWVVIKIKIQDQGHARLGNLEFLEEKPLVGEALARYRAEKKWRDREKLEWETN
840 850 860 870 880 890
900 910 920 930 940 950
cry1a-105.pe IYVKEAKESVDALFVNSQDQLQADNTAMTHAADKRVHSIREAYLPESLVPGVNAIIF
IYVKEAKESVDALFVNSQDQLQADNTAMTHAADKRVHSIREAYLPESLVPGVNAIIF
225472 IYVKEAKESVDALFVNSQDQLQADNTAMTHAADKRVHSIREAYLPESLVPGVNAIIF
900 910 920 930 940 950
960 970 980 990 1000 1010
cry1a-105.pe EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNYKHVDVEEQNNQORSVLVVPWEAEVS
EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNYKHVDVEEQNNQORSVLVVPWEAEVS
225472 EELEGRIFTAFSLYDARNVIKNGDFNGLSCWNYKHVDVEEQNNQORSVLVVPWEAEVS
960 970 980 990 1000 1010
1020 1030 1040 1050 1060 1070
cry1a-105.pe QEVRYVCRGEGYILRVYATAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVTCNDY
QEVRYVCRGEGYILRVYATAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVTCNDY
225472 QEVRYVCRGEGYILRVYATAYKEGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVTCNDY
1020 1030 1040 1050 1060 1070
1080 1090 1100 1110 1120 1130
cry1a-105.pe TVNQBEYGGATSRNRYNEAPSVADVASVVEEKSYPDGRRENPCENRGRYDTPV
TVNQBEYGGATSRNRYNEAPSVADVASVVEEKSYPDGRRENPCENRGRYDTPV
225472 TVNQBEYGGATSRNRYNEAPSVADVASVVEEKSYPDGRRENPCENRGRYDTPV
1080 1090 1100 1110 1120 1130
1140 1150 1160 1170
cry1a-105.pe GYVTKELYFPETDKVWIEIGETGTFIVDSVELLMEE
GYVTKELYFPETDKVWIEIGETGTFIVDSVELLMEE
225472 GYVTKELYFPETDKVWIEIGETGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pep
NRAA:535781
535781 source="GENBANK_PROT" insecticidal crystal protein [Bacillus
thuringiensis]
SCORES Initl: 4287 Initn: 6533 Opt: 6833 z-score: 7758.5 E(): 0
>>NRAA:535781
initn: 6533 initl: 4287 opt: 6833 z-score: 7758.5 expect(): 0
Smith-Waterman score: 6833; 86.9% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
535781 MDNPNINECIPYNCLSNPEVEVLGGERIETGYTPIDISLSLTOFLSEFVPGAGFVLGL
10 20 30 40 50 60
70 80 90 100 110 120
cry1a-105.pe VDIINGIPGQWDFAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFREWEAD
VDIINGIPGQWDFAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFREWEAD
535781 VDIINGIPGQWDFAFLVQIEQLINQRIEERFARNQAIISRLGSLNLYQIYAESFREWEAD
70 80 90 100 110 120
130 140 150 160 170 180
cry1a-105.pe PTNPALREEMRIQFNDNMNSALTTATPLFAVQNYQVPLLSVYQAAMHLSLVRDVSFVGO
PTNPALREEMRIQFNDNMNSALTTATPLFAVQNYQVPLLSVYQAAMHLSLVRDVSFVGO
535781 PTNPALREEMRIQFNDNMNSALTTATPLFAVQNYQVPLLSVYQAAMHLSLVRDVSFVGO
130 140 150 160 170 180
```


142765 PTPALREEMRIQFNDMWSALTTAIPLLAVQYQVPLLSVYVQAAHLHSLVLRDVSFVGQ
130 130 140 150 160 170 180
cry1a-105.pe RMGFAAATNSRYNDLRLIGNYTDHAWRYNTGLRWGPDSDRDWRNQFRELTLTV
190 200 210 220 230 240
142765 RMGFAAATNSRYNDLRLIGNYTDHAWRYNTGLRWGPDSDRDWRNQFRELTLTV
190 200 210 220 230 240
cry1a-105.pe LDIIVSLFNYDSRTYPIRTVSQLTREIYNVLENFNGSGRGAQIEGSRHSPLMDIL
250 260 270 280 290 300
142765 LDIIVSLFNYDSRTYPIRTVSQLTREIYNVLENFNGSGRGAQIEGSRHSPLMDIL
250 260 270 280 290 300
cry1a-105.pe NSITITDAHRGEYVWGHQIMASPVGSGPEFTPLYGTMGNAAPQORIVAAQLCGQVYR
310 320 330 340 350 360
142765 NSITITDAHRGEYVWGHQIMASPVGSGPEFTPLYGTMGNAAPQORIVAAQLCGQVYR
310 320 330 340 350 360
cry1a-105.pe TLESSTLYRRP-FNIGINNQQSLVLDCTEFAYCT-SSNLPAAVYRKSGTVDSUDEIPPONN
370 380 390 400 410
142765 TLESSTLYRRP-FNIGINNQQSLVLDCTEFAYCT-SSNLPAAVYRKSGTVDSUDEIPPONN
370 380 390 400 410
cry1a-105.pe NVPPROGFSHRLSHVMSFRSGNSVSIIRAPMFSWTHSAEFNNIADSDITQIPLVK
420 430 440 450 460 470
142765 NVPPROGFSHRLSHVMSFRSGNSVSIIRAPMFSWTHSAEFNNIADSDITQIPLVK
420 430 440 450 460 470
cry1a-105.pe SVPPRAGFSHRLSHVMSFRSGNSVSIIRAPMFSWTHSAEFNNIADSDITQIPLVK
480 490 500 510 520 530
142765 SVPPRAGFSHRLSHVMSFRSGNSVSIIRAPMFSWTHSAEFNNIADSDITQIPLVK
480 490 500 510 520 530
cry1a-105.pe AHTLQSGTIVVRGPGFTGGDILARTSGGPFAYTVINQGLQPKQRYRARIRYASTNLRIY
540 550 560 570 580 590
142765 AHTLQSGTIVVRGPGFTGGDILARTSGGPFAYTVINQGLQPKQRYRARIRYASTNLRIY
540 550 560 570 580 590
cry1a-105.pe VTVAGERIPFAGQFNKTMWDGDLTFOFSYATINTAFPPMSQSSFTVGADTFSSGNEVY
600 610 620 630 640 650
142765 VTVAGERIPFAGQFNKTMWDGDLTFOFSYATINTAFPPMSQSSFTVGADTFSSGNEVY
600 610 620 630 640 650
cry1a-105.pe IDRFELIPVATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTLSDE
660 670 680 690 700 710
142765 IDRFELIPVATLEAEYNLERAKAVNALFTSTNOLGKTNVTDYHIDQVSNLVTLSDE
660 670 680 690 700 710
cry1a-105.pe FCLDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFNEN
720 730 740 750 760 770
142765 FCLDEKREUSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTGITIQGGDDVFNEN
720 730 740 750 760 770
cry1a-105.pe YVTLGTFDECPYTLVYQKIDESKLAFTRYQIOLRGYIEDSODLEISIRYNAKHETVNP
780 790 800 810 820 830
142765 YVTLGTFDECPYTLVYQKIDESKLAFTRYQIOLRGYIEDSODLEISIRYNAKHETVNP
780 790 800 810 820 830
cry1a-105.pe GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTD
840 850 860 870 880 890
142765 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTD
840 850 860 870 880 890

142765 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGEKCAHSHHFSLDIDVGCTD
780 790 800 810 820 830
cry1a-105.pe INEDLGWVIFKIKITQDGHARGNLEFEEKPLVGEALARKVRAEKWDRKREKLEMETN
840 850 860 870 880 890
142765 INEDLGWVIFKIKITQDGHARGNLEFEEKPLVGEALARKVRAEKWDRKREKLEMETN
840 850 860 870 880 890
cry1a-105.pe IVYKEAKESVDALFVNSQYDQLQADNTINAMHAADKRVHSIREAYLPESLVIPGVNAAIF
900 910 920 930 940 950
142765 IVYKEAKESVDALFVNSQYDQLQADNTINAMHAADKRVHSIREAYLPESLVIPGVNAAIF
900 910 920 930 940 950
cry1a-105.pe EELEGRIFTAFSLYDARNVKNKGFNNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAEVS
960 970 980 990 1000 1010
142765 EELEGRIFTAFSLYDARNVKNKGFNNGLSCWNVKGVHDVEEQNNQSVLVVPEWEAEVS
960 970 980 990 1000 1010
cry1a-105.pe QEVYVCPGRGYILRTVAYKKGEGGCVTHIEENNTDELAFSCVVEEYPPNVTICNDY
1020 1030 1040 1050 1060 1070
142765 QEVYVCPGRGYILRTVAYKKGEGGCVTHIEENNTDELAFSCVVEEYPPNVTICNDY
1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNQEEYGGVATSRNRGVNAPSPADYASVYEEKSYTDGRRENCFNKGVRDYTPLPV
1080 1090 1100 1110 1120 1130
142765 TVNQEEYGGVATSRNRGVNAPSPADYASVYEEKSYTDGRRENCFNKGVRDYTPLPV
1080 1090 1100 1110 1120 1130
cry1a-105.pe GYVTELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
142765 GYVTELEYFPETDKVWIEIGETEGTFIVDSVELLMEE
1140 1150 1160 1170
cry1a-105.pe
NRAA:743635
743635 source="GENBANK_PROT" lepidopteran-specific protoxin
SCORES Init1: 4277 Initn: 6523 Opt: 6823 z-score: 7747.2 E(): 0
>NRAA:743635
initn: 6523 init1: 4277 opt: 6823 z-score: 7747.2 expect(): 0
Smith-Waterman score: 6823; 86.8% identity in 1179 aa overlap
(1-1177:1-1176)
cry1a-105.pe MDNPNINCEIPYNCLSNPEVEVLGGRIETGTYPIDISLTOQLLSEFVPGAGFVLGL
743635 MDNPNINCEIPYNCLSNPEVEVLGGRIETGTYPIDISLTOQLLSEFVPGAGFVLGL
10 20 30 40 50 60
cry1a-105.pe VDIWIGIFGFSQWDAFLVQIOLINQRIEFARNQAIISRLGLSNLYQIYAESFREWEAD
743635 VDIWIGIFGFSQWDAFLVQIOLINQRIEFARNQAIISRLGLSNLYQIYAESFREWEAD
70 80 90 100 110 120
cry1a-105.pe PTFNPALEEMRIQFNDMWSALTTAIPLLAVQYQVPLLSVYVQAAHLHSLVLRDVSFVGQ
130 140 150 160 170 180
142765 PTFNPALEEMRIQFNDMWSALTTAIPLLAVQYQVPLLSVYVQAAHLHSLVLRDVSFVGQ
130 140 150 160 170 180

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Product Characterization Center

cry1a-105.pe PTPALREEMRIQFNDWNSALTTAIPLEAVQNYQVPLLSVVOAANHLHSLVLRDVSVEGQ 130 140 150 160 170 180
5901703 PTPALREEMRIQFNDWNSALTTAIPLEAVQNYQVPLLSVVOAANHLHSLVLRDVSVEGQ 130 140 150 160 170 180

cry1a-105.pe RWGFDAAATNSRYNDLRLIGNYTDHVRWYNTGLERWVGPDSDWRVYRQFRELITV 190 200 210 220 230 240
5901703 RWGFDAAATNSRYNDLRLIGNYTDHVRWYNTGLERWVGPDSDWRVYRQFRELITV 190 200 210 220 230 240

cry1a-105.pe LDIVSLFPNYDSRTYPIRTVSQTLREIYNPVLENFDSGRGSAQIGESIRSPHLMIDL 250 260 270 280 290 300
5901703 LDIVSLFPNYDSRTYPIRTVSQTLREIYNPVLENFDSGRGSAQIGESIRSPHLMIDL 250 260 270 280 290 300

cry1a-105.pe NSITITVDHRGEYVWSGHOIMASPVGFSGPEFTPLXGTWGNAAPOQRIVAQLGQVVR 310 320 330 340 350 360
5901703 NSITITVDHRGEYVWSGHOIMASPVGFSGPEFTPLXGTWGNAAPOQRIVAQLGQVVR 310 320 330 340 350 360

cry1a-105.pe TLSTLYRRP-FNIGINNQQLSVLDTGTEFAYGT-SSNLPASVYRKSGTVDLSLDEIPPQNN 370 380 390 400 410
5901703 TLSTLYRRP-FNIGINNQQLSVLDTGTEFAYGT-SSNLPASVYRKSGTVDLSLDEIPPQNN 370 380 390 400 410

cry1a-105.pe NVPRQFQSHRSHVSMFRSGFSSNSVSIIRAPMSWIRHRAERNIIASDITQIPLVK 420 430 440 450 460 470
5901703 NVPRQFQSHRSHVSMFRSGFSSNSVSIIRAPMSWIRHRAERNIIASDITQIPLVK 420 430 440 450 460 470

cry1a-105.pe AHTLQSGTTVVRGFTGGDILRRTSQGGPAYTIVNINQQLPQRYRIRYASTTNLRIT 480 490 500 510 520 530
5901703 AHTLQSGTTVVRGFTGGDILRRTSQGGPAYTIVNINQQLPQRYRIRYASTTNLRIT 480 490 500 510 520 530

cry1a-105.pe VTVAGERIFAGQFNKMTDGLTQSFYSATINTAFTFPMSSQSFVSGADTFSSGNEVY 540 550 560 570 580 590
5901703 VTVAGERIFAGQFNKMTDGLTQSFYSATINTAFTFPMSSQSFVSGADTFSSGNEVY 540 550 560 570 580 590

cry1a-105.pe IDREFPVTATLEAEYNLEAQAQAVNALFTSNOLGLKNTVTDYHDQVSNLVTLSDE 600 610 620 630 640 650
5901703 IDREFPVTATLEAEYNLEAQAQAVNALFTSNOLGLKNTVTDYHDQVSNLVTLSDE 600 610 620 630 640 650

cry1a-105.pe FCLDEKRELSEKVKHAKLSDERNLLQDSNFKDINRQPERGWSGSGTITIGGGDDVFKN 660 670 680 690 700 710
5901703 FCLDEKRELSEKVKHAKLSDERNLLQDSNFKDINRQPERGWSGSGTITIGGGDDVFKN 660 670 680 690 700 710

cry1a-105.pe YVTLSGTFDCPTLYLYQKIDSKLAKTRFYQLRGYIEDSDLEYIRYNKAKHTVNP 720 730 740 750 760 770
5901703 YVTLSGTFDCPTLYLYQKIDSKLAKTRFYQLRGYIEDSDLEYIRYNKAKHTVNP 720 730 740 750 760 770

cry1a-105.pe GTGSLWPLSAQSPIGKCEPNRCAPHLENNPDLDCSCRDGKCAHSHHFSLDIDVGCTD 780 790 800 810 820 830
5901703 GTGSLWPLSAQSPIGKCEPNRCAPHLENNPDLDCSCRDGKCAHSHHFSLDIDVGCTD 780 790 800 810 820 830

cry1a-105.pe LNEEDLGWVIFIKITQDGHARLGNLFLEEKPLVGEALARKVRAEKWKARDKREKLEWETN 840 850 860 870 880 890
5901703 LNEEDLGWVIFIKITQDGHARLGNLFLEEKPLVGEALARKVRAEKWKARDKREKLEWETN 840 850 860 870 880 890

cry1a-105.pe IVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHSIRAYLPELSVIPGVNAAIF 900 910 920 930 940 950
5901703 IVYKEAKESVDALFVNSQYDQLQADTNIAHAAADKRVHSIRAYLPELSVIPGVNAAIF 900 910 920 930 940 950

cry1a-105.pe EELEGRIFTAFSLYDARVINKGDFNNGLSQWVAGHVDVEEQNNQSRSLVVPPEWAEVYS 960 970 980 990 1000 1010
5901703 EELEGRIFTAFSLYDARVINKGDFNNGLSQWVAGHVDVEEQNNQSRSLVVPPEWAEVYS 960 970 980 990 1000 1010

cry1a-105.pe QEVRCVCGRYILRVYAKYEGGEGCVTTHEENNTDELKFSNCVBEETPNNTVTCNDY 1020 1030 1040 1050 1060 1070
5901703 QEVRCVCGRYILRVYAKYEGGEGCVTTHEENNTDELKFSNCVBEETPNNTVTCNDY 1020 1030 1040 1050 1060 1070

cry1a-105.pe TVNOEEYGGVTSRNGNEAPSVADYASVVEEKSQYTDGRRNCPCEFNAGYDTPLPV 1080 1090 1100 1110 1120 1130
5901703 TVNOEEYGGVTSRNGNEAPSVADYASVVEEKSQYTDGRRNCPCEFNAGYDTPLPV 1080 1090 1100 1110 1120 1130

cry1a-105.pe GYVTKELVFPETDKVWIEIGETEGTFIVDSVELLMEE 1140 1150 1160 1170
5901703 GYVTKELVFPETDKVWIEIGETEGTFIVDSVELLMEE 1140 1150 1160 1170

cry1a-105.pe
NRAA:67089177
67089177 source="GENBANK_PROT" Cry1Aa [Bacillus thuringiensis]

SCORES Initl: 4264 Initn: 6450 Opt: 6750 z-score: 7664.3 E(): 0
>NRAA:67089177
Initn: 6450 Initl: 4264 opt: 6750 z-score: 7664.3 expect(): 0
Smith-Waterman score: 6750; 86.7% identity in 1166 aa overlap
(8-1171:1-1163)

cry1a-105.pe MDNNPNINCEPICNCLSNPEVEVLGGRIETGTPIDISLSTQFLSEFVPGAGFVLGL 10 20 30 40 50 60
67089177 NECIPNCLSNPEVEVLGGRIETGTPIDISLSTQFLSEFVPGAGFVLGL 10 20 30 40 50

cry1a-105.pe VDIIWGIFGSDMAFLVIOEQLINQRIEFARNOAISREGLSNLQIYIAESFREWEAD 70 80 90 100 110 120
67089177 VDIIWGIFGSDMAFLVIOEQLINQRIEFARNOAISREGLSNLQIYIAESFREWEAD 70 80 90 100 110 120

cry1a-105.pe	780 790 800 810 820 830	GTGSLWPLSAQSPGKCGEPNRCAPHELEWEDDCSCROGECACAHSHHFLSDIDVGCCTD	
67089177	780 790 800 810 820 830	GTGSLWPLSAQSPGKCGEPNRCAPHELEWEDDCSCROGECACAHSHHFLSDIDVGCCTD	
cry1a-105.pe	840 850 860 870 880 890	LNEDLGVWIFKIKTQDGHARLGNLEFLEKPLVGEALAPKAEKRWDRKRELEWETN	
67089177	840 850 860 870 880 890	LNEDLGVWIFKIKTQDGHARLGNLEFLEKPLVGEALAPKAEKRWDRKRELEWETN	
cry1a-105.pe	900 910 920 930 940 950	IVYKEAKESVDALFVNSQYDQLQADNTNIAHAAKRVHSIREAYLPFLSVIPGVNAIIF	
67089177	900 910 920 930 940 950	IVYKEAKESVDALFVNSQYDQLQADNTNIAHAAKRVHSIREAYLPFLSVIPGVNAIIF	
cry1a-105.pe	960 970 980 990 1000 1010	EELEGRIFTAFSLDARNVKNGDFNNGLSCHNVKGVHDVVEECONORSVLVVPWEAEVS	
67089177	960 970 980 990 1000 1010	EELEGRIFTAFSLDARNVKNGDFNNGLSCHNVKGVHDVVEECONORSVLVVPWEAEVS	
cry1a-105.pe	1020 1030 1040 1050 1060 1070	QEVRCVCGGYILRTAYKEGYGEGCVTHIEENNTDELAKFSNCVEEYIPNNTVTCNDY	
67089177	1020 1030 1040 1050 1060 1070	QEVRCVCGGYILRTAYKEGYGEGCVTHIEENNTDELAKFSNCVEEYIPNNTVTCNDY	
cry1a-105.pe	1080 1090 1100 1110 1120 1130	TVNOEQYGSYTSYRNGYNAPSVPADYASVYEEKSYTDGRNPNCFNMGYRDYTPLPV	
67089177	1080 1090 1100 1110 1120 1130	TVNOEQYGSYTSYRNGYNAPSVPADYASVYEEKSYTDGRNPNCFNMGYRDYTPLPV	
cry1a-105.pe	1140 1150 1160 1170	GVNKEEIPPEIDYVNGEESYFVDSVE	
67089177	1140 1150 1160 1170	GVNKEEIPPEIDYVNGEESYFVDSVE	
cry1a-105.pep		21239436 source="GENBANK PROT" crystal protein of CryIaA13 Bacillus thuringiensis serovar sotolgi 4666284 db BAA77211.1 RefSeq CryIaA13 protein [Bacillus thuringiensis]	
NRAA:21239436		Initl: 3711 Initn: 6423 Opt: 6722 Z-score: 7632.3 (1180 aa)	
		Initn: 6423 Initl: 3711 opt: 6722 Z-score: 7632.3 (1180 aa)	
		Smith-Waterman score: 6722; 85.3% identity in 1183 aa overlap (1-1177:1-1180)	
cry1a-105.pe	10 20 30 40 50 60	MDNNPNINECIPNCLSPNPEVVLGGRIETGYTPIDISLSTFLLSEVFCAGNLCGL	
21239436	10 20 30 40 50 60	MDNNPNINECIPNCLSPNPEVVLGGRIETGYTPIDISLSTFLLSEVFCAGNLCGL	
cry1a-105.pe	70 80 90 100 110 120	VDTIIGWIFGFSQWDAFLVQIEQLINQRIEERFARNOAISRLGSLNLYQIVAESFREWEAD	
67089177	70 80 90 100 110 120	VDTIIGWIFGFSQWDAFLVQIEQLINQRIEERFARNOAISRLGSLNLYQIVAESFREWEAD	

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21239436 VDIINGIPQWDAFLVLEQLINORIEEFARNOASRLGLESLNLYQIYAESPFEAD 70 80 90 100 110 120
cry1a-105.pe PTNPALREEMRIQFNDWNSALTAIPFAVQNYQVPLLSVYVOANLHLSVLURDVSFQG 130 140 150 160 170 180
21239436 PTNPALREEMRIQFNDWNSALTAIPFAVQNYQVPLLSVYVOANLHLSVLURDVSFQG 130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRYNDLTELIGNYTDHAVRYNTGLERVWGPDSRDVIRYNQFRRELITV 190 200 210 220 230 240
21239436 RWGFDAAATINSRYNDLTELIGNYTDHAVRYNTGLERVWGPDSRDVIRYNQFRRELITV 190 200 210 220 230 240
cry1a-105.pe LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDCSFRGSAQIGIESIRSPHLMIL 250 260 270 280 290 300
21239436 LDIVSLFPNYSRTYPIRTVSQLTREIYTNPVLENFDCSFRGSAQIGIESIRSPHLMIL 250 260 270 280 290 300
cry1a-105.pe NSITTYDHRGEYFWGSHQIMASPVGFSGPEFTPLVGTNGMNAAPQRIVAQLQGUYR 310 320 330 340 350 360
21239436 NSITTYDHRGEYFWGSHQIMASPVGFSGPEFTPLVGTNGMNAAPQRIVAQLQGUYR 310 320 330 340 350 360
cry1a-105.pe TLSTLYRPP-ENIGINNQOISVLDTGEFAYGT-SSNLPASVAVKSGTSDVDEIPPONN 370 380 390 400 410
21239436 TLSTLYRPP-ENIGINNQOISVLDTGEFAYGT-SSNLPASVAVKSGTSDVDEIPPONN 370 380 390 400 410
cry1a-105.pe NVPPRQGFHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAAFNNIASDSITQIPLVK 420 430 440 450 460 470
21239436 NVPPRQGFHRLSHVSMFRSGFNSSVSIIRAPMFSWIHRSAAFNNIASDSITQIPLVK 420 430 440 450 460 470
cry1a-105.pe AHTLQSGTTVVRGPGFTGDIIRTSGGPFAYTIYININGQLPQRYRARIYASTNLRIRY 480 490 500 510 520 530
21239436 AHTLQSGTTVVRGPGFTGDIIRTSGGPFAYTIYININGQLPQRYRARIYASTNLRIRY 480 490 500 510 520 530
cry1a-105.pe VTVAGERIFAGQFNTMDTGPTLFQSFVSATINTAFTFPMSSQSFVVGADTFSSGNEVY 540 550 560 570 580 590
21239436 VTVAGERIFAGQFNTMDTGPTLFQSFVSATINTAFTFPMSSQSFVVGADTFSSGNEVY 540 550 560 570 580 590
cry1a-105.pe IDRFELIPVATILEAEYNLERAKAVNAFTSTNQLGKTNVTDYHIDQVSNLVLSDE 600 610 620 630 640 650
21239436 IDRFELIPVATILEAEYNLERAKAVNAFTSTNQLGKTNVTDYHIDQVSNLVLSDE 600 610 620 630 640 650
cry1a-105.pe FCLDEKELSEKVKHAKRLSDERNLLODSNFKDINQPERGWSGTITIQGGDVFKEN 660 670 680 690 700 710
21239436 FCLDEKELSEKVKHAKRLSDERNLLODSNFKDINQPERGWSGTITIQGGDVFKEN 660 670 680 690 700 710
cry1a-105.pe VYTLSGTFDECPYLYQKIDESKKAFTRYQLRGVIEDSQDLEIYSIRYNAKHETVNP 720 730 740 750 760 770
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21239436 VYTLSGTFDECPYLYQKIDESKKAFTRYQLRGVIEDSQDLEIYSIRYNAKHETVNP 720 730 740 750 760 770
cry1a-105.pe GTGSLWPLSASQPIGKCGENRCAPHEWNPDLCSCRDGEXCAHSHHFLSLDIDVGCTD 780 790 800 810 820 830
21239436 GTGSLWPLSASQPIGKCGENRCAPHEWNPDLCSCRDGEXCAHSHHFLSLDIDVGCTD 780 790 800 810 820 830
cry1a-105.pe LNEDLGWVWIFKIKITQDGHARLGNLEFLEEKPLVGEALARKAERKAKRDKSEKLEMETN 840 850 860 870 880 890
21239436 LNEDLGWVWIFKIKITQDGHARLGNLEFLEEKPLVGEALARKAERKAKRDKSEKLEMETN 840 850 860 870 880 890
cry1a-105.pe IVYKEAKESVDALFVNSQYDRLOADTNIAIHAAKRVHSIRAYLPFLSVIPGVNAALF 900 910 920 930 940 950
21239436 IVYKEAKESVDALFVNSQYDRLOADTNIAIHAAKRVHSIRAYLPFLSVIPGVNAALF 900 910 920 930 940 950
cry1a-105.pe EELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNORSVLVPEWEAEVS 960 970 980 990 1000 1010
21239436 EELEGRIFTAFSLYDARNVKNKGDFNNGLSQWNVKGVHDVEEQNNORSVLVPEWEAEVS 960 970 980 990 1000 1010
cry1a-105.pe QEVVPCPGGYILRTVAYKEGEGCVTTHEENNTDELKFSNCVEEYIPNNVTVCNDY 1020 1030 1040 1050 1060 1070
21239436 QEVVPCPGGYILRTVAYKEGEGCVTTHEENNTDELKFSNCVEEYIPNNVTVCNDY 1020 1030 1040 1050 1060 1070
cry1a-105.pe TVNQEEYGAYTSRNRGNEA---FSVPADVASVYEKSYTDORRENCFENRGYDYT 1080 1090 1100 1110 1120 1130
21239436 TVNQEEYGAYTSRNRGNEA---FSVPADVASVYEKSYTDORRENCFENRGYDYT 1080 1090 1100 1110 1120 1130
cry1a-105.pe PLPVGYVTKLEYFFETDKWIEIGETEGTFIVDSVELLLMEE 1140 1150 1160 1170
21239436 PLPVGYVTKLEYFFETDKWIEIGETEGTFIVDSVELLLMEE 1140 1150 1160 1170
cry1a-105.pe MNDPNINECIPVNCINLSNEPEVLGGRIETGTPIDISLSTQFLLSEFPVAGFVLG 1180 1190 1200
21239436 MNDPNINECIPVNCINLSNEPEVLGGRIETGTPIDISLSTQFLLSEFPVAGFVLG 1180 1190 1200
```

37781497 source="GENBANK_PROT" Cry1Aa (Bacillus thuringiensis)

SCORES Initl: 3697 Inltn: 6408 Opt: 6707 z-score: 7615.3 E(): 0
>>NRAA:37781497
Initl: 6408 Inltn: 3697 Opt: 6707 z-score: 7615.3 expect(): 0
Smith-Waterman score: 6707; 85.1% identity in 1183 aa overlap
(1-1177;1-1180)

cry1a-105.pe MNDPNINECIPVNCINLSNEPEVLGGRIETGTPIDISLSTQFLLSEFPVAGFVLG 10 20 30 40 50 60
37781497 MNDPNINECIPVNCINLSNEPEVLGGRIETGTPIDISLSTQFLLSEFPVAGFVLG 10 20 30 40 50 60

cry1a-105.pe VDIWGIFGSPQDAFLVQIEQLINQRIEFAFNQASIRLEGSLNLYQIYAESFREWAD 120
5669035 VDIWGIFGSPQDAFLVQIEQLINQRIEFAFNQASIRLEGSLNLYQIYAESFREWAD 120
cry1a-105.pe PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLVDVSFGQ 180
5669035 PTNPALREEMRIQFNDMNSALTTAIPLFAVQNYQVPLLSVYVQAANLHLSVLVDVSFGQ 180
cry1a-105.pe RMGFDAATINRNDLTRLLGNVTHAVRWNTGLERWGPDSRDWRINQPRRELITLV 240
5669035 RMGFDAATINRNDLTRLLGNVTHAVRWNTGLERWGPDSRDWRINQPRRELITLV 240
cry1a-105.pe LDIVSLFPNYSRTPRTVTSQLTREIYNPVLENFDSRGSAGIEGSRPHLMDIL 300
5669035 LDIVSLFPNYSRTPRTVTSQLTREIYNPVLENFDSRGSAGIEGSRPHLMDIL 300
cry1a-105.pe NSITITDAHREYVWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAAQLQGQVIR 360
5669035 NSITITDAHREYVWSGHQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVAAQLQGQVIR 360
cry1a-105.pe TLSSTLYRPP-FNIGINNQQLSVLDGTEPAVCT-SSNLPSAVRVKSGTSDSDLEIPPONN 410
5669035 TLSSTLYRPP-FNIGINNQQLSVLDGTEPAVCT-SSNLPSAVRVKSGTSDSDLEIPPONN 410
cry1a-105.pe NVPPRGQFSHLRSHVMSFRSGFSNVSIIIRAPMFSWIRHSAFNIIIASDITQIPLVK 470
5669035 NVPPRGQFSHLRSHVMSFRSGFSNVSIIIRAPMFSWIRHSAFNIIIASDITQIPLVK 470
cry1a-105.pe AHTLQSGITVVRGPGFTGGDILRRTSGGPFATYINWQGPQRYRARIYASTTNLRIV 530
5669035 AHTLQSGITVVRGPGFTGGDILRRTSGGPFATYINWQGPQRYRARIYASTTNLRIV 530
cry1a-105.pe VTVAGERIPFAGQFNKTMGTDLPTLFOSFSYATINTAFTFPMSSOSFTVGADTFSSGNEVY 590
5669035 VTVAGERIPFAGQFNKTMGTDLPTLFOSFSYATINTAFTFPMSSOSFTVGADTFSSGNEVY 590
cry1a-105.pe IDREFIPVATLEAEVNLERAQKAVNALFTNQLGKTMTVDYHIDQVSNLVTLSDE 650
5669035 IDREFIPVATLEAEVNLERAQKAVNALFTNQLGKTMTVDYHIDQVSNLVTLSDE 650
cry1a-105.pe FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTITIQGGDVFKEN 710
5669035 FCLDEKRELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWGSGTITIQGGDVFKEN 710

cry1a-105.pe VYTLSTGTFDECPYLYOKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNV 720
5669035 VYTLSTGTFDECPYLYOKIDESKLFKAFTRYQLRGYIEDSQDLEIYSIRYNAKHETVNV 720
cry1a-105.pe GTGSLWPLSASQSPIGKCGEPNRCAPHLEWPDLDSCSRDGEKCAHSHHFSLDIDVGCTD 830
5669035 GTGSLWPLSASQSPIGKCGEPNRCAPHLEWPDLDSCSRDGEKCAHSHHFSLDIDVGCTD 830
cry1a-105.pe LNEDLGWVIFKIKITQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWDRKREKLEMETN 890
5669035 LNEDLGWVIFKIKITQDGHARLGNLEFLEEKPLVGEALARKVRAEKKWDRKREKLEMETN 890
cry1a-105.pe IVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHSIREAYLPESLVPVGNAAIF 950
5669035 IVYKEAKESVDALFVNSQYDQLOADNTIAMHAADKRVHSIREAYLPESLVPVGNAAIF 950
cry1a-105.pe EELEGRIFTAFSLDARNVKNKGDFNGLSCMNKGVHVDVEEQNNORSVLVVPWEAEVS 1010
5669035 EELEGRIFTAFSLDARNVKNKGDFNGLSCMNKGVHVDVEEQNNORSVLVVPWEAEVS 1010
cry1a-105.pe QEVYVCPGEGYLLRVTAKEGYGECVTHETENNTDELKFSNCVEEIVPNNVTYNDY 1070
5669035 QEVYVCPGEGYLLRVTAKEGYGECVTHETENNTDELKFSNCVEEIVPNNVTYNDY 1070
cry1a-105.pe TVNQEEYGGAYTSRNRGYNAPSPADYASVYEEKSYTDGRRNCPFNRGYRDYTPLV 1130
5669035 TVNQEEYGGAYTSRNRGYNAPSPADYASVYEEKSYTDGRRNCPFNRGYRDYTPLV 1130
cry1a-105.pe GYVTKLETFPPTDKWIEIGETGTFIVDSVELLLMEE 1170
5669035 GYVTKLETFPPTDKWIEIGETGTFIVDSVELLLMEE 1170
cry1a-105.pe GYVTKALEYFPPTDKWIEIGETGTFIVDSVELLLMEE 1170
5669035 GYVTKALEYFPPTDKWIEIGETGTFIVDSVELLLMEE 1170
8469152 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAG (INSECTICIDIAL
DELTA-ENDOTOXIN CRYIA(G)) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (134 KDA CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" source="swissprot_prot"
version="NA type="PRT
SCORES Initl: 3950 Initn: 6267 Opt: 6563 z-score: 7451.7 E(): 0
>>SW:8469152
Initn: 6267 Initl: 3950 Opt: 6563 z-score: 7451.7 expect(): 0
Smith-Waterman score: 6563; 84.0% identity in 1183 aa overlap
(1-1177:1-1176)
10 20 30 40 50 60

cry1a-105.pe MONNNINECNPNNSNBEVEVLGGRIETGYTPIDISLSTOFLSEFVPGAGVLGL
8469152 MONNNINECNPNNSNBEVEVLGGRIETGYTPIDISLSTOFLSEFVPGAGVLGL
cry1a-105.pe VDLINGLSPQWMAA 80 100 110 120
8469152 VDLINGLSPQWMAA 80 100 110 120
cry1a-105.pe PTNPALREEMRIQFNDMNSALTTA 130 140 150 160 170 180
8469152 PTNPALREEMRIQFNDMNSALTTA 130 140 150 160 170 180
cry1a-105.pe RWGFDAAATINSRYNDLTRLLGNTHDAVRWNTGSRNGEDSDWIRVYNRRRLNTV
8469152 RWGFDAAATINSRYNDLTRLLGNTHDAVRWNTGSRNGEDSDWIRVYNRRRLNTV
cry1a-105.pe LDIVLSPFYNDSTVPIRTVYSQLTRITVNPVLENFDSFGSAQIGESIRSLMDI
8469152 LDIVLSPFYNDSTVPIRTVYSQLTRITVNPVLENFDSFGSAQIGESIRSLMDI
cry1a-105.pe NSITIVTDAHRGEYVWGHQIMASPVGSGPEFTPLPYGTMGNAPQORIVAQCGYR
8469152 NSITIVTDAHRGEYVWGHQIMASPVGSGPEFTPLPYGTMGNAPQORIVAQCGYR
cry1a-105.pe TLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYKSGTVDLSLDEIPPONN
8469152 TLSTLYRRP-FNIGINNQLSVLDGTEFAYGT-SSNLPSAVYKSGTVDLSLDEIPPONN
cry1a-105.pe NVPPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSW----IHRSAEFNNIIASDSITOI
8469152 NVPPROGFSHRLSHVMSFRSGFNSSVSIIRAPMFSW----IHRSAEFNNIIASDSITOI
cry1a-105.pe PLVKAHLQSGTIVVRGCGFTGGDILARTSGGPFATVINGQLPQRYEARIRYASTTN
8469152 PLVKAHLQSGTIVVRGCGFTGGDILARTSGGPFATVINGQLPQRYEARIRYASTTN
cry1a-105.pe LRIYVTVAGERIFAGQNKMTDGLPTFOSTSYATINTAFTPMSSQSFVAGADFSGG
8469152 LRIYVTVAGERIFAGQNKMTDGLPTFOSTSYATINTAFTPMSSQSFVAGADFSGG
cry1a-105.pe NEVVIDRFLIPVTATLEAYNLERAQKAVNALFTSTNGLKNTVDTHIDQVSNLVTY
8469152 NEVVIDRFLIPVTATLEAYNLERAQKAVNALFTSTNGLKNTVDTHIDQVSNLVTY

cry1a-105.pe LSDEFCLDEKELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWSGTGTTIOGGDDV
8469152 LSDEFCLDEKELSEKVKHAKRLSDERNLQDSNFKDINRQPERGWSGTGTTIOGGDDV
cry1a-105.pe FXENVVTLSGTFDECYPTLYQKIDESKKAFTYQIRGVIEDSQDLEIYSIRNAKHET
8469152 FXENVVTLSGTFDECYPTLYQKIDESKKAFTYQIRGVIEDSQDLEIYSIRNAKHET
cry1a-105.pe VNVPGTGSILWPLSQAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLDDV
8469152 VNVPGTGSILWPLSQAQSPIGKCGEPNRCAPHLEWNPDLDCSCRDGKCAHSHHPSLDDV
cry1a-105.pe GCTDNLNEDLGVMVIFKIKTODGHARLGNLFLEKPLVGEALARVKRAEKKWRDKREKLE
8469152 GCTDNLNEDLGVMVIFKIKTODGHARLGNLFLEKPLVGEALARVKRAEKKWRDKREKLE
cry1a-105.pe WETNIVYKEAKESVDALFVNSQYDQLQADTNAMTAMHAAKRVHSIREAYLPSELSVPGVN
8469152 WETNIVYKEAKESVDALFVNSQYDQLQADTNAMTAMHAAKRVHSIREAYLPSELSVPGVN
cry1a-105.pe AATPTEGRIETAFSLDARNVKNGDNNGLSCWNVKGVHVEEQQNORSVLAVPEWE
8469152 AATPTEGRIETAFSLDARNVKNGDNNGLSCWNVKGVHVEEQQNORSVLAVPEWE
cry1a-105.pe AAVSQVAVCPGCGVPRVAVYKGYGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVT
8469152 AAVSQVAVCPGCGVPRVAVYKGYGEGCVTHIEINNTDELKFSNCVEEIIYPNNTVT
cry1a-105.pe CNDITVNOEYGGNTSNRGNMAYADYASVEEYSDGRRNCPENCFNRGPDYT
8469152 CNDITVNOEYGGNTSNRGNMAYADYASVEEYSDGRRNCPENCFNRGPDYT
cry1a-105.pe PLPGVYVTKALEYFFETDKWIEGEGEFTFIVDVEEALMEE
8469152 PLPGVYVTKALEYFFETDKWIEGEGEFTFIVDVEEALMEE
cry1a-105.pe NRAA:8469152
8469152 source="GENBANK PROT" Pesticidal crystal protein cry1Aa (Insecticidal
delta-endotoxin CryIA(g)) (Crystalline entomocidal protoxin) (117 kDa crystal
protein)gi|5669019|gb|AAD46137.1| lepidoteran-specific toxin [Bacillus
thuringiensis]
SCORES Initl: 3950 Initn: 6267 Opt: 6563 z-score: 7451.7 E(): 0
>NRAA:8469152
Initn: 6267 Initl: 3950 Opt: 6563 z-score: 7451.7 expect(): 0

Smith-Waterman score: 6563; 84.0% identity in 1183 aa overlap (1-1177:1-1176)			
cryla-105.pe	MDNNPNEICIPNCLNSFEVLGGRIETGTPIDISLSUTFLSLFVPGAGFVLGL	10 20 30 40 50 60	
8469152	MDNNPNEICIPNCLNSFEVLGGRIETGTPIDISLSUTFLSLFVPGAGFVLGL	10 20 30 40 50 60	
cryla-105.pe	VDIWIGFGSQMDALVQLINQRIEERFARNQALSRLEGLSNLYQIYAESFREWAD	70 80 90 100 110 120	
8469152	VDIWIGFGSQMDALVQLINQRIEERFARNQALSRLEGLSNLYQIYAESFREWAD	70 80 90 100 110 120	
cryla-105.pe	PTNPALREEMRIQFNDMSALTTAIPFAVQNVQVPLLSVYVQAAHLHLSVLRDVSFQG	130 140 150 160 170 180	
8469152	PTNPALREEMRIQFNDMSALTTAIPFAVQNVQVPLLSVYVQAAHLHLSVLRDVSFQG	130 140 150 160 170 180	
cryla-105.pe	RMGFDAATINSRYNDLIRLIGNYDIAVRWNTGLERVWCPDSRWIRYQFRRELTLTV	190 200 210 220 230 240	
8469152	RMGFDAATINSRYNDLIRLIGNYDIAVRWNTGLERVWCPDSRWIRYQFRRELTLTV	190 200 210 220 230 240	
cryla-105.pe	LDIVLFPNDSTRPIRTVSQLTREIYTNFVLENFPGSPGSAQIEGSIIRSPHLMIL	250 260 270 280 290 300	
8469152	LDIVLFPNDSTRPIRTVSQLTREIYTNFVLENFPGSPGSAQIEGSIIRSPHLMIL	250 260 270 280 290 300	
cryla-105.pe	NSITTYIDAHGEVYWSHQIMASPVGSGPEFTFPLGYGTMNAPQRIYVAQLQGVYR	310 320 330 340 350 360	
8469152	NSITTYIDAHGEVYWSHQIMASPVGSGPEFTFPLGYGTMNAPQRIYVAQLQGVYR	310 320 330 340 350 360	
cryla-105.pe	TLSSFLYLRP-FNIGINNQOLSLDGTETAYGT-SSNLPSAVYRSGTVDLSLDEIPPQNN	370 380 390 400 410	
8469152	TLSSFLYLRP-FNIGINNQOLSLDGTETAYGT-SSNLPSAVYRSGTVDLSLDEIPPQNN	370 380 390 400 410	
cryla-105.pe	VNPPRQGSFHLRSHVMSFSGSNSSVSIIRAPMSF-THRAEFNNIIASDSITQI	420 430 440 450 460 470	
8469152	VNPPRQGSFHLRSHVMSFSGSNSSVSIIRAPMSF-THRAEFNNIIASDSITQI	420 430 440 450 460 470	
cryla-105.pe	PLVAKHTLQSGTIVGRPGFTGDIILRETSGPEYATIVNINGQIPQRYRIYASTTN	480 490 500 510 520 530	
8469152	PLVAKHTLQSGTIVGRPGFTGDIILRETSGPEYATIVNINGQIPQRYRIYASTTN	480 490 500 510 520 530	
cryla-105.pe	LRIVTVAGERIFAGQNKMTDGLPTQSFVSATINTAFTPPMSQSFVGTGADTFSSG	540 550 560 570 580 590	
8469152	LRIVTVAGERIFAGQNKMTDGLPTQSFVSATINTAFTPPMSQSFVGTGADTFSSG	540 550 560 570 580 590	
cryla-105.pe	NEVYIDREFLIPVATILEAYNLERAQKVALETSTNQGLKNTVTDYHIDQVSNLVTV	600 610 620 630 640 650	
8469152	NEVYIDREFLIPVATILEAYNLERAQKVALETSTNQGLKNTVTDYHIDQVSNLVTV	600 610 620 630 640 650	

8469152	NEVYIDREFLIPVATILEAYNLERAQKVALETSTNQGLKNTVTDYHIDQVSNLVTV	600 610 620 630 640 650	
cryla-105.pe	LSDEFCLDEKREUSEKVKHAKESLDERNLLODSFNQPERGCMGSGTGITIQGGDDV	660 670 680 690 700 710	
8469152	LSDEFCLDEKREUSEKVKHAKESLDERNLLODSFNQPERGCMGSGTGITIQGGDDV	660 670 680 690 700 710	
cryla-105.pe	FRFENVTLTSGTDECYPTLYQKIDESKLKAFTRYQLRGVIEDSDLEIYIRYNAKHET	720 730 740 750 760 770	
8469152	FRFENVTLTSGTDECYPTLYQKIDESKLKAFTRYQLRGVIEDSDLEIYIRYNAKHET	720 730 740 750 760 770	
cryla-105.pe	VNVPTGSLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIV	780 790 800 810 820 830	
8469152	VNVPTGSLMPLSAQSPICKGCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHFSLDIV	780 790 800 810 820 830	
cryla-105.pe	GCTDNLDELGVWIFIKTKDGHARLGNLEFLEKPLVGEALARKRAEKWKRRKREKLE	840 850 860 870 880 890	
8469152	GCTDNLDELGVWIFIKTKDGHARLGNLEFLEKPLVGEALARKRAEKWKRRKREKLE	840 850 860 870 880 890	
cryla-105.pe	WETNIVYKEAKESVDALFVNSQVDQLQADTNIAHAAKRVHSIREAYLPESLVPQVN	900 910 920 930 940 950	
8469152	WETNIVYKEAKESVDALFVNSQVDQLQADTNIAHAAKRVHSIREAYLPESLVPQVN	900 910 920 930 940 950	
cryla-105.pe	AAIFELEGRIFAFSLYDARNVIRKGFNFNGLSCWNVGHVDVEEQNNQSRSLVVPWE	960 970 980 990 1000 1010	
8469152	AAIFELEGRIFAFSLYDARNVIRKGFNFNGLSCWNVGHVDVEEQNNQSRSLVVPWE	960 970 980 990 1000 1010	
cryla-105.pe	AEVSOEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNNTVT	1020 1030 1040 1050 1060 1070	
8469152	AEVSOEVRVCPGRGYILRVYAYKEGYGEGCVTTHEIENNTDELKFSNCVEEIIYPNNTVT	1020 1030 1040 1050 1060 1070	
cryla-105.pe	CNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEKSYTDGRRNPPCFNFRGYDYT	1080 1090 1100 1110 1120 1130	
8469152	CNDYTVNQEYGGAYTSRNRGYNEAPSVADYASVYEKSYTDGRRNPPCFNFRGYDYT	1080 1090 1100 1110 1120 1130	
cryla-105.pe	PLPVGKVTKELEVEPEPTDKVWIEIGETEGTFIVDSVELLIMEE	1140 1150 1160 1170	
8469152	PLPVGKVTKELEVEPEPTDKVWIEIGETEGTFIVDSVELLIMEE	1140 1150 1160 1170	
cryla-105.pep SW: 8469136			
8469136 description="PESTICIDIAL CRYSTAL PROTEIN CRYIAD (INSECTICIDIAL DELTA-ENDOTOXIN CRYIA (D)) (CRYSTALLINE ENTOMOCIDIAL PROTOXIN) (133 KDA CRYSTAL PROTEIN)." library="NA species="Bacillus thuringiensis serovar aizawai" source="swissprot_prot" version="NA type="PRT			

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~~cryIa-105.pe MDNNPNTNPNCLSPNPEVLGGRIETQVTDISLSLTFQLFSFVPGAGFVLGL
:
MEIMNNQQCPVNLNDTTEILGGRTYTPIDSSLTQFLFSFVPGAGFVLGL~~

```
cryla-105.pe VDIWGFSPQMDAFLVQIQFOLNRIEFPANRASRGLEGISNLYOIVYAFESREWAD  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |  
IDLWGFSPQMDAFLVQIQFOLNRIEFPANRQAISRLEGISNLYOIVYAFESREWAD
```

	130	140	150	160	170	180
cryla-105.pe	PTNPALREEMRIQFNDMSALTTAIPFAVONYQVLLSVVQANLHLSVLSVVFQ					
8469136	PTNPALTEEMRIQFNDMSALTTAIPFTVQYQVLLSVVQANLHLSVLSVVFQ					

	190	200	210	220	230	240
cry-ia-105.pe	RMGFDATINSRNDYD	TRUIGNYTHAVRWYNTGLERWVGDPD	SRDWRINQFPRFTLV			
	RMGFDVATINSRNDYD	TRUIGTYDYAVRWYNTGLERWVGDPD	SRDWRINQFPRFTLV			
846g136						

```

cryla-105.pe LDIVLFPNDSTYPIRTVSQLTREITYTPVLNFDSCFRGSAQGTESIRSPHMLD
                250 250 260 270 280 280
8469136 LDIVLFPNDSTYPIRTVSQLTREITYTPVLNFDSCFRGSAQGTESIRSPHMLD
                250 250 260 270 280 290 300

```

cryla-105.pe NSITIVDAHRGEYWGSHQINASPVGFSPETFFLYTGMGNAAPQOIRVLAQGLGGYV
 310 310 320 330 340 350
 8469136 NSITIVDHRGFWYSGHQITASPVGFAGPEFTFRYGTGMGNAAPV-LISTTGLGIFR
 310 310 320 330 340 350

```
cry1a-105.pe      TUSSTLYRPP-FNIGINQQVSLDGTGEFYAGT-SNNLSAVYKSTVDSDLETPQPN
8469136            |||||X|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
                        TUSSTPYRIILGNGPNNQLFVGTEFGFASLTADLSTPIYQRGTVDSDLDVIPQPN
360               370       380       390       400       410
```

	420	430	440	450	460	470
cr1a-105.pe	NVPPQGSFHLSHVMSFGFSSNSVITRAFWHSRAEFNIIASDITQIPLV					
8469136	SVPARAGFHLSHVTLMSQ-AGAVTVTRATFSWRHSRAEFSNLPSSQITQIPLTK					

[illegible][illegible]

```

cry1a-105.pe  IDRELIPVTAILEYNNLEAQNNAALFTTNGLKTNTDYHIDQVSNLVYLSDE
                  600      610      620      630      640      650
8469136      IERIEFPVFAEAYDLERAEQNAALFTTNGLKTNTDYHIDQVSNLVCELSGE
                  600      610      620      630      640      650

```

```

660      670      680      690      700      710
cryla-105.pe FCLDEKREISEKVKHAKLSLDERNLLQDNFKDINRPERGWSGSTITIQGGDVFVFN
|||||
8459136 FCLDEKREISEKVKHANLSLDERNLLQDNPFNGINRQPDRCWRGSTITIQGGDVFVFN
|||||
660      670      680      690      700      710

```

```

720      730      740      750      760
cryla-105.pe  VYTLSGTFDCEPTYLYQKIDSKLAFYQYRGYEDSOHLEIYIRNTKHTVNP
|||||
VYTLPGTFNCEPTYLYQKIDSKLAFYQYRGYEDSOHLEIYIRNTKHTVNP
770      780      790      800
8469136

```

```

      780      790      800      810      820      830
cry1a-105.pe GTGSIWPLSPQSTIGKCGEPNRCAPHEWNPDLJDCSRDGEKAHHHFSLLDVGCTD
8469136      :      :      :      :      :      :
GTGSIWPLSPVENVPIGKCGEPNRCAPQLEWNPDLJDCSRDGEKAHHHFSLLDVGCTD
      780      790      800      810      820      830

```

[illegible]

900 910 920 930 940 950
 BE IYVKAKESVDALFVNSQDQLQADTMIAMHAADKRVHREIYALPELSVIGVNAALF
 8469336 IYVKAKESVDALFVNSQDQLQADTMIAMHAADKRVHREIYALPELSVIGVNAALF
 900 910 920 930 940 950

cry1a-105-ps EELEGRITWASLSYDANITKQSGCNKGLSCWNVKGVHDVFEQNNQRSLVVPWEAEAYV
8469136 EELEGRITWASLSYDANITKQSGCNKGLSCWNVKGVHDVFEQNNQRSLVVPWEAEAYV
960 970 980 990 1000 1010

cry1a-105_pe QEVVPCPGGVILVNTAKEGYGGGCHHEINNDKLFKSNCEVEESLYPNNTVTCND
 8469136 QEVVPCPGGVILVNTAKEGYGGGCHHEINNDKLFKSNCEVEESLYPNNTVTCNDYDY

[illegible]

```

cryla-105.pe  PLPGVVTKELEYFPETDKVMTEIGTGTIVDSVLLMEE
8469136      1140      1150      1160      1170
PLPAGVVTKELEYFPETDKVMTEIGTGTIVDSVLLMEE

```

cryla-105.pep
NEAA_8469136
8469136 source="GENBANK_PROT" Pesticidal crystal protein cryIad (Insect

8469136 source="GENBANK PROT" Pesticidal crystal protein cry1Ad (Insecticidal

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MSL No. 20351
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8469136
TSIDGRPINQGNFSAFMSSGGNLOSGSFRTAGTTPNFNSNGSIFTLSAHVNSGNEVY

```

600      610      620      630      640      650
cryla-105.pe IDREFLIPVATLEARYNLEAQAQVNAALFTSNGLKTNVTDYHIDQVSNLVTVLSD
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
8469136 IERIEFPVATPEAYDLEAQAQVNAALFTSNGLKTNVTDYHIDQVSNLVTVLSDGE
      600      610      620      630      640      650

```

```

660      670      680      690      700      710
cryla-105.pe FCLDEKRELSKVKHAKLSDERNLLQDSNFQINRQPERMGWGSTITTOGGDDVFKEN
8469136 FCLDEKRELSKVKHAKLSDERNLLQDPNFRINRQPERMGWGSTITTOGGDDVFKEN

```

```

cry1a-105.pe      720 730 740 750 760 770
YVTVSGTFDCYTYLYQKIDESCCKAFTYQURGYEDSQBLEIYIRNAKHETVNPV
8469136          : : : : : : : : : : : : : : : : : : : : : :
YVTVPGTFNFCYTYLYQKIDESCCKAFTYQURGYEDSQBLEIYIRNAKHETVNPV

```

```

cry1a-105.pe  GTGSLWPLSAQSPIGKCGEPNRCAPHEWLPWFDLDGSCDRGCKAAHSHHSHHSLDIDVGCTD
                680      690      700      710      720      730      740      750      760      770      780      790      800      810      820      830
8469136      GTGSLWPLSVENPIGKCGEPNRCAPQLEWNPFDLDGSCDRGCKAAHSHHSHHSLDIDIGCTD
                780      790      800      810      820      830

```

```

cryla-105.pe  LNEIDGVWVIFKIKTODGHARGLNLEFLEBKPLVGSLARVKRAEKWROKREKLQVETN
8469136      LNEIDGVWVIFKIKTODGHARGLNLEFLEBKPLVGSLARVKRAEKWROKREKLQVETN
840          840      850      860      870      880      890

```

```

cry1a-105.pe  IVYKEAESVDALFVNSQYDQLQADTDIAIHAADRVHRSREAYLPELSVPVGVNAAIF
8469136       IVYKEAESVDALFVNSQYDRLQADTDIAIHAADRVHRSREAYLPELSVPVGVNAGIF

```

```

cryla-105.pe BELEGRTFTAFSLYDARNVINGNGLSCMNWKGVDEEQNNQSRSLVLPWPEAEVVS
8469136 BELEGRTFTAFSLYDARNVINGNGLSCMNWKGVDEEQNNHRSVLVLPWPEAEVVS
960 970 980 990 1000 1010

```

```

cryla-105.pe  QEVRCFGRGIIIRVTAYKEGSGCVGCVTHIEIDNTDELKFSNCVBEVVPNNVTCTNDY
8469136      QEVRCFGRGIIIRVTAYKEGSGCVGCVTHIEIDNTDELKFSNCVBEVVPNNVTCTNDY
1020         1020  1030  1040  1050  1060  1070

```

```

cryla-105.pe  TQNOEEYGGAYTSRNRGYNEA-----PSPVADYASVYEESYTDGRNPNCFNRGYRDTY
1080 1090 1100 1110 1120 1130
8469136      TANQEEYGGAYTSRNRGYSEYENSSIPAYAPVYEE-AVTDGRKENPCESNRKGYDTY
1080 1090 1100 1110 1120 1130

```

```

cry1a-105.pe  PLPAGYVTKLEVFPEPTDKVWIEIGETEGTFIVDSYELLMEE  1140 1150 1160 1170
8469136      PLPAGYVTKLEVFPEPTDKVWIEIGETEGTFIVDSYELLMEE  1140 1150 1160 1170

```

cry1a-l05.pap

© 19138

```

SCORES Init1: 4184 Initn: 5748 Opt: 5915 Z-score:
>SW:8459138
      Initn: 5748 Init1: 4184 Opt: 5915 Z-score: 6715.2 exp
Smith-Waterman score: 5915; 76.% identity (in 1184
[1-1177:1-1174])

```

cryla-105.pe MDNNPNINECIPYNCLSNPEVEVLGGERTETCTPDIISLS
 10 20 30 40 49
 8469138 MENNIQ-NQCVPYNCLNPEVEILNEER-STGNLPDIISLS

[illegible]

```
cryla-105.pe      FPNPALREEMRIQFNMDNSALTATPLFAVONYQPULLSVW  
                  :|::||::|::|::|::|::|::|::|::|::|:  
8469138          PNAQLREDVRIFRANTD DALITAINFTLTSFEIPLL SVW
```

cry1a-105.pe RWGFPDAATINSRNDLTRLIGNVTDHAVRWNTGLERVGE
 8469138 GWGLDIATVNNHNRNLINLIHRYTKHCLDITNQGLENLRTG
 180 190 200 210 220

```

280
270
260
250
240
cry1a-105.pe  LDIVSLFPNYDSRTYPIRTVSQLTREIYNPVLEN--FDGSGS
||||:|||||:|||||:|||||:|||||:|||||:|||||:
8469138      LDIVLFPNVDVRYPIQIOTSSQTLTREIYTSVIEDSPVSN
240 250 260 270 280

```

300 310 320 330
 cryla-105.pe ILNSITYTDAHGEYYWGGHQINASPVGSGPETTFPLLYCYV
 8469138 FNNSLFVTAETVRSQTVWGGH--LVSSRNATGNRINFPSYCYV
 300 310 320 330

360 370 380 390
 cryla-105.pe YRTLSSTLYRRPFNIGINNQQLSV-LDGTETAYGTSSNLPSF
 8469138 YRTLSDPVVRG---GFGNPHYVLGLRGVAFAQ-TGTN-HPTN 390
 160 370 380 390

cryIa-105.pe NNVPPRQGFHSRLSHVSMFRSGFNSSVSIRAPMFWSWIH
 :
 NSGAPWNDYSHVLNHVTFVRWPGEISGDSWRAPMFWSWTH

	480	490	500	510
cryla-105.pe	KAHTLQSGTTWVRGPGFTGDDILRRTSGGPAYTI	VNING		
8469138	KAHTLQSGTTWVRGPGFTGDDILRRTSGGPAYTI	VNING		

cryla-105.pe	540	550	560	570	580	590
8469138	540	550	560	570	580	590
cryla-105.pe	600	610	620	630	640	650
8469138	600	610	620	630	640	650
cryla-105.pe	660	670	680	690	700	710
8469138	660	670	680	690	700	710
cryla-105.pe	720	730	740	750	760	770
8469138	720	730	740	750	760	770
cryla-105.pe	780	790	800	810	820	830
8469138	780	790	800	810	820	830
cryla-105.pe	840	850	860	870	880	890
8469138	840	850	860	870	880	890
cryla-105.pe	900	910	920	930	940	950
8469138	900	910	920	930	940	950
cryla-105.pe	960	970	980	990	1000	1010
8469138	960	970	980	990	1000	1010
cryla-105.pe	1020	1030	1040	1050	1060	1070
8469138	1020	1030	1040	1050	1060	1070
cryla-105.pe	1080	1090	1100	1110	1120	1130
8469138	1080	1090	1100	1110	1120	1130
cryla-105.pe	1140	1150	1160	1170	1180	1190
8469138	1140	1150	1160	1170	1180	1190

cry1a-105.pep
NRAA:8469138

8469138 source="GENBANK PROT" Pesticidal crystal protein cry1Fa (Insecticidal delta-endotoxin CryIa) (Crystalline entomocidal protoxin) (134 kDa crystal protein)[gi|142758|gb|AAA22348.1| insecticidal crystal
protein][gi|142756|gb|AAA22347.1| cryIF

SCORES Initl: 4184 Initn: 5748 Opt: 5915 Z-score: 6715.2 E(): 0
>NRAA:8469138
Initn: 5748 Initl: 4184 opt: 5915 Z-score: 6715.2 expect(): (1174 aa)
Smith-Waterman score: 5915; 76.6% identity in 1184 aa overlap
(1-1177:1-1174)

cry1a-105.pep MNNPNNEICIPYCNLSNPEVEVLGGERIETGTPIDISLSTOFLSEFVPGAGFVLGL 60
10 20 30 40 50
8469138 MENNIQ-NQCVPNCLNNEVEILNEER-STGRPLDLISLSTRFLSEFVPGVGVAFGL 50
10 20 30 40 50

cry1a-105.pep VDLIWFPGSQWDAFLVQIQLNQRIEFPARNQAIKSLGLSLNLYQIYAEFREWAD 120
70 80 90 100 110
8469138 FDLIWFPTSDMSLFLQIQLRIETIERNRAITTLRLGLADSYEITYEALREWEAN 110
60 70 80 90 100 110

cry1a-105.pep PTNPALREEMRIQFNDMSALTATPLFVQNVQVPLISVYVQANHLNLSLVDVSFVG 180
130 140 150 160 170
8469138 FNNAGLRDVRIRFANTDDALITAINNFTLSFPLLSVYVQANHLNLSLVDVSFVG 170
120 130 140 150 160 170

cry1a-105.pep RWGFOAATINSRYNDLTRIGNYTHAVRWNTGLERWGPDSRDWIRYNQFRRETLTV 240
190 200 210 220 230
8469138 GWGLDIATVNNHYNRLNLIHRYTKHCLDTYQGLEMLRGTRQWARFNQFRDLTLTV 230
180 190 200 210 220 230

cry1a-105.pep LDIVSLFNDSTRYPRTVSQLTRITNPLEN--FDGSPRGAQIGESIRSPHLM 280
250 260 270 280 290
8469138 LDIVLFPNDVRYTPIQTSQTLREIYTSVIEDSPVSNANPNGFNRAEFGVAPPLMD 290
240 250 260 270 280 290

cry1a-105.pep ILNSTIYTAHREYVWGSQIMASPVGSGPEFTFPLYGTMGNAAPQQRIVLQGGV 350
300 310 320 330 340
8469138 FNNSLFVATVRSQIVWGGH--LVSSRNAGRIINPPSYGVF-NPGGAIWIEDPRPF 350
300 310 320 330 340 350

cry1a-105.pep YRLTSLSLYRPPNIGNINQQLSV-LDGTETAYGTSNLFPSAVYRKSQTVSDLSLPPQN 410
360 370 380 390 400
8469138 YRLTSDPVFVRG--GFGNPHVVLGRGVAQQ-TGTN-HTRTFNNSGTSIDLSLDEIPQD 410
360 370 380 390 400 410

cry1a-105.pep NNVPPRQFSRHSVSMFRSGFSNSVSIIRAPMFWTHRSAPFNIIADSIQTPLV 470
420 430 440 450 460
8469138 NSCAPWINDYSHLVNHTVFRWPFCEISGSDSWRAPMFWTHRSATPTNTIDPERITQPLV 470
420 430 440 450 460 470

cry1a-105.pep KAHTLQSGTTVWRGPGFTGGDLARTSGGPFAYTIIVNINGQLPQRYARIRYASTTNLRI 530
480 490 500 510 520
8469138 KAHTLQSGTTVWRGPGFTGGDLARTSGGPFAYTIIVNINGQLPQRYARIRYASTTNLRI 530
480 490 500 510 520 530

cry1a-105.pep YTVVAGERIFAGFNKMTMDTDPLOSFSYATINTAFTPMSSOSFTVGADTFSSGNEV 590
540 550 560 570 580
8469138 YTVVAGERIFAGFNKMTMDTDPLOSFSYATINTAFTPMSSOSFTVGADTFSSGNEV 590
540 550 560 570 580 590

cry1a-105.pep YIDRFELIPVTATLEAEYNLEERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYLS 650
600 610 620 630 640
8469138 YIDRFELIPVTATLEAEYNLEERAQKAVNALFTSTNQLGKTNVTDYHIDQVSNLVTYLS 650
600 610 620 630 640 650

cry1a-105.pep EFCLEKRELSSEKVKHAKLSDERNLQDSNFKDINRQPERGWGGSTGTTIQGGDDVFKE 710
660 670 680 690 700
8469138 EFCLEKRELSSEKVKHAKLSDERNLQDSNFKDINRQPERGWGGSTGTTIQGGDDVFKE 710
660 670 680 690 700 710

cry1a-105.pep NYVTLSGTDECPTLYLYKIDESKLKAFRIYQLRGYIEDSQDLIYIRINAKHETVNV 770
720 730 740 750 760
8469138 NYVTLSGTDECPTLYLYKIDESKLKAFRIYQLRGYIEDSQDLIYIRINAKHETVNV 770
720 730 740 750 760 770

cry1a-105.pep PGTSLMPLSAQSPICKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGCT 830
780 790 800 810 820
8469138 LGTSLMPLSAQSPICKCEPNRCAPHLEWNPDLDCSCRDGKCAHSHHSLDIDVGCT 830
780 790 800 810 820 830

cry1a-105.pep DLNEDLGVWIFIKITQDGHARLGNLEFLEKPLVGELARVKRAEKWKDRKLEWET 890
840 850 860 870 880
8469138 DLNEDLGVWIFIKITQDGHARLGNLEFLEKPLVGELARVKRAEKWKDRKLEWET 890
840 850 860 870 880 890

cry1a-105.pep NIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHSIREAYLPESVIPGVNAAI 950
900 910 920 930 940
8469138 NIVYKEAKESVDALFVNSQYDQLQADTNIAHAAKRVHSIREAYLPESVIPGVNAAI 950
900 910 920 930 940 950

cry1a-105.pep FEELEGRIFTAFSILYDARNVKNKGDFNNGLSKNVKGHVDFVEQNNQSRSLVVPWEAEV 1010
960 970 980 990 1000
8469138 FEELEGRIFTAFSILYDARNVKNKGDFNNGLSKNVKGHVDFVEQNNQSRSLVVPWEAEV 1010
960 970 980 990 1000 1010

cry1a-105.pep SQEVRCVCGRYLLRVATYKEGCGCVTHIENNTDELKFSNCVVEEYIPNNVTTCND 1070
1020 1030 1040 1050 1060
8469138 SQEVRCVCGRYLLRVATYKEGCGCVTHIENNTDELKFSNCVVEEYIPNNVTTCND 1070
1020 1030 1040 1050 1060 1070

cry1a-105.pep YTVNVEEYGGAYTSNRNGNEA----PSVPADYASVYEEKSYTDGRRNPCEFRGRDY 1130
1080 1090 1100 1110 1120
8469138 YTVNVEEYGGAYTSNRNGNEA----PSVPADYASVYEEKSYTDGRRNPCEFRGRDY 1130
1080 1090 1100 1110 1120 1130

Product Characterization Center

cyryla-105.pe TPUPGVYVKELEFPFPPKDKWIEIGETEGTIVDSVELLIMEE
1140 1150 1160 1170
8469138 TTPPACQVWKLEYFPPKDKWIEIGETESTFIVDSVELLIMEE
1140 1150 1160 1170

cyryla-105.pep
NRPA:17979619

17979619 source="GENBANK PROT" CryO34 [Bacillus
thuringiensis]gi|56397442|gb|BAW2936.1|dessectical delta endotoxin CryIa
[Bacillus thuringiensis]gi|1427592|gb|AAZ249.1| cryIIa)

SCORES Initl: 3527 Innt: 4823 Opt: 5549 Z-score: 6299.2 E(1.0
>NRPA:17979619
initn: 4823 initl: 3527 opt: 5549 Z-score: 6299.2 exp(1.0)
Smith-Waterman score: 5595; 72.7% identity in 1185 aa overlap
(1-1177:1-1171)

cyryla-105.pe MDNNPNINECIPNCLSPVEVLGGERITGYPTIDISLSLTOKLLSEVPCKAFVWSL
17979619 MEIVNNQCVPNCINLPENELDIERSNSTVAT-NIALEISLLASR-TPGSGILLG
10 20 30 40 50
70 80 90 100 110 120
cyryla-105.pe VDIWGFGPSWDALFQIQELINQRIBEFARNQAIRLEGSLNYOIYAESFREWEAD
17979619 FDAIWGISGPSOWDLFLQIELLDQIKIEEFARNQAIRLEGISLYGIYTEAFREWEAD
60 70 80 90 100 110
120 130 140 150 160 170
cyryla-105.pe PTNPALKEEMRIOFNDMSALTPIAIFAYONVOPLSVYVQANHLHLSVRDUSVFQG
17979619 PTNPALKEEMRIOFNDMSILVTAIPLFSYONVOPELVSVYVQANHLHLSVRDUSVFQG
120 130 140 150 160 170
cyryla-105.pe RWGFDAATINSRYNDLTRILIGNYTDHARVWNTGLERVGPD--RDWYRNQFRRLT
17979619 RWGFDAATINSRYNDLTRILPIYDYAVRWNTGLDR--PRTGLENWARFNQFRRLT
180 190 200 210 220 230
cyryla-105.pe LTVLIDVLSLFNFYDSRTYRTVSQTLREITYNPVENFDGSFRGSAQTGEGS-IRSPHL
17979619 ISVLDIISFFRDNYSRLYPITSSQLTRVYVDPVINIYDVAGSFENIENSARSPL
240 250 260 270 280 290
cyryla-105.pe MDILNSITIYTDHARGEYWWSHQIMASPGFSGPFTEFLGTGNNAQQRIVAQLOQ
17979619 MDPLNLITIDTLIRGHVHWAGRHTVSHFTG-SQVITTPQYGITANAPRRRTAFSTFP
300 310 320 330 340 350
cyryla-105.pe GV---YRTLSTLYLRFPFNIGINNQQLSVLDTGEFAVGTSSNLSAVYRKSGTVDLSDEI
17979619 GUNLFRTLNPSPPFRASENI-TPTLGINVOCGVTFIOPNNAEV---LYRSKGTVDLSNEL
360 370 380 390 400 410
cyryla-105.pe PPNVNVPPOGTSRHLHSVMFRSGFNSVSIIRAMPFWIHRSAEFNNI IASDSITQ
420 430 440 450 460 470

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1946622	PIDGEN -	SLVGSYHRSHVHLTRSYNYNLSL---	PTFWHHSATNTNTINPDITIO
		420	430 440 450 460
cryla-105.pe		480	490 500 510 520 530
	IPLVKAHTLQSGTIVVRGPGFTGDIILRSTGSGPAYTVINNGQLPQRYRARIYASTT		
	IPLVKATLQSGTIVVRGPGFTGDIILRSTGSGPAYTVINNGQLPQRYRARIYASTT		
1946622	IPLVKGRFLGGGTSYKVGPGTGDILRNTTIGEFVSYQVNIWNSPIQYRYLRRFYASSR		
	470	480 490 500 510 520	
cryla-105.pe		540	550 560 570 580 590
	NLRIVYVAGERIFAGQFNKMTMDGPTLQTSFVSATINTAFTPFMSQSFVTGADTFSS		
	DARITVAIGQIRVDMTLEKMETIGESLTSRFTSYTFNPFSGFRANPDITRIABELPFR		
1946622		530	540 550 560 570 580
cryla-105.pe		600	610 620 630 640 650
	GNEYVIDRELLIPVATLEAFYNIERAAQVNAVLTSTNQLGKTNTVDTYHDQVSNLVT		
	GGELYIDKIELLADATFEEDYLDERAAQVNAVLTSTNQLGKTNTVDTYHDQVSNLVE		
1946622		590	600 610 620 630 640
cryla-105.pe		660	670 680 690 700 710
	YLSDEFCLDEKRELESEKVKHAKRUSDERNULODSNFKDINRQPERGMSGGTGITTGGDD		
	CLSDEFCLDEKRELESEKVKHAKRUSDERNULODSNFKDINRQPERGMSGGTGITTGGDD		
1946622		630	640 650 660 670 680 690 700
cryla-105.pe		720	730 740 750 760 770
	VFKENYVTLGTFDECYPTLYIQKIDESKLKAFTRYQLRGYIEDSODLEIYSIRYNAKHE		
	VFKENYVTLGTFDECYPTLYIQKIDESKLKAFTRYQLRGYIEDSODLEIYSIRYNAKHE		
1946622		710	720 730 740 750 760
cryla-105.pe		780	790 800 810 820 830
	TVNVPGTGSJWPLSQAQSPGKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHSFLDID		
	TVNVPGTGSJWPLSQAQSPGKCGEPNRCAPHLEWNPDLDCSDRGKCAHSHHSFLDID		
1946622		770	780 790 800 810 820
cryla-105.pe		840	850 860 870 880 890
	VGCTDLNEDLGVWVIFKIKTODGHARLGNLEFLEKPLVGELARVKRAKKWRDKREKL		
	VGCTDLNEDLGVWVIFKIKTODGHARLGNLEFLEKPLVGELARVKRAKKWRDKREKL		
1946622		830	840 850 860 870 880
cryla-105.pe		900	910 920 930 940 950
	EWETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHSIREAYLPFELSVPFV		
	EWETNIVYKEAKESVDALFVNSQYDQLOADNTIAMIHAADKRVHSIREAYLPFELSVPFV		
1946622		890	900 910 920 930 940
cryla-105.pe		960	970 980 990 1000 1010
	NAALFEELEGRIFTAFSYDARNVYKNGDFNGLSCMWKGVHDVEEQNNRSLVAVPEW		
	NAALFEELEGRIFTAFSYDARNVYKNGDFNGLSCMWKGVHDVEEQNNRSLVAVPEW		
1946622		950	960 970 980 990 1000
cryla-105.pe		1020	1030 1040 1050 1060 1070
	EAEYSQEVRCRGGYILRVTAKEYGEGCVTHIEINNTDELKFSNCVVEEIVPNNTV		
	EAEYSQEVRCRGGYILRVTAKEYGEGCVTHIEINNTDELKFSNCVVEEIVPNNTV		
1946622		1010	1020 1030 1040 1050 1060
cryla-105.pe		1080	1090 1100 1110 1120 1130
	TCNDTYVNOQEYGGAYTGRNRGYNEA - PSPADYASVVEEYSYTDGSENPCEFRNGRYR		

1946622
TNNYVAGGEEHETISRNRGYDEAYESNSVHASVYEEKSVTDRENCESNRGVD
1070 1080 1090 1100 1110 1120

cry1a-105.pe
KTPSGYVKEVEYETETDKVWEISFETEGFIVDSVELLMEE
1140 1150 1160 1170
YTPLPAGYVKEVEYETETDKVWEISFETEGFIVDSVELLMEE
1130 1140 1150 1160 1170

cry1a-105.pep
SW:8469151
8469151 description="PESTICIDIAL CRYSTAL PROTEIN (CRY1A) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (33 kDa CRYSTAL
DELTA-ENDOTOXIN CRY1A) (CRYSTALINE ENTOMOCIDAL PROTOXIN) (33 kDa CRYSTAL
PROTEIN)." library="NA species="Bacillus thuringiensis" strain="var. keaya"
source="swissprot_prot" version="NA type="PRT

SCORES Initl: 3521 Initn: 4817 Opt: 5543 Z-score: 6292.4 (1.171)
>>SW:8469151
Initn: 4817 Initl: 3521 Opt: 5543 Z-score: 6292.4 expect: 0
Smith-Waterman score: 5589; 72.7% identity in 1185 aa overlap
(1-1177:1-1171)

cry1a-105.pe
MDNNPINECIPYNCNLSNVEVILGGERIETGYTIDISLSLTQFLISFVPGAGVGL
10 20 30 40 50
MEIVNQNCVYVNCNPNENELDIERSNSVAT-NIALSESLASA-TPIGGILGL
10 20 30 40 50

cry1a-105.pe
VDIWIIFGSPQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNYQIYASFREWAD
70 80 90 100 110 120
FDAIWISGSPQWDAFLVQIEQLINQRIEFAFNQAIISRLGSLNYQIYASFREWAD
60 70 80 90 100 110

cry1a-105.pe
PTPALREMRIOFNDMSALTTPALFAVQVYVPLLSVVOQANHLVSLRDSVFGQ
130 140 150 160 170 180
PTPALREMRIOFNDMSALTTPALFAVQVYVPLLSVVOQANHLVSLRDSVFGQ
120 130 140 150 160 170

cry1a-105.pe
RWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERWVGPDSS--RDMIRYNQFRRLT
190 200 210 220 230
AWGFDAATINSRYNDLTRIGNYTDHVRWYNTGLERWVGPDSS--RDMIRYNQFRRLT
180 190 200 210 220 230

cry1a-105.pe
LTULDIVSLFVNDSTPIPTVQSOLTRIIYNPVLNFDGFRGSGNOGIES-IRSPHL
240 250 260 270 280 290
ISVLDIISFRNDRSLPIPTVQSOLTRIIYNPVLNFDGFRGSGNOGIES-IRSPHL
230 240 250 260 270 280

cry1a-105.pe
MDIILSTIYTDHVRWYNTGLERWVGPDSS--RDMIRYNQFRRLT
300 310 320 330 340 350
MDIILSTIYTDHVRWYNTGLERWVGPDSS--RDMIRYNQFRRLT
290 300 310 320 330 340

cry1a-105.pe
GV---YRTLSSTLYRPFNIGNQQLSVLDGTETAYGTSNLPASVYKSGTSVDSLDEI
360 370 380 390 400 410
GV---YRTLSSTLYRPFNIGNQQLSVLDGTETAYGTSNLPASVYKSGTSVDSLDEI
350 360 370 380 390 400

cry1a-105.pe
PPQNNVPPQGFHRLSHVSMFRSGFSSVSLIRAPMSFWHRAEFNNIIASDSITQ
420 430 440 450 460 470
PIDGEN--SLVGYSRSHVTLRSLRYNTSL---PTVWTHSATNTINPDIIITQ
420 430 440 450 460 470

cry1a-105.pe
IPLVKAHTLOSQTIVVRGPGFTGDDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTT
480 490 500 510 520 530
IPLVKAHTLOSQTIVVRGPGFTGDDILRRTSGGPFAYTIIVNINGQLPQRYRARIYASTT
470 480 490 500 510 520

cry1a-105.pe
NLRIYVTVAGERIFAGOFNKMTDGLPTLQSFYSATINTAFTFPMSSQSTFTVGDFTSS
540 550 560 570 580 590
DARITVAIGQIRVDMTLEKMTIGESLTSRTFTSNFPPFRANPDIIIRIABELPIR
530 540 550 560 570 580

cry1a-105.pe
GNEVVDREELIPVTATLEAYNLRAKAVNALFTSTNGLKTNVTDYHIDQVSNLAVT
600 610 620 630 640 650
GGELYIDKIELILADAFEEYDOLERAQAVNALFTSTNGLKTNVTDYHIDQVSNLAVT
590 600 610 620 630 640

cry1a-105.pe
YLSDEFCLDEKELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGGDD
660 670 680 690 700 710
CLSDERCLDEKELSEKVKHAKRLSDERNLLQDSNFKDINRQPERGWSGTGITIQGGDD
650 660 670 680 690 700

cry1a-105.pe
VFKNYVTVSGFTFDECTPTLYQKIDESKKAFTYQIRGVIEDSQLEIYIRYNAXHE
720 730 740 750 760 770
VFKNYVTVSGFTFDECTPTLYQKIDESKKAFTYQIRGVIEDSQLEIYIRYNAXHE
710 720 730 740 750 760

cry1a-105.pe
TVNVPSTGSIWPLSASPSIGSGEINRCAPHEWNPDLDCSCRDGKCAHSHHFSLDID
780 790 800 810 820 830
TVNVPSTGSIWPLSASPSIGSGEINRCAPHEWNPDLDCSCRDGKCAHSHHFSLDID
770 780 790 800 810 820

cry1a-105.pe
VGCTDLNEDLGVMVTKINQDGHADENLSTLEEKTVGSLARVAKRAFKKWRDKREKL
840 850 860 870 880 890
VGCTDLNEDLGVMVTKINQDGHADENLSTLEEKTVGSLARVAKRAFKKWRDKREKL
830 840 850 860 870 880

cry1a-105.pe
EWETNIVYKEAKESVDALFVNSQYDRLQADTNIAKTHANRVRHSITIEAYLPESLVNGV
900 910 920 930 940 950
EWETNIVYKEAKESVDALFVNSQYDRLQADTNIAKTHANRVRHSITIEAYLPESLVNGV
890 900 910 920 930 940

cry1a-105.pe
NAAIFEELEGRIFTAFSLYDARNVKNGLSCWNVKGVHVDVSEQNQRSLVIAEM
960 970 980 990 1000
NAAIFEELEGRIFTAFSLYDARNVKNGLSCWNVKGVHVDVSEQNQRSLVIAEM
950 960 970 980 990 1000

cry1a-105.pe
EAEVSQVRVCFGRGYILLRVATYKEGYGCVCTIHEIENNTDELKFSNCVVEEIPYNNVT
1020 1030 1040 1050 1060 1070
EAEVSQVRVCFGRGYILLRVATYKEGYGCVCTIHEIENNTDELKFSNCVVEEIPYNNVT
1010 1020 1030 1040 1050 1060